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(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MOD-ULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer, and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

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Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides, hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nomicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

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Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include onthe-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the beyond the bounds where surgery and curative intent can be undertaken. Hoever, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

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and account for more than 75% of all lung cancers. Non-small cell tumors that are localized at the time of presentation can sometimes be cured with surgery and/or radiotherapy, but usually are not identified until significant metastasis has occurred, which are typically not very responsive to surgical, chemotherapy, or radiation treatment.

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of veffective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

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SUMMARY OF THE INVENTION

The present invention provides nucleotide sequences of genes that are up- and downregulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as
targets for screening for therapeutic compounds that modulate lung cancer, such as
antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins
can be used for a number of purposes. Examples include early detection of lung cancers,
monitoring and early detection of relapse following treatment of lung cancers, monitoring
response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy
of lung cancers, selecting patients for postoperative chemotherapy or radiation therapy,
selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early
detection of precancerous lesions of the lung. Examples of benign or precancerous lesions
include: atelectasis, emphysema, brochitis, chronic obstructive pulmonary disease, fibrosis,
hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and

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bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancerassociated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the nolynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the natient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evalated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

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In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

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In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

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In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseases lung samples divided by the 90th percentile of lung tumor samples divided by the 90th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

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Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

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"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

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same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

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For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

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Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology.

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Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when; the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

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two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

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In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

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conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any 5 length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds. although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or Omethylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A 10 Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5.235.033 and 5.034.506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing 15 one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring 20 nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

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The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

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strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

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using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

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The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

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A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

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The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

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occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

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"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein in vitro, in cells. or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

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preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably
1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

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"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

WO 02/086443 PCT/US02/12476 for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies. A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g., (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

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In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to downregulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant diseasemay be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

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nucleic acid sequences can be administered for gene therapy purposes, including the

administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA

vaccines.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

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In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in nonmalignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) Nucleic Acids Research 26:1-7 and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) Genome Res. 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are downregulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

Informatics

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The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets,

Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, ÇA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

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pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, genedisease causal linkages, identification of correlates of immunity and physiological status,

among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed

computers is utilized.

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An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5.706.498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multidimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis; Probabilistic Models of Proteins and Nucleic Acids (; Baxevanis and Oeullette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine: Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

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Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the

Internet; Han and Kamber (2000) <u>Data Mining: Concepts and Techniques</u> (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

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In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

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be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

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The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

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MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain
molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a
data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM,
SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can
be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal
adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O
device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of lung cancer-associated proteins

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Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

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domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich
targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a

targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000)

(1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-

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In another embodiment, the lung cancer sequences are transmembrane proteins.

Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

WO 02/086443 PCT/US02/12476 localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.ip/).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

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Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, sax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

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As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genee" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications.

Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

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In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

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particular target. The probes can be overlapping (i.e., have some sequence in common), or

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

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As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for ndivitual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

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Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

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In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

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In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

WO 02/086443 PCT/US02/12476 sequences used for the expression of an operably linked coding sequence in a particular host

organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to

utilize promoters, polyadenylation signals, and enhancers.

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Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, supra).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

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The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microiniection of the DNA into nuclei.

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In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin. chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation. and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha,

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Kluvveromyces fragilis and K. lactis, Pichia guillerimondii, and P. pastoris,

Schizosaccharomyces pombe, and Yarrowia lipolytica.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of lung cancer proteins

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In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

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classes: substitutional, insertional or deletional variants. These variants ordinarily are
prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer
protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding
the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.
However, variant lung cancer protein fragments having up to about 100-150 residues may be
prepared by in vitro synthesis. Amino acid sequence variants are characterized by the
predetermined nature of the variation, a feature that sets them apart from naturally occurring
allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants
typically exhibit a similar qualitative biological activity as the naturally occurring analogue,
although variants can also be selected which have modified characteristics as will be more
fully outlined below.

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While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

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variant may be designed or reorganized such that a biological activity of the lung cancer

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

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Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) <u>Proteins: Structure and Molecular Properties</u>, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) .

CRC Crit. Rev. Biochem., pp. 259-306.

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Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987)

Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth.

Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

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thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes
Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein

Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to lung cancer proteins

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In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

WO 02/086443 PCT/US02/12476 being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g.,
Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic
trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are canable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if nonhuman mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fy, Fab, Fab'. F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fy framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4.816.567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 5 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This 10 approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5.633,425; 5.661,016, and in the following scientific publications: Marks. et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 15 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

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In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

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In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

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In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

WO 02/086443 PCT/IIS02/12476 normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially

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preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

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In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in in situ imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

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In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, in situ hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

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In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

WO 02/086443 PCT/US02/12476 cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in

expression to be induced by the test compound.

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The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By "neutralize" is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

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In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

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al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

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Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

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U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid

U.S. Patent No. 5,385,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

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In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

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As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

WO 02/086443 PCT/US02/12476 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,

5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

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A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

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screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

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Assays to identify compounds with modulating activity can be performed in vitro. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

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In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

WO 02/086443 PCT/US02/12476 sequence when the protein is bound to the support), direct binding to "sticky" or jonic

supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc.

Following binding of the protein or agent, excess unbound material is removed by washing.

The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

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In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

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A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells a Manual of Basic Technique</u> (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (3H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in WO 02/086443

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non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) <u>J. Natl. Cancer Insti.</u>, 37:167-175; Eagle, et al. (1970) <u>J. Exp. Med.</u> 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

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Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer</u>, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in <u>Sem Cancer Biol.</u>).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

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Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the distal. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

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Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Paractical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Natl. Cancer Inst.</u> 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or intersugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.

Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

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is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002). Sciencexpress (21March2002); Sharp (1999). Genes Dev. 13:139-141; and Cathew (2001). Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001). Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

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Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25; 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

WO 02/086443 PCT/US02/12476 formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is

understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

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Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety.

Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-two gene.

The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art. Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

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The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or suray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid. methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, WO 02/086443

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lactose, corn and other starches; binding agents; sweeteners and other flavoring agents;
coloring agents: and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacological Basis of Therapeutics).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacologial Basis of Therapeutics. supra.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

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It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo, or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

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Berger and Kimmel, <u>Guide to Molecular Cloning Techniques, Methods in Enzymology</u>

volume 152 (Berger), Ausubel, et al. (eds. 1999) <u>Current Protocols</u> (supplemented through

1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

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In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341). pentide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam (1996) J. Immunol, Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al. (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol, 148:1585; Rock (1996) Immunol, Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

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delivery technologies, also known as receptor mediated targeting, such as those of Avant

Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

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Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NI); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) <u>Science</u> 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

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Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein.

Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of lung cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

WO 02/086443 PCT/US02/12476 EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) <u>Nature</u> 403:672-676; Zhao, et al. (2000) <u>Genes Dev.</u> 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,778 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001500US)

5	Table 1A					
•	Pkey	ExAccn	UnigenelD	Unigene Title	70% chron/90% NL	70% SQAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001	Hs.83213	Immunoglobulin Heavy Chain, Vdjrc Reg	2.68 1.96	3.28 0.14
10	100971 101088	J02874 L05568	Hs.553	fatty acid binding protein 4; adipocyte solute carrier family 6 (neurotransmitte	0.79	0.07
10	101102	L07594	Hs.79059	transforming growth factor; beta recepto	2.55	1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
15	101330	L43821 L49169	Hs.80261 Hs.75678	enhancer of filamentation 1 (cas-fike do FBJ murine osteosarcoma viral oncogene h	0.59 1.15	0.29 0.41
13	101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a t	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
20	101771 101842	M81750 M93221	Hs.153837 Hs.75182	myeloid cell nuclear differentiation ant mannose receptor; C type 1	0.96 1.27	0.45 0.37
20	101842	W33221 U31384	Hs.83381	guanino nucleotide binding protein 11	1.04	0.37
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
2.5	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95 1.62	0.23 0.21
2,5	103025	X54131 X79981	Hs.123641 Hs.76206	protein tyrosine phosphatase; receptor t cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B tymphocytes; i	1.86	1
30	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47 0.16
30	104212 104691	AB002298 AA011176	Hs.173035 Hs.37744	KIAA0300 protein ESTs	1.17	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
35	104865	AA045136	Hs.22575	ESTs	1.23	0.49
33	104989 105729	AA102098 AA292694	Hs.118615 Hs.3807	ESTs ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.63 0.86	0.32 0.34
	105729	AA398606	Hs.32241	ESTs Weakly similar ID PROSPROCEMINATOR PR	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
40	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
40	106536 106605	AA453997 AA457718	Hs.23804 Hs.21103	ESTs Homo saniens mRNA: cDNA DKFZp564B076 (fr	0.82 0.99	0.15 0.07
	106667	AA461086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.48	0.43
40	106797	AA478962	Hs.169943	ESTs	1.18	0.32
45	106844 106870	AA485055 AA487576	Hs.158213 Hs.26530	sperm associated antigen 6 serum deprivation response (phosphatidy)	0.98 1.05	0.51 0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292	T30407	Hs.4789	ESTs; Wealdy similar to oxidative-stress	1.07	2.58 0.21
30	107994 107997	AA036811 AA037388	Hs.165030 Hs.82223	ESTs Human DNA sequence from clone 141H5 on c	0.7 1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
55	108382	AA074885	Hs.67726	macrophage receptor with collegenous str	1.52	0.72
22	108435 108480	AA078787 AA081093	Hs.194101 Hs.68055	ESTs .	2.53 1.56	1.53 0.48
	109252	AA194830	Hs.85944	ESTs .	2.69	3.18
	109550	F01534	Hs.26981	ESTs	1.19	0.65
~ 0	109613	F03031	Hs.27519	ESTs	1.01	0.29
60	109837	H00656 H04768	Hs.29792 Hs.30484	ESTs ESTs	0.81 1.44	0.15 0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1	0.22
65	111247	N69825 N80935	Hs. 16762 Hs. 22483	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26 1.57	0.26 0.52
	111341 111510	R07856	Hs.16355	ESTs ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
	113195	T57112		""yc20g11.s1 Stratagene lung (#937210) .	1.22	0.35
70	113238	T62979	Hs.189813	ESTs	2.27 1.06	0.45 0.22
	113540 113552	T90496 T90889	Hs.16757 Hs.16026	ESTs ESTs	1.16	0.42
	113606	T93093	Hs.17125	ESTs	1.48	0.7
	113695	T96965	Hs.17948	ESTs	1.54	0.28
75	113946	W84753	Hs.37896	ESTs	1.79	0.72
	114251	Z39898 Z41690	Hs.21948	ESTs ESTs; Moderately similar to H1 chloride	1.95 1.42	0.25 0.13
	114359 115230	Z41589 AA278300	Hs.153483 Hs.182980	ESTS; Moderately similar to hit chonce	2.62	0.42
	115279	AA279760	Hs.63671	ESTs	1.79	0.91
80	115566	AA398083	Hs.43977	ESTs	0.86 0.79	0.2 0.04
	115965 116166	AA446681 AA461556	Hs.173233 Hs.202949	ESTs KIAA1102 prolein	2.29	0.68
	116279	AA486073	Hs.57362	ESTs	2.27	0.78
	117023	H88157	Hs.41105	ESTs	1.36	0.16

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	117209	H99959	Hs.42768	ESTs	1.46	0.48	
	118901 118981	N90719 N93839	Hs.94445 Hs.39288	ESTs ESTs	1.51 1.34	0.48	
	119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.27	
5	119221	R98105		""yr30g11.s1 Soares fetal liver spleen	1.32	0.53	
	119824	W74536	Hs.184	advanced glycosylation end product-speci	1.83	0.19 0.45	
	119861	W80715 W92775	Hs.59368	ESTs; Moderately similar to IIII ALU SUB ESTs	1.23	0.55	
	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37	
10	120467	AA251579	Hs.187628	ESTs	1.87 1.3	1.91 0.31	
	121314 121643	AA402799 AA417078	Hs.182538 Hs.193767	ESTs ESTs	231	0.68	
	121690	AA418074	Hs.110286	ESTs	1.47	0.51	
	122633	AA454080	Hs.34853	inhibitor of DNA blnding 4; dominant neg	1.31	0.63	
15	123978	C20653	Hs.170278 Hs.151323	ESTs ESTs	1.52 0.93	0.32 0.35	
	124214 124357	H58508 N22401	ns.151323	""yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1	
	124438	N40168	Hs.102550	ESTs	1.36	0.7	
20	125167	W45560	Hs.102541	ESTs EST	1.46 3.07	0.69 3.76	
20	125174 125422	W51835 AA903229	Hs.231082 Hs.153717	ESTs	1.34	0.3	
	125561	AJ417667	Hs.22978	ESTs	1.89	0.63	
	125831	D60988		""HUM145B09B Clontech human fetal brain	0.94	0.36	
25	127002	R35380 AA369367	Hs.24979	ESTs ESTs; Weakly similar to pIL2 hypothetica	3.02 1.01	4.06 0.69	
23	127307 127609	AA622559	Hs.126712 Hs.150318	ESTs	1.21	0.32	
	127959	Al302471	Hs.124292	ESTs	2.5	1	
	128458	D52193	Hs.56340	ESTs	1.13 1.45	0.33 0.58	
30	128624 128789	AA479209 AA486567	Hs.102647 Hs.105695	ESTs ESTs	1.1	0.34	
30	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55	
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4 0.73	
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77 1.11	0.73	
35	129210 129240	AA401654 W24360	Hs.202949 Hs.237868	KIAA1102 protein Interleukin 7 receptor	0.91	0.41	
33	129402	T63781	10.201000	""vc21c01.s1 Strategene tung (#937210)	1.36	0.43	
	129565	XTTTT	Hs.198726	vasoactive intestinal peptide receptor 1	0.67 1.3	0.08 0.42	
	129593 129626	AA487015 AA447410	Hs.98314 Hs.11712	Homo saplens mRNA; cDNA DKFZp586L0120 (f ESTs; Weakly similar to IIII ALU SUBFAMI	1.28	0.42	
40	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	1.58	1	
	129898	N48595	Hs.13256	ESTs	1.13	0.53	
	129958 130273	L20591 U59914	Hs.1378 Hs.153863	annexin A3 MAD (mothers against decapentaplegic; Dr	0.81 0.59	0.31 0.22	
	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	1.44	0.76	
45	130657	T94452	Hs.201591	ESTs	0.96	0.42	
	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51 0.97	0.45 0.37	
	131066 131263	F09006 R38334	Hs.22588 Hs.24950	ESTs regulator of G-protein signalling 5	2.34	2.82	
	131589	U52100	Hs.29191	epithelial membrane protein 2	1,2	0.62	
50	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95 1.47	0,38 0.52	
	131751 132430	H18335 T23630	Hs.31562 Hs.258675	ESTs EST	1.86	2.09	
	132436	N67192	Hs.49476	Homo saplens done TUA8 Cri-du-chat regl	1.73	0.58	
	132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.91 0.82	0.29 0.2	
55	133120	X64559 D45370	Hs.65424 Hs.74120	tetranectin (plasminogen-binding prolein adipose specific 2	1.29	0.48	
	133488 133565	H57056	Hs.204831	ESTs	2.25	0.57	
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62	
	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16 0.79	0.34	
60	133978 133985	W73859 L34657	Hs.78061 Hs.78146	transcription factor 21 platelet/endothelial cell adhesion molec	0.79	0.28	
	134299	AA487558	Hs.8135	ESTs	1.02	0.46	
	134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86 1.19	0.42 0.27	
65	134323	AA028976 D50683	Hs.8175 Hs.82028	Homo saplens mRNA; cDNA DKFZp564M0763 (f transforming growth factor; beta recepto	1.19	0.67	
03	134343	D67969	Hs.82921	solute carrier family 35 (CMP-stallc aci	1.28	1	
	134561	U76421	Hs.85302	adenosine dearninase; RNA-specific; B1 (h	2.12	0.55	
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35 1.35	2.74 0.33	
70	134696 134749	H88354 L10955	Hs.8861 Hs.89485	ESTs carbonic anhydrase IV	0.89	0.33	
70	134788	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21	
	134869	T35288	Hs.90421	ESTs; Moderately similar to IIII ALU SUB	2.14	2.64	
	135346	M21056	Hs.992	phospholipase A2; group (B (pancreas)	0.63	0.13 2.15	
75	100113 100147	D00591 D13666	Hs.84746 Hs.136348	Chromosome condensation 1 Homo sapiens mRNA for osteoblast specifi	0.5	2	
	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39	
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58	
	100360	D78335 D79997	Hs.75939 Hs.184339	Uridine monophosphate kinase KIAA0175 gene product	0.91 0.75	2.04 2.03	
80	100372 100486	D79997 HG1112-HT11		TIGR: ras-like protein TC4	1.09	1.93	
-	100559	HG2197-HT22	67	'collagen, tyge VII, alpha 1"	0.97	3.6	
	100576	HG2290-HT23	86	"ealdtonin/alpha-CGRP, alt. transcript	1 0.85	1 1.9	
	100668 100906	HG2981-HT39 HG4716-HT51		*TIGR: CD44 (epican, all. transcript 12 Guanosine 5-Monophosphate Synthase	1.18	2.29	
85	100906	HG721-HT482	7	"TIGR: placental protein 14, endometrial	1	1.45	

	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070 L08424	Hs.151738 Hs.1619	*Matrix metalloproteinase 9 (gelafinase	0.77	1.52
	101124	L10343	Hs.112341	Achaete-scute complex (Drosophila) homol "Protease Inhibitor 3, skin-derived (SKA	0.62	2.67
5	101175	L18920	Hs.36980	*Melanoma antigen, family A, 2*	1	1
	101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 1B (cornifin)	0.85	2.51 8.83
	101448 101511	M21389 M27826	Hs.195850 Hs.267319	keratin 5 (epidermolysis bullosa simplex Endogenous retroviral protease	1.03	1.13
10	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
	101548	M31328	Hs.71642	*Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		"Human parathyroid hormone-related pepti	!	1_
	101649 101724	M60047 M69225	Hs.1690 Hs.620	Heparin-binding growth factor binding pr bullous pemphigold antigen 1 (230/240kD)	1	2.7 8.98
15	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	i	2.78
	101759	M80244	Hs.184601	"Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK prolein kinase	1	1
	101808 101809	M86757 M86849	Hs.112408	S100 calcium-binding protein A7 (psorias "Homo sapiens connexin 26 (GJB2) mRNA, c	0.74	1.76 7
20	101845	M93426	Hs.78867	"Protein tyrosine phosphatase, receptor-	i	í
	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	"Interleukin enhancer binding factor 2,	1.03	1.61
	102154 102193	U17760 U20758	Hs.75517 Hs.313	"Laminin, beta 3 (nicein (125kD), kalini secreted phosphoprotein 1 (osteopontin;	0.94 0.34	3.62 4.59
25	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610 102623	U65011 U66083	Hs.30743 Hs.37110	Preferentially expressed antigen in mela "Malanoma antigen, family A, 9 (MAGE-9)"	1	3.88
30	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	i
	102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
	102888 102913	X04741 X07696	Hs.76118 Hs.80342	Ubiquifin carboxyl-terminal esterase L1 keratin 15	1.13 0.7	2.59 4.72
35	102915	X07820	Hs.2258	Matrix Metalloprotelnase 10 (Stromolysin	1.15	3.35
	102963	X15943	Hs.37058	"Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	"Integrin, beta 4"	1.38	2.34
	103036 103058	X54925 X57348	Hs.83169 Hs.184510	Matrix metalloprotease 1 (Interstifial c Stratifin	1.25	14.93 4.17
40	103060	X57766	Hs.155324	matrix metalloprotelnase 11 (stromelysin	1	1.72
	103119	X63629	Hs.2877	"Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206 103242	X72755 X76342	Hs.77367 Hs.389	monokine Induced by gamma Interferon	0.71	1.48
	103242	X82693	Hs.369 Hs.3185	*Alcohol dehydrogenase 7 (class IV), mu *Lymphocyte antigen 6 complex, locus D;	0.92	1.28
45	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587 103594	Z29083 . Z31560	Hs.82128 Hs.816	5T4 Oncofetal antigen *SRY (sex determining region Y)-box 2, p	0.71	3.93 7.23
50	103768	AA089997	110.010	*ESTs, Highly similar to integral membra	0.99	1.8
	104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558 104689	R55678 AA010665	Hs.88959	Human DNA sequence from clone 967N21 on ESTs	1.23 0.96	7.23 2.11
	104733	AA019498	Hs.23071	ESTs	1.18	1.88
55	104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
	104978	AA088458	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAMI	1.64	2.89
	105012 105175	AA116036 AA186804	Hs.9329 Hs.25740	"Homo saptens mRNA for fis353, complete ESTs; Weakly similar to unknown (S.cerev	1.19 0.9	3.91 4.63
	105263	AA227926	Hs.6682	ESTs	0.95	2.87
60	105298	AA233459	Hs.26369	ESTS	1	1.13
	105312	AA233854 AA291644	Hs.23348 Hs.36793	S-phase kinase-associated protein 2 (p45	1.32 1.28	3.01 2.31
	105719 105743	AA293300	Hs.9598	Hypothetical prolein FLJ23188 ESTs	1.20	1
	106012	AA411621	Hs.8895	ESTs; same as BFH6?	0.94	2.04
65	106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
	106540 106575	AA454607 AA456039	Hs.38114 Hs.105421	Hypothetical protein FLJ11100 ESTs	1.26	2.26
	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1,32
	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
70	106906	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
	107059 107104	AA608545 AA609786	Hs.23044 Hs.15243	RAD51 (S. cerevisiae) homolog (E coli Re Nucleolar protein 1 (120kD)	0.48 1.01	2.67 1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97 ·	2.89
	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
75	107901	AA026418	Hs.91539	ESTs	0.72	3.44
	107922	AA028028 AA029317	Hs.61460 Hs.18878	lg superfamily receptor LNIR precursor	1	2.48
	108695	AA121315	Hs.70823	Hypothetical protein FLJ21520 KIAA1077 protein	0.91	3.53
	108857	AA133250	Hs.62180	ESTs	1	1
80	108860	AA133334	Hs.129911	ESTs	0.73	7.3
	108990 109166	AA152296 AA179845	Hs.72045 Hs.73625	ESTs *RAB6 interacting, kinesin-like (rabkine	- 1	1 4.55
	109100	AA227919	Hs.73625 Hs.85962	Hyaluronan synthase 3	i	1.28
0.0	109665	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
85	109970	H09281	Hs.13234	ESTs	1.13	2.16

	W	O 02/086				
	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84 0.94	1.95 1.41
	110156	H18957	Hs.4213 Hs.5199	ESTs HSPC150 protein similar to ubiquitin-con	0.91	3.18
	110561 111223	H59617 N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
5	111345	N89820	Hs.14559	Hypothetical protein FLJ 10540	1	1.25
	111876	R38239	Hs.293246	*ESTs. Weakly similar to putative p150 f	0.83	1.27
	111902	R39191	Hs.109445 Hs.70823	KIAA1020 protein KIAA1077 protein	0.91 0.77	0.91 3.01
	112244 112973	R51309 T17271	HS./U023	*cDNA FLJ13308 fis, clone OVARC1001436,	1	1
10	112989	T23482	Hs.89981	*Diacylglycerol kinase, zeta (104kD)*	0.55	1.03
	113047	T25867	Hs.7549	ESTs	0.87	2
	113095	T40920 T90345	Hs.126733 Hs.16740	ESTs Hypothetical protein FLJ11036	0.42	1.44
	113531 113970	W86748	Hs.8109	FSTs	1.17	1.73
15	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-l	0.86	0.82
	114407	AA010188	Hs.103305	ESTs	0.8 1.06	1.88 1.34
	114471 114509	AA028074 AA043551	Hs.104613 Hs.101799	RP42 homolog KIAA1350 protein	1.82	2.32
	115060	AA253214	Hs.198249	"Gap junction protein, beta 5 (connexin	0.79	1.49
20	115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density !	0.59	1.97 1.25
	115291	AA279943 AA292537	Hs.122579 Hs.45207	ESTs Hypothetical protein KIAA1335	1.15	1.48
	115506 115522	AA232337 AA331393	Hs.47378	ESTs	0.5	3.29
25	115536	AA347193	Hs.62180	ESTs	1	1
	115697	AA411502	Hs.63325	Homo saplens type II membrane serine pro	1	6.53 6.98
	115909	AA436666	Hs.59761	ESTs Differentially expressed in Fanconi anem	1	2.31
	115978 116028	AA447522 AA452112	Hs.69517 Hs.42644	thioredoxin-like	0.99	1.68
30	116107	AA456968	Hs.92030	ESTs	1.14	1.8
	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99 0.44	1.9 0.86
	116158 116335	AA461187 AA495830	Hs.61762 Hs.87013	Hypoxia-Inducible protain 2 "Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
35	116483	C14092	Hs.76118	Ublguitin carboxyl-terminal esterase L1	1.04	2.36
50	117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11 0.98	2.63 1.79
	117693 117881	N40939 N50073	Hs.112110 Hs.260622	PTD007 protein Butyrate-induced transcript 1	1	1.43
40	118368	N64339	Hs.48956	ESTs	0.67	2.86
	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967 W79920	Hs.191381 Hs.58561	ESTs; Weakly similar to hypothetical pro G protein-coupled receptor 87	i	i
45	119845 120102	W95428	Hs.132927	*ESTs, Moderately similar to p53 regulat	i	i
	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
	120859 120880	AA350158 AA360240	Hs.1619 Hs.97019	Achaete-soute complex (Drosophila) homol EST	i	i
50	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
-	120983	AA398209	Hs.97587	EST	1	1
	121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1.8
	121369 121791	AA405657 AA423978	Hs.128791 Hs.293317	CGI-09 protein "ESTs, Wealdy similar to JM27 [H.sapiens	i	1.0
55	123005	AA479726	Hs.105577	ESTS	i	i
	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98 1.64
	123479	AA599469 AA608956	Hs.135056 Hs.112619	clone RP5-850E9 on chromosome 20	1.19 1.03	1.14
60	123571 123829	AA620597	Hs.112208	*ESTs, Weakly similar to PQ0109 Purkinje XAGE-1 protein	1.39	2.2
00	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49 0.76	- 8.62 0.77
	124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
65	125218 125453	W73561 R05041	Hs.110024 Hs.18048	*Melanoma antigen, family A, 10*	0.8	1.42
05	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmb	1.52	2.26
	125972	AA434562	Hs.35406	"ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95 1.35
70	126395 126645	N70192 Al167942	Hs.278956 Hs.61635	Hypothetical protein FLJ12929 STEAP1 (Homo sapiens BAC clone RG041D11	i	2.23
70	127221	Al354332	Hs.72365	ESTs	0.73	3.27
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid melaph	0.51	1.94
	128192	AI204246		KIAA1085 protein	1.8 0.89	3.16 0.97
75	128610	L38608 U46006	Hs.10247 Hs.10526	activated leucocyte cell adhesion molecu Cysteine and glycine-rich protein 2	1	1
15	128777 128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	*Solute carrier family 2 (facilitated gl	0.84	2.04
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87	1.04
80	129404	AA172056	Hs.111128	ESTs *Genbank Homo saplens keratin 6 isoform	0.72	12.8
ov	129466 129605	L42583 S72493	Hs.115947	Keralin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
	130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22 1.96
85	130080	X14850	Hs.147097	"H2A histone family, member X" stenniocalcin 2	0.98	1.95
0.3	130385	AA126474	Hs.155223	SIBILITOGUES &		

WO 02/086443 130410 130441 130482 Hs.155421 Alpha-fetoprotein "Human DNA-PK mRNA, partial cds" Bacutoviral IAP repeat-containing 5 (sur Pitultary tumor-transforming 1 Insulin-like growth factor binding prote V01514 1135835 No 301387 1.15 3.65 1.32866 1.88 1.96 4.7 Ha 1578 130553 AA430032 Hs.252587 5 130577 M35410 Hs.162 Matrix metalloproteinase 12 (macrophage ESTs; Weakly similar to katanin p80 subu 130627 123808 Hs.1695 0.69 4.05 VV333388 Hs.19574 Hs.21400 1 13 241 130900 130939 AA59868 0.89 FSTs 131046 XD2530 Hs.2248 INTERFERON-GAMMA INDUCED PROTEIN PRECURS 0.8 1.15 10 131244 D38076 Hs.24763 Hs.156346 Hs.34780 RAN binding protein 1 Topoisomerase (DNA) II alpha (170kD) "Doublecortex; lissencephaly, X-linked (1.13 1.85 131877 Ingolodinesies (Invel) is griph (I Youn) Toolshooting Essengarbia, F. Alleska (Toolshooting Essengarbia), F. Alleska (KAMOTS gene product KAMOTS gene product KAMOTS gene product ESTE + klyb) smiller to prodein knowledge gustnien encomplication prodein knowledge gustnien encomplication prodein knowledge T. Low density (Inportation to Particulation T. Low density (Inportation to Particulation T. Low density (Inportation to Particulation T. Settle (Inportation T. Settle T. Settle (Inportation T. Settle T. S 131027 AA461549 0.62 W90146 Hs.35962 ESTs 0.74 3.27 131965 131978 Hs.36232 15 132354 L05187 AA417152 N59764 Hs.211913 0 60 1 42 132543 He 5101 0.79 4.27 Hs.5398 1.08 132632 1131201 Hs.54451 Hs.54481 132653 0.80 132659 Z75190 0.89 20 Hs.55279 4.41 132710 W93726 0.64 Hs.56105 1.55 132758 W52432 132767 Hs.231622 M74542 AA458761 U69611 U52960 132816 Hs.575 0.55 0.66 132000 He 18387 3.53 25 133070 Hs.64311 1.16 Hs.286145 Hs.70830 27 133282 0.00 133317 A4215299 1.42 Hs.72157 1 12 2 55 132270 AA156897 X57579 Hs.727 1.76 133391 30 133832 H03387 Hs.241305 1.02 1.39 134032 Z81326 Hs.78589 Hs.181634 Hs.80205 0.95 1.53 AA398908 134168 134218 134405 134453 134470 134645 AA227480 2.48 2.86 3.78 R67275 Hs.82772 Hs.83484 0.76 35 ¥70683 1.89 4.11 X54942 Un 83758 1 82 U87459 Hs.167379 0.83 134781 M17183 U19147 Hs.272484 40 100040 0.92 1 25 M97935 101201 122524 Hs.2256 2.92 8.5 101664 M60752 Hs.121017 0.8 1.61 1103911 102025 Hs.78934 TINARGR Hs.2156 102031 45 102221 U24576 Hs.75888 143 102270 U30255 1 08 1.32 102330 1137022 He 95577 0.88 1.07 1.58 U41668 Hs.77494 102391 1.49 X51956 50 103395 X94754 Hs.119503 0.89 1.32 105638 105726 AA281599 Hs.20418 Hs.9754 0.91 1.48 AA292328 114841 AA234722 AA262491 Hs.55408 Hs.186572 0.78 ESTs ESTs 55 115906 AA436616 Hs.82302 0.74 2.52 119132 R49046 Hs.107911 ATP-binding cassette; sub-family B (MDR/ 1.1 1.51 Hs.189838 Hs.184601 Hs.75478 ESTs solute carrier family 7 (callonic amino 124163 H30539 126487 A4482505 1.01 Source carrier tarriny / (casonic arieno KIAA0956 protein tyrostne 3-monocxygenase/tryptophan 5-mo survival of motor neuron protein interac AA307960 127141 60 128034 AA905754 Hs.75103 1.18 128609 AA234365 Hs.102456 15 survival of motor neuron protein interac ESTs a disintegrin and metalloprotease domain forthead box E1 p21/Cdc42/Rac1-activated kinase 1 (yeast secretogranin II (obromogranin C) 1.7 R37753 He 106985 130199 130524 Hs.172028 Z48579 U89995 Hs.159234 65 133000 He 62402 133658 M25756 Hs.75426 secretogram II (chromogram C) ESTA and ESTA Shocomal RNA Approxibitation of the Company of the C 135047 Hs.93597 100053 M27830 0.88 1.53 Hs.82962 0.68 100114 DODGOG 186 70 D11094 Hs.61153 Hs.81892 1.29 2.03 100128 100154 D14657 100161 D14694 Hs.77329 1.02 1.56 Hs.394 Hs.78183 Hs.57101 100168 0.46 1.17 D17703 100187 75 100188 0.97 D21063 100217 D26600 D28364 Hs.89545 1.9 100220 1.11 1.53 He 1600 2.09 100287 D43950 1.13 100297 D49489 Hs.182429 0.92 1.78 80 100330 D55716 Hs.77152 1.07 1.61 100355 100364 100368 D78129 0.96 1.87 D78586 D79987 Hs.154868 1.49 2.46 Hs.153479 1.32 D84557 85 100438 D87448 Hs.91417

	w	O 02/086	5443			
	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1 48
	100455	HG1153-HT1	153	Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1,41
	1004518	HG174-HT17		Desmoplakin I	1.28	3.17
	100528	HG1828-HT1	857	""Nexin, Glia-Derived""	0.68	1.9
5	100861	HG2874-HT3	1018	Ribosomal Protein L39 Homolog	1.1	5.44
	100667	HG2981-HT3	127	"Epican, Alt. Splice 11"	0.8	1.97
	100630	HG4074-HT4	344	Rad2	1.01	2.12
	101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131 101162	L10838 L14595	Hs.167460 Hs.174203	splicing factor; arginthe/serine-rich 3 solute carrier family 1 (glutamate/neutr	1.23 1.35	1.87 2.73
10	101181	L19686	Hs.73798	macrophage migration Inhibitory factor (1.03	1.78
	101183	L19779	Hs.795	H2A histone family; member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase Inhibitor 3 (CDK	0.7	2.2
	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (0.99	1.99
15	101233	L29008	Hs.878	sorbital dehydrogenase	0.82	2.11
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		"Homo sapiens (cell line HL-6) alpha t	0.69	2.78 1.84
	101342 101396	L76191 M15796	Hs.182018 Hs.78996	Interleukin-1 receptor-associated kinase proliferating cell nuclear antigen	1.04 0.95	3.55
20	101390	M18391	Hs.89839	EphA1	1.35	1.5
20	101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs. 12 163	eukaryotic translation initiation factor	1.19	1.93
	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
25	101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		"Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45 1.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	
30	101853 101977	M94362 S83364	Hs.76084	lamin B2 ""putative Rab5-interacting protein (cl	0.84 0.89	1.19 1.9
50	101977	U01038	Ha.77597	polo (Drosophia)-like kinase	0.66	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
	102039	U05861	Hs.201967	aldo-keto reductase family 1; member C1	0.93	2.32
35	102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
	102130	U15009 ·	Hs. 1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01 1.15	1.34 2.34
40	102220	U24389 U28386	Hs.65436 Hs.159557	lysyl oxidase-like 1 karvopherin alpha 2 (RAG cohort 1; Impor	1.14	2.69
40	102330	U35451	Hs.77254	chromobox homolog 1 (Orosophila HP1 beta	1.05	1.7
	102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discoldin domain receptor family; member	1.05	2.01
	102499	US1478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
45	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U62136		""Homo sapiens enterocyte differentiali	1.11	1.6
	102676	U72514	Hs.12045	putative protein	1.04	2.17 2.28
	102687 102704	U73379 U76638	Hs.93002 Hs.54089	ublquitin carrier protein E2-C BRCA1 associated RING domain 1	0.86 1.12	1.63
50	102704	U83843	NS.34009	"Human HIV-1 Net Interacting protein (0.9	1.39
50	102784	U85658	Hs.61796	transcription factor AP-2 garma (activat	0.98	216
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
	102972	X16662	Hs.87268	annexin A8	1.25	2.32
55	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44 3.79
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	2.58
	103075 103168	X59543 X68314	Hs.2934 Hs.2704	ribonucieotide reductase M1 polypeptide glutathione peroxidase 2 (gastrointestin	1.11 0.75	3.05
60	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasmi	1.01	1.97
00	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1	1
	103262	X78565	Hs.204133	hexabrachion (tenascin C; cytotactin)	1.23	3.09
65	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypopt	1.12	2.25
	103364	X90872	Hs.75854	SULT1C sulfotransferase	2.85	4.62
	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	!	2.48 1.53
	103391	X94453 X95586	Hs.114366 Hs.78596	pyrrotine-5-carboxylate synthetase (glut protessome (prosome; macropain) subunit;	0.92	1.53
70	103404	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
70	103448	X99133	Hs.204238	Epocalin 2 (oncogene 24p3)	0.55	0.96
	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
	103658	Z74615	Hs.172928	collagen: type I: alpha 1	1.06	2.98
75	103774	AA092898	Hs.92918	ESTs; Wealdy similar to R07G3.8 [C.elega	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase t subunit	0.87	2.17
	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 (H.sapi	1.4	2.49
	104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68 1.49
80	104434 104453	L02870 M19169	Hs.1640 Hs.123114	collagen; type VII; alpha 1 (epidermolys cystelin SN	1.04 0.38	0.76
50	104611	R98280	Hs.123114 Hs.125845	ribulose-5-phosphate-3-epimerase	1.08	2.25
	104758	AA024661	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
	105114	AA 156532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
	105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
85	105174	AA186613	Hs.34744	ESTs	0.95	2.05

	w	O 02/086	1443			
	105280	AA232215	Hs.14600	ESTs	1	1.4 2.02
	105344 105516	AA235303 AA257971	Hs.8645 Hs.21214	ESTs FSTs	0.72 1.35	3.56
	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
5	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98 0.92	1.28 1.32
	105705 105724	AA290767 AA292096	Hs.101282 Hs.22934	Homo saplens mRNA; cONA DKFZp434B102 (fr ESTs; Weakly similar to ZINC FINGER PROT	0.92	1,41
	105782	AA350215	Hs.21580	ESTs	1	1
• •	105799	AA372018	Hs.24743	ESTs	1.08	1.78
10	105807 105891	AA393803 AA400768	Hs.16869 Hs.26662	ESTs; Moderately similar to COLLAGEN ALP ESTs; Weakly similar to tumor necrosis f	0.95 0.87	1.34 2.25
	105891	AA404338	HS.20002	ESTs, Weakly Stillian to union necrosis i	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
15	106103	AA421104	Hs.12094	ESTs KIAA0286 protein	1.04 1.23	1.44 2.11
13	106140 106149	AA424524 AA424881	Hs.14912 Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74 0.97	2.23 1.99
20	106220 106228	AA428582 AA429290	Hs.32196 Hs.17719	ESTs; Moderately similar to metargidin p ESTs	0.99	1.54
20	106318	AA436570	Hs.9605	pre-mRNA cleavage factor lm (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs: Moderately similar to pl1.2 hypothe	0.98 0.95	2.66 1.93
	106432 106474	AA448850 AA450212	Hs.17138 Hs.42484	ESTs Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1.93
25	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1 1,49	1.82 2.78
	106611 106654	AA458904 AA460449	Hs.26267 Hs.3784	ESTs; Weakly similar to torsinA (H.saple ESTs; Highly similar to phosphoserine am	1.49	1.4
	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.sa	1.11	1.49
30	107115	AA610108	Hs.27693	FSTs: Highly similar to CGI-124 protein	1	1.03
	107129 107159	AA620553 AA621340	Hs.4756 Hs.10600	flap structure-specific endonuclease 1 ESTs; Weakly similar to ORF YKR081c [S.c	1.13 1.05	3.63 2.09
	107444	W28391	Hs.5181	nroliferation-associated 2G4: 38kD	1.18	1.9
25	107481	W58247	Hs.27437	Homo saplens kinesin superfamily motor K	0.99 0.94	2.74 1.77
35	107516 107529	X56597 Y12065	Hs.99853 Hs.5092	fibrillarin nucleolar protein (KKE/D repeat)	1.05	2.29
	107529	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957 108565	AA031948 AA085342	Hs.57548 Hs.1526	ESTs ATPass; Ca++ transporting; cardiac muscl	0.95 0.59	1.46 1.35
40	108780	AA128561	Hs.117938	collagen; type XVIII; alpha 1 DKFZP56400463 protein	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56 1.42
	109060	AA160879 AA169379	Hs.241551 Hs.72865	chloride channel; calcium activated; fam ESTs	0.67 1.03	2.31
45	109112 109344	AA109379 AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs: Wealdy similar to REGULATOR OF MIT	0.76	1.87
	110780 110958	N23174 N50550	Hs.22891 Hs.24587	solute carrier family 7 (cationic amino signal transduction protein (SH3 contain	0.9 1.17	0.95 2.26
	111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	1.21	1.85
50	111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305 112401	R54822 R61279	Hs.26244 Hs.237536	ESTs ESTs; Wealdy similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56	1.96
	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskertn	1.03	1.57
55	112992 113048	T23513 T25895	Hs.7147 Hs.184008	ESTs ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113048	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-blod	1.33 0.76	2.7 1.47
60	113573 113811	T91166 W44928	Hs.15990 Hs.4878	ESTs FSTs	0.79	1.51
00	114088	Z38266	Hs 12770	Homo sapiens PAC clone DJ0777023 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Wealty similar to GOLGI 4-TRANSMEM	1.02	1.76 2.36
	114846	AA234929 AA243873	Hs.44343 Hs.82184	ESTs ring finger protein 3	1.32	1.84
65	114964 115047	AA252627	Hs.22554	homeo box 85	\$.01	2.36
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167 115239	AA258421 AA278650	Hs.43728 Hs.73291	hypothetical protein ESTs; Weakly similar to similar to the b	1.52 0.7	2.52 2.67
	115239	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
70	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943 AA449122	Hs.43946 Hs.76086	ESTs; Wealdy similar to Weak similarity ESTs; Highly similar to small zinc lingo	1.2 0.96	1.98 1.31
	116004 116121	AA459254	Hs.48855	ESTs	0.97	1.55
	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
75	116190	AA464963	Hs.67776	ESTs ESTs	0.8 1.37	1.57 2.65
	116312 116732	AA490494 F13779	Hs.65403 Hs.165909	ESTs	0.92	1.8
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
90	117950	N51394	Hs.75478	KIAA0956 protein	1.04 0.62	2.36 1.29
80	117992 118785	N52000 N75386	Hs.172089 Hs.111867	Homo saplens mRNA; cDNA DKFZp58680222 (f GLI-Kruppel family member GLI2	1	1.29
	119717	W69134	Hs.57987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78 0.86	1.77 1.46
85	120128 120242	Z38499 Z98443	Hs.91448 Hs.86366	MKP-1 like protein tyrosine phosphatase ESTs	0.83	2.01
00	120242					-

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	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054 121326	AA398604 AA404246	Hs.97387 Hs.97031	ESTs ESTs: Weakly similar to Similar to phyto	1.05 0.98	1.93 1.3
	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
5	121457	AA411448	Hs.208985	ESTs	0.91 0.46	1.59 0.55
	121780 121781	AA422086 AA422150	Hs.124660 Hs.98370	ESTs cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
10	122059	AA431737	Hs.98749	EST .	1.93	2.33
10	122338 122354	AA443311 AA443772	Hs.98998 Hs.186692	ESTs ESTs	1 0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Wealdy similar to MRJ [H.saplens]	2.28	2.93
	122790	AA460156	Hs.99556	ESTs	0.88	1.3 1.93
15	123398 123518	AA521265 AA608531	Hs. 105514 Hs. 170313	ESTs ·	1	1.93
13	123673	AA609471	Hs.112712	ESTs	1	1.15
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74 0.67	1.12 1.1
	124367 124447	N24006 NAROOO	Hs.99348 Hs.140945	distal-less homeo box 5 Homo saplens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
20	125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	Al382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65 0.72	6.76 2.26
	125852 125924	H09290 AA526849	Hs.76550 Hs.82109	Homo saplens mRNA; cDNA DKFZp56481264 (f syndecan 1	1.22	2.25
	126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
25	126214	N29455	Hs.74316	desmoplakin (DPI; DPII)	1.93 1.21	3.55 1.66
	126414 126737	N78770 AA488132	Hs.223439 Hs.62741	ESTs ESTs	1	1.00
	126743	AA179253	Hs.172182	poly(A)-binding protein; cytoglasmic 1	1.3	2.16
20	126926	AA179546	Hs.832	ESTs: Highly similar to INTEGRIN BETA-8	2.53 1.57	2.8 2.12
30	127432 128218	AA501734 H02682	Hs.170311 Hs.99189	heterogeneous nuclear ribonucleoprotein ESTs; Moderately similar to recombinatio	1.24	2.09
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
	128568	X60673	Hs.247568	adenviate kinase 3	1.23 0.87	3.48 2.42
35	128584 128628	M11433 C14037	Hs.101850 Hs.251978	retinol-binding protein 1; cellular	1.22	1.9
55	128691	W27939	Hs. 103834	FSTs ·	1.1	1.73
	128714	V00599	Hs.179661	Homo saplens clone 24703 beta-tubulin mR	0.92 1.34	1.17 1.94
	128733 128781	AA328993 X85372	Hs.104558 Hs.105465	ESTs small nuclear ribonucleoprotein polypept	0.9	1.34
40	129052	AA496297	Hs.182740	ribasamal protein S11	2.59	3.19
	129095	L12350	Hs. 108623 Hs. 109706	thrombospondin 2 ESTs; Moderalely similar to HN1 (M.muscu	1.04 0.95	3.2 1.61
	129241 129665	AA435665 MB8458	Hs.109706 Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
	129703	AA401348	Hs.179999	ESTs	0.97	1.63
45	129720	AA476582 N20593	Hs.12152 Hs.56845	ESTs; Moderately similar to SIGNAL RECOG GDP dissociation inhibitor 2	1.09 0.74	1.79 1.68
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosylt	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; sipha 1	1.17	1.98 1.79
50	130405 130541	H88359 X05608	Hs.155396 Hs.211584	nuclear factor (erythrold-derived 2)-lik neurofilament; light polypeptide (68kD)	1.26	1.79
50	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	LEDP atvoosyltransferase 1	1 0.93	4.8 1.05
	131009 131028	AA063596 U20240	Hs.22142 Hs.2227	ESTs; Weakly similar to NADH-CYTOCHROME CCAAT/enhancer binding protein (C/EBP);	1	1.23
55	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091	T35341	Hs.22880 Hs.23528	ESTs; Highly similar to dipeptidyl pepti ESTs; Highly similar to HSPC038 protein	1.28 1.43	1.98 2.06
	131144 131148	C14412 C00038	Hs.23526	ESTs rignly samilar to non-coop protein	0.88	3.38
	131164	Y00503	Hs.182265	keratin 19	1.19 0.86	2.77 3.84
60	131185	M25753	Hs.23960 Hs.24395	cyclin B1 small Inducible cytokine subfamily B (Cy	0.66	2.96
	131219 131454	C00476 AA455896	Hs.2699	alvolcan 1	0.99	1.54
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18 1.95
65	131689 131692	AA599653 D50914	Hs.30696 Hs.30736	transcription factor-like 5 (basic helix KIAA0124 protein	1 1.55	2.39
03	131786	AA135554	Hs.32125	ESTs	1	1.33
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83 1.08	1.63 2.2
	131860 131884	U02082 H90124	Hs.334 Hs.3463	Oncogene TIM ribosomal protein S23	1.23	1.24
70	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
	131945	M87339 AA093998	Hs.35120 Hs.3566	replication factor C (activator 1) 4 (37	1 0.87	2.8 1.36
	131958 131964	W42508	Hs.3593	ESTs; Highly similar to phosphorylation ESTs	1	1.25
	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncoga	1.12	1.43
75	132040	AA146843	Hs.172894	BH3 interacting domain death agonist proteasome (prosome; macropain) 25S subu	0.89	1.55 1.27
	132065 132109	D82226 AA599801	Hs.211594 Hs.40098	ESTs	1	1.05
	132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
80	132123	AA447123 H89551	Hs.250705 Hs.41241	ESTs ESTs	1.06 1.08	2.46 2.46
80	132162 132180	AA405569	Hs.41241 Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
	132309	AA460917	Hs.2780	Jun D proto-oncogene	1.16	1.8
	132371	AA235448 AA253330	Hs.46677 Hs.5344	ESTs adaptor-related protein complex 1; gamma	0.8 0.5	1.26 1.49
85	132618 132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81
				•		

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	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3	
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43	
	132922	T23641	Hs.6066	KIAA1112 protein	1.16	1.53	
_	132959	AA028103	Hs.61472	ESTs: Wealdy similar to unknown [S.cerev	1.02	1.88	
5	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97	
	133005	C21400	Hs,103329	KIAA0970 protein	0.88	1.34	
	133065	X62535	Hs.172690	dlacylglycerol kinase; alpha (80kD)	0.93	1.23	
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76	
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43	
10	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8	
	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69	
	133313	AA249427	Hs.70704	ESTs	1.07	1.68	
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18	
15	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repail	0.91	1.45 1.68	
15	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94 0.85	1.14	
	133483	X52426	Hs.74070	keratin 13	1.1	1.14	
	133492	L40397	Hs.74137	transmembrane trafficking protein			
	133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	0.7	6.21	
20	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95 0.91	1.3 1.25	
20	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu		1.29	
	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.99	
	133627	U09587	Hs.75280	glycyl-IRNA synthetase	1.09 1.02	1.59	
	133671	T25747 U86782	Hs.75471 Hs.178761	zinc finger protein 146 26S proteasome-associated pad1 homolog	1.11	3.33	
2.5	133865	F09315	Hs.170290	discs: large (Droscobile) homolog 5	1.84	6.7	
23	133913	W84712	Hs.7753	calumenin	1.15	1.86	
	133913	L34587	Hs. 184693	transcription elongation factor B (SIII)	1.3	1.91	
	133982	U47621	Hs.207251	nudeolar autoantigen (55kD) similar to	1.3	1.99	
	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65	
30	134110	U41060	Hs.79136	LIV-1 protein: estrogen regulated	1.04	1.62	
50	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55	
	134161	U97188	Hs.79440	IGF-Ii mRNA-binding protein 3	0.82	1.95	
	134193	F09570	Hs.7980	FSTs	0.98	1.48	
	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8	
35	134402	U25165	Ha.82712	franile X mental retardation; autosomal	1.26	2	
	134457	D86963	Hs.174044	dishavelled 3 (homologous to Drosophila	1	1.47	
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57	
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2	2.64	
	134501	W84870	Hs.211568	oukaryotic translation initiation factor	0.84	1.36	
40	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93	
	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73	
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22	
	134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64	
	134693	N70361	Hs.8854	ESTs	1.09	1.82	
45	134806	Z49099	Hs.89718	spermine synthase	0.98	1.35	
	134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4	
	134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42 1.29	
	134914	U29615	Hs.91093	chilinase 1 (chilotriosidase)	1.16 0.95	1.29	
50	134953	L10678	Hs.91747	profile 2	0.98	1.73	
50	134993	AA282343	Hs.9242	purine-rich element binding protein B	1.35	211	
	135051	C15324	Hs.93668	ESTs	0.86	1.16	
	135158	U51711		Human desmocollin-2 mRNA; 3' UTR	v.d6	1.16	

Table 1B shows the excession numbers for those plays in Table 1A lecting unigenalD's. For each probased we have leted the gene cluster number from which the objected sweet designed. Gene clusters were complete using sequences durined from Genbank ESTs and mRVAs. These sequences were clustered based on sequence striking using Clustering and Alignment Tools (Duction Net), Oakland California). The Genbank accession numbers for sequences owner clustered based on sequence committees for sequences comprising each cluster are leted in the Accession column.

60		ber: Gene clus	s probesel tikeriffier number or number consistan numbers
	Pkey	CAT	Accessions
65	100661 100667	23182_1 26401_3	BEB23001 L05098 A-JBS304 AW966416 NS2295 A-A60213 AWS71619 A-B030555 L0542 X56794 S66400 XS5150 W60071 AW351630 XS5038 M33328 BED06289 BED70059 M33324 BED05248 BED05248 BED05717 BE181648 BED65700 AW666203 BEB67271 AW35213 AW37975 BE465981 E4605049 BED06278 BED06278 AW37772 AW37250 AW377772 AW57278 AW37975 BE4781 E46094 BED0624 BED06278 AW377772 BE18175 ALD7721 AW37270 AW57203 E003084 BE40011 4 W23518 BED06579 BED06219 X5161 K20358 HW1453 BEF546644 T65274 AW77274 AW37476 K5979 AW574 TA A62071 SEB0520 AW7761 AW3761 AW7138 BED06571 AW3568 HW370
70			BESIGNE 1822/1 WAST/AF ANSWERS DESIGNED AND 168 THE SERVICE AND 18 THE
75	100668	26401_3	LIAMAN 26779 SERADO XSSISO WEGOTI ANN'SICED XSSISO MEDIZAR ESPOCEZIO BESTOCEZIO ANNOSICEZIO XINGRIZIO ANNOSICEZIO SERIORI SERIORI SERIORI ANNOSICEZIO ANNOSICEZIO SERIORI RESPONI ANNOSICEZIO ANNOSICEZIO SERIORI RESPONI ANNOSICEZIO ANN
80			AISTSSS I AWRBATT Z. AATTSBA I ALGARGOA HIZTOTA ALGASSOA HAZYONES AWARSOTA WATIBBA ALGASSOS ALZTATT I BECAGAIS ANDRO SAIZEATIBB ALGASSOS ALZTATT I BECAGAIS ANDRO SAIZEATIBA ALGASIZATI, HAATIBA ALGASSOS ALZTATT I BECAGAIS ANDRO A
85	101332	25130_1	J04086 NM, 001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 AJ471482 AJ970337 AA737616 AJ827444 AW003286 AJ742333 AJ344044 AJ765634

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	•••	0 02/000	AD-8680 ANZ 323.05 MH 1227 A005280 EBURSSS A77400 W1650 A160025 AZB8423 AA03778 AW465927 AA68838 AA050593 AA655737 W1600 EBCRESUIT AA56000 A174157 A1700071 AA069174 A162504 AXB5593 AW65937 A466693 AW594519 A22184 AX3744 AA37775 EBCS022 A77600F A835058 AZZ1527 W167451 A W077688 A93572 A866059 A165052 AW774505 A172746 AL07694 A410161 H 11741 A431002 AW175375 T1279 AA026526 AA05053 AW174505 A165052 AW767450 F107746 AL07694
5			ABITURIS HT/011 ANSTRUIS ANTIGOST 1122 AND ANDROSS AND AND AND ANDROSS AND AND AND AND ANDROSS AND AND AND AND ANDROSS AND
10	100780	458_127	AND IT 28 ALGEST OF MYRS ON INSIGHT AWARD AND AND AND AND AND AND AND AND AND AN
15	100760	450_127	
20	100830	4002_1	DEJORGE DESCRIPTION DE CENTRA DE CEN
20	100906	4312_1	AISSGA AL 135548 ALSS224 AISS1135 AVC45095 AW19415 H78274 H7035 AA521/05 AA521/05 AA52000 AV65000 AV65001 AV61705 AV52000 AV65000 AV65000 AV65000 AV65000 AV65000 AV65000 AV65000 AV6500
25	100930	16865_1	AA46421 NNB81866 ANGHZB EES4010 T920A FRANCT HYBZDS ANSEAS ANGHOAGA ANTIBUXD ANGTSAR ANGTROB AA7145A AA365698 AASTRIA AASSOOG AUSGOTT AA526635 ASTRIST HISPIGA ABAGGO AA47265 TO 1800 ANGTSAFE ANGTROB AA67145A AA365698 AAFTRIAG AA5716 TROOTZA AI75176 AA60161 ANGTSAG ANGTSAFA HISTIZ DOZDYTI EESTFAG T81159 R007722 ANGTSAFA AA67172 DOZDYTI EESTFAG T81159 R00772 ANGTSAFA AA67172 DOZDYTI EESTFAG T81159 R00772 ANGTSAFA AA67164 AA467172 DOZDYTI AA567164 AA67165 AA67165 AA467165 AA67165 AA67
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50			AA434011 AI369971 AA479731 AI865541 AI418020 AA421246 AA452764 AL048051
35	102221	3861_1	ANAGOTI MOSSETT ANATSYST ABBESSH AM1802D AA27246 AA452754 ALDAROST M.N. CORSIST CAMTERST ABBESSH AM1802D AA27246 AA452754 ALDAROST M.N. CORSIS LICAGOS MINISTER ANAS ANAS ANAS ANAS ANAS ANAS ANAS ANA
33			AT 142026 ALBRATION AT 1918 TAKENSISA ALBETTAIG BELGISSIS MINEZIONEZ ANVISIZOZISI I AL493203 BEZHARGIS EESISA19 ANVI 193699 ANVISTSAS BEZHARGIS ALBETTAIN AT 193699 ANVISTSAS BEZHARGIS ALBETTAIN AT 193691 ANVISTSAS BEZHARGIS ALBETTAIN AT 193691 AL
40			ALLOGICE ALGICITE ALGICITAT ALGORIA ALGICIGA ALGICIGA ALGICIGA ALGICIGA ALGORIA ALGICIGA ALGICI ALGICIGA ALGICIGA ALGICIGA ALGICICA ALGICI
	101809	32963_1	M8849 AA315280 NH, DM004 AA31529 BELGES AA61400 ANEDDAZ BE15893 AW35155 AA43068 AW11780 AW38453 AW38454 AW38456 AW73827 AW73828 AW59385 AA51702 AW37837 AW27869 AW27125 AW37289 AW34847 AX8814 AW38454 AW18136 AW36180 AA61506 AW86281 AW71746 AW172468 AW12863 AW23626 AW18280 AW27125 AW37849 AW807451 AW58486 AX51751 AW36180 AA61506 AW86281 AW717468 AW172468 AW27863 AW27866 AW37840 AW58449 AW807451 AW807869 AX54460 AX51751
45			AW020066 A783995 A18998 A91757 XW254471 AW36471 AB1673 ZWX AW36530 AW365821 AW365463 AA461087 A341438 A1970613 A0040737 A418400 AA947181 AA962716 A1280695 AW769275 AW023591 A1160977 AA055400 N71882 AA490466 AW243772 AW316538
43			
	102590	15932_1	R61573 BE005029 X98091 AA297307 BE537267 BE566138 BE566139 F11561 BE564745 BE568776 AW064005 BE566479 BE360035 BE507112 BE566634 BE566556 AA298060 BE566043 BE566813 BE566613 AA233070 BE565414 BE566736 BE566565 BE56667 BE56616 BE566433 BE566736 BE566569 AA298060 BE566439 BE566730 BE56615 AA233070 BE566448 BE566736 BE566656 BE56667 BE56616 BE5666433 BE566736 BE566756 BE56675 BE566743 BE566736 BE566740 BE566756 BE56678 AA468772 AA071383 AW735642 BE566786
50			A.237763, AAZ78550, AAZ1083, AAZ98184, AAG91007, AA984577, AAZ05916, N28759, ALG31221 C15757 C15767 1H02729, BEE589410, AA173930, AA419490, BP7471 BE739598, BE004624, BEZ39511, D252874, AA14949, BP7471 BE739598, BE004624, BEZ39511, D252874, AA17494, AA223654, AW192011, AA449759, MAY19432, AA173846, AA173843, AA173843, AA173845, BES49511, BES49511, AB549511, AB5495
55			ANI MASS ADSIGNATION AND ANI
60	101977	29073_1	AF 11212 A LUGSUS TARBON ANYAGYS BERSANSH BERSANTY WHISTY DESCRIZED BERSANDS BERSANDS BERSANDS ANASSTRANS AND STORY
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70			AN SEATON ALTERITY ALCOTOR ANY TOSSO AND TICKNO AND SEASON AND SEATON ALCOTOR AND ALCOTOR
75	102781	20812_1	BE39215 AW326540 BE54240H 3217 DE S02244 T31955 BE20698 BE277373 T3270 LB20494X BE27844 DE 389537 BE27873 DE 31045 BE38573 RE378 BE378 BE37873 BE378 B
80			A 350/11 A A10211 RIAGED RESPONDED RESPONDED RAZIONED AND A150/14 TESTED AND SERVICE RESPONDED R
85			AW173990 AW311540 BES3552/ AA350114 DES31104 AB661829 AK633105 AA527640 AW129146 AW615672 BE334607 AA483902 AW475032 BE378532

	W	0 02/08644	43 PCT/US02/12476
5			AAST2006 A460305 AMT0528 BEOLYZDI ANKS194B. ANK10066 ANKS1153 A059405 AA74664 AD14776 AAST7156 A0569011 AA56625 AA911956 AA140762 ANK74035 A657236 BE328228 ANK270348 AA158225 ANK17035 ANK74097 ANK519193 A461475 ANK54033 A062647 AN899973 AA77611 AA15221 NBRY41 BE544552 ANK727578 A455706 AA152166 AA05524 A150170 A152756 ANT7464 A851900 BE300756 A119980 A43679 AVA74733 ANK72768 ANK7506 AA15276 AA561232 AA56722 ANK76766 ANK76268 ANK76265 ANK7626 AR414551 AA157994 A431886 A456292 ANK92724 AS569 AA75686 AA75686 PATK626 ANK76265 ANK762
			AVV24898 AVT51830 AA90TR16 F0898 AVX077898 AR282300 AA14899 AVX6757 T33426 AA218571 AI9723021 AA686279 F48951 2A1578183 AVX19598 AVX19598 AVX19596 AVX19596 AVX19598
10			TSSIZY AGGIGEZ ARSSAEL ANGSAELA ANGSAELA ANGSAELA ANGSAELA ANGSAELA ELEGANIZA ELEGANIZ
15	119221	102947_1	BEZNISOR BES 14359 EC-000707 BEZNI 1258 ED-54359 ES-20150
20			AW235415 R70377 AA099236 F20703 AA524436 R69484
	125831	1522905_1	H04043 D60988 D60337
	128192 113195	45743_3 178688_1	AJ204246 AJ204250 A1194250 H83265 T53524 AA304359 AW960551 Al672874 A1749427 AA227777 AW027055 AA971834 T49644 T54122 AJ883239 AW960233 T91264 T96544 AJ350945 A1709114 R72382 T44788 R48725 AW385415 AJ095494 T49645 AA928653 AA570052 AW007546 T57175 AA516413 AA9131 10 T57112
25			AA664433 AA774503 AA367671 T59757 W78816 AI720806 AI633854 AI632086 AI668663 N70894 AW571809 AI383592 AI201348 W80715 N91880 AW963101 AA339011
	119861 112973	238266_1 4868_1	AB033223 BE391905 BE275955 BE277872 BE903882 AA313774 BE919159 BE296024 BE299727 BE300011 BE390277 BE394764 N87559 BE499419 BE499682 BE409197 AL119332 AA622427 AB16265 AA610118 T07318 AA019339 AA634430 BE205794 BED49614 A042322 AB622711 AB17845 AA630405 AW7919599 AB17842 T17271 AB103683 A1093533 M46019 AW892438 AB274836 AB75562 D51149 AW192458
30			AAS39614 AI925762 AW088153 T17455 AA018440 AW75 1475 BE300241 AI816255 BE391981 AW409671 AA353910 AW875446 AW875703 AW875928 AW875645 AW875647 AW938037 AL138042 AW892619 BE243018 AW995454 BE245381 BE009082 BE278921 AW967842 AA282454 H30121
	129402 105936	47367_1 260931 1	W72062 AF088057 W76255 AI827219 AI631461 AW449295 AI354957 AI313803 T62772 AI222040 T62921 T63781 AI678765 H12175 R14664 AI914049 AAS95383 H08009 H19418 AW953728 AI358021 AAS87361 AI269377 AA369905 AW957113 H27693
35		•	A 300A7 1173776 WYASYA AAST900A A131018 WYZ331 A179085 AAS68346 A859346 A185406 A188874 A8564770 AW131268 H16419 H76784 A32156 B3141154 ASA68372 ECERTISTR REGORD H1647 RESORD H1647 RESORD H364066 ESCHISGE A181455 A388120 A389375 AAR39110 A1016404 T35018 AA68837 AW44676 A181506 EES01139 AA688554 A337800 AW078352 Z41279 A115444 AA58735 AA406338 L2283 BA, 003554 L42601 EE 182076 A854 IZ21 EEL (14567 L42610 V01516) 10058 AW73752 A3403302 AW080167 A3541402 EES12846
	129466	2094_50	A 16/4 3/4 A NA 238 369 DE643/05 RE645/05 RE64530 RE645301 AW370R23 AW794706 AA 194806 AA 194992 AW384024 AW384000 AA 641239
40			AZAGGA ALMOSS ANYZBBB / AAAGSS ALGOBS ANGESES ANGESES ANYSBC75 ANYSBSSS ANYSBC70 ANGESTO ANGESTO ANTHER ANGES ANYSBC75 ANYSBSSS ANYSBC70 ANGESTO ANGES
45			AB310G AW2559A MX73593 AW27591 AW37415 AW37398 AAA9999 AW23985 AW25594 BED9829 BED9826 AS5398 AW55918 AW56791 AW25996 AW05092 AW5517 AW25927 AW5716 AW5716 AW5719 AW57496 BEL791 AW57496 BEL791 AW57540 B
50	100220 100355	45374_1 12538_1	AW103259 WR5229 ARRH 605 AKEST288 DE 154608 AADERS3 WR5121 WR5150 D25864 ABSH111 D28456 D25533 AW255450 D25250 AW2528640 AA10141 D22044 AM258640 AA507810 D25223 AAS5961 ECE2423 SEREÇAT DE 15674 D2504 AW35550 AA51780 AA51781 D25224 AA586550 AA51781 D25224 AW35550 AA51781 D25224 AW35550 AA51781
55		H05719 F1344	No. TIBES 122 ANT TISSION FISSAM ALTHATON (12200 AAT 18278) OF TIES AAT 12221 S ANT 1820 S AND 1848
60	100491 BE27780	34803_1 5 AA147951 AA6	DS6169 MS0891 X58985 MM QD512 EE79177 AA1483 BE256445 E526016 AVX48545 A173933 AVX65701 BE386050 BE619742 0131 BE25233 A1646589 A1654045 A547174 A126981 A1654010 A173523 AVX185707 AA71758 AVX19742 AVX787379 A46911 A4988500 AA62361 A003569 H4531 AA657976 A715912 R36138 AA722002 A662071 AVX73787 E664625 A4071 A457 A475975 A485421 AA62361 A003569 H4531 AA657976 A715912 A785328 A471593 A175912 A78578 A78579 A78591 A7859
65			AMENTER ANSTER I MASSIOS SAMSAZET AVASSERI I AMESSERI AMESSERI AMESSERI AMESSERI AMESSERI I AMESSERI A
70			AMBIEZZO AAASBEZA AJTIOTOS WEGETS ATZOSAT PZOTIB AABASHAJ AAGSEZSO MORGO HIGOZO EGEZGEGO EGESTOSO ANAZORIA ASSOCIA EGESTOSO ATZOSA EGESTOSO ANAZORIA EGESTOSO EGESTOS
75	100518	13165_1	RS0220 H50814 H44721 AWS51723 AA514796 AA418708 AWGT3377 AA3779622 AA277995 AA708224 AA708216 A318233 AA441180 AA0262521 AA316774 AA486908 H500094 AA096362 AW583742 BES36422 BEG18653 R70203 AA314732 AA34048 BES62720 T28342 NM 004415 AL031086 M77830 BE149780 AW762599 AW648723 AW376987 AW376987 AW376989 AW648371 AW376782 AW648376
			AW361413 AW849074 AW997139 AW799304 AW799309 RE077020 RE077017 RE185187 AW997196 RE156621 RE179915 RE006561 RE143155
80			AVR60098 B EXCUZIO 7 AMMOSZI A ABETTI 6 AVR813 TS BED11378 AMMOSZI 6 ESESTBA AVR88475 EE F60433 10211 BEDAGTI E ESESTBA E ESESTBA AVR88475 EE F60433 10211 BEDAGTI E ESESTBA E ESESTBA AVR87476 AVR7160 BEDAGTI AVR87176 AV
85			R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719959 AW352220 AW995245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW649590 T87267 AW853812 AA852213 W74149 BE009090 AA066401 H91011 AW368529 AW390272 C18457

5		AIDZ2862 BEERIS SA WYSFB81 AWM5692 AMM018 BEI 8531 BEI 18214 AM38564 AWR5115F 129818 AM13 1077 WISD540 XM2548 AWX5798 140098 VAZZY WAZG90 AZG904 BEIĞ1781 BELETIST BAZHT 172408 143104 AM19590 OX3278 AM3404 AM2567 AM2470 AM38262 AF13006 AWX70813 AWTG927 AWTG9817 AWTS9810 AWTS9803 AWTS9803 AWX70869 AM3570 AM2470 OX020 AWTT7783 AM38606 AWX7029 AM24788 BECG773 FEBOTER WYSF27 AM54784 AWTG974 AWX71884 AWX7084 AW5698 AM5698 AM
10		AMERICA MUTUCA AN 1911 F. ANZEDER A HEROSING
15	100528	49879_1 BECRIBERT ALUTYZEP ANAKTSSE BEZZYZF AMSSSSYS USIGSE (EZETATES) EEZETÄTE BELGBIS (BEZZYRÄ CEISODO AAAGYZAF EVEZYBA MISSES MERSES ANAKHASTA ARUSEN AASSIS ARUSEN ARUSEN AASSIS AASSIS ARUSEN AASSIS AA
20	100559	18.5.200.01.00 / 10.00
25	100576 124357 101624 101625 135158	9986_1 X00356 NNL, 00174 M26095 X05662 M15667 X02330 X02330 AA716558 AW256074 X04861 AI695720 AA719597 gemberk, X22-01 1
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I PCT/US02/12476 AW674920 N57176 AA026480 AW676767 H90284 AA026853 AW177787 AA026854 AW177786 BE092134 BE092137 BE092136 AW177784

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Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 grass down-regulated in lung tumos relative to normal lung and chronicely diseased lung. Oronically diseased lung samples represent chronic non-migraned lung diseases such as fibrosis, emphysema, and bronchist. Those genes was selected from \$550 probests on the Could/Immitrix Hutti Cameroid; paragrams are selected from \$500 probests on the Could/Immitrix Hutti Cameroid; paragrams are selected from \$500 probests on the Could/Immitrix Hutti Cameroid; paragrams are referred to the could be an expression data for each probased collaboration from the country and the country of the coun

	Pkey: ExAcon:	Unique Exemple	Eos probeset er Accession i	Identifier number number, Genbank accession number								
	Unigenel	D: Unigene	number	manage Contract to the Contrac								
10	Unigene R1:	Title: Unigene 90th per		or normal lung samples divided by the 80th perce	nlile of Al for a	denocarcii	noma and	squamous	cell card	inoma lun	g tumor	
	R2:	samples	i. of Al for norm	nal lung samples divided by 90th percentile of Al fo	r adenocamin	oma and s	nuamous	cell carcin	oma luno	tumor sar	noles.	
	R3:	median	of Al for norm	al lung samples minus the 15th percentile of Al to	r all normal lui	ng, chronic	ally disea	sed lung a	nd tumor	samples c	lvided by	
15		the 90th	percentile of	Al for adenocarcinoma and squamous cell carcin	oma lung tum	or samples	minus th	e 15th per	centile of	Al for all n	omal	
		tino ch	mnically disea	ased lung and tumor samples.								
	R4:	average	of Al for norm	nal lung samples divided by average Al for squam	ous cell carcir	oma and	adenocaro	zinoma lun	g turnors.			
	RS:											
20	R6:	median	of Al for norm	all lung samples minus the 15th percentile of Al fo	r ali normai lu	ng, chronic	ally disea	sed lung a	na tumor	samples (INIUSU UY I	116 9001
20	R7:	percent	ile of Al for ad	lenocarcinomas minus the 15th percentile of Al for nal lung samples divided by the 90th percentile of	Al for soupme	ig, chibilic	rinomas.	seu lung a	id tullior a	sampics.		
	R8:	modion	of Al for norm	soliung camples minus the 15th percentile of Al to	r all normal lu	na, chronic	:aliv disea	sed luna e	nd turnor	samples o	livided by t	he 90th
	140.	percent	le of Al for sa	uamous cell carcinomas minus the 15th percentile	of Al for all n	omal lung	, chronica	illy disease	d lung an	d tumor s	emples.	
25	Pkey	ExAcon	UnigeneID	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
	100095	797171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
	100095	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)	40.20							3.46
	100138	U83508	Hs.2463	angiopoletin 1			2.30					
30	100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
	100306	U86749	Hs.80598	transcription elongation factor A (SII);						3.06		
	100447	NM_014767	Hs.74583	KIAA0275 gene product								3.16
	100458	S74019	Hs.247979	Vpre-B	42.40					4.13		
25	100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor				125.60		4.13		
35	100959 101032	AA359129 BE206854	Hs.118127 Hs.46039	actin; alpha; cardiac muscle phosphoglycerate mutase 2 (muscle)	36.40			123.00				
	101032	AF047347	Hs.4880	arryloid bela (A4) precursor protein-bind	30.10			34.60				
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte				193,20				
	101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
40	101180	U11874	Hs.846	Interloukin 8 receptor; beta				54.86				
	101308	L41390		"Homo saplens core 2 beta-1,6-N-acetylg!	33.20							
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do			2.29	36.40				
	101345	NM_005795	Hs.152175	Calcitonin receptor-like			229	70.55				
45	101346 101397	A1738616 M26380	Hs.77348 Hs.180878	hydroxyprostaglandin dehydrogenase 15-(N lipoprotein lipase				10.00				3.54
73	101414	NM 000066		complement component 8; beta polypeptide							3.81	
	101435	NM_001100		actin; alpha 1; skeletal muscle				34.60				
	101507	X16896	Hs.82112	interleukin 1 receptor; type !				37.60				
	101530	M29874	Hs.1360	cytochrome P450; subfamily IIB (phenobar								4.25
50	101537	AI469059	Hs.184915	zinc finger protein; Y-linked		5,50	2.54					
	101542	NM_000102		cytochrome P450; subfamily XVII (steroid EDG1; endothelial differentiation, sphin	39.40	5.50						
	101545 101554	BE246154 BE207611	Hs.154210 Hs.123078	thyrold stimulating hormone receptor	35.40	13.00						
	101560	AW958272	Hs.83733	Intercellular adhesion molecule 2, exon								3.38
55	101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		
	101605	M37984	Hs.118845	troponin C; slow								3.80
	101621	BE391804	Hs.62661	guanylate binding protein 1; Interferon-	30.20						2.75	
	101680 101829	AA299330 AW452398	Hs.1042 Hs.129763	Sjogren syndrome antigen A1 (52kD; ribon solute carrier family 8 (sodium/calcium						3,37	213	
60	101829	M93221	Hs.75182	mannose receptor; C type 1				38.20		4.0,		
00	101961	AW004056	Hs.168357	*Hs-TBX2=T-box gene {T-box region} [huma			2.32					
	101994	T92248	Hs.2240	uteroglobin								6.85
	102020	AU077315	Hs.154970	transcription factor CP2			2.45					6.75
65	102091	BE280901	Hs.83155	aldehyde dehydrogenase 7	54.60							0.75
03	102112	AW025430 AA723157	Hs.155591	forkhead box F1 folate receptor 1 (adult)	54.00							3.98
	102190 102202	NM 000507	Hs.73769 Hs.574	fructose-bisphosphalase 1								3.62
	102241	NM_007351		Multimerin			2.32					
	102310	U33839		Accession not listed in Genbank		7.00						
70	102397	U41898		"Human sodium cotransporter RKST1 mRNA,	29.40							
	102571	U60115	Hs.239069	"Homo sapiens skeletal muscle LIM-protei						3.07		3.75
	102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome X			2.40			3.07		
	102636	U67092 U70867	Hs.83974	"Human ataxia-telangiectasia locus prote solute carrier family 21 (prostaglandin			3.15					
75	102667 102675	U72512	Hs.7771	"Human B-cell receptor associated protei						3.56		
15	102698	M18667	Hs.1867	progastricsin (pepsinogen C)								4.51
	102727	U79251	Hs.99902	opiold-binding protein/cell adhesion mol					12.00			
	102852	V00571	Hs.75294	conficutrools releasing hormone	37.40							
-	103026	X54162	Hs.79386	thyrold and eye muscle autoantigen D1 (6					13.00			
80	103028	X54380	Hs.74094	pregnancy-zone protein	28.80				10.00			
	103098	M86361	11. 005140	Human mRNA for T cell receptor, clone IG		6.00			10.00			
	103117 103241	X63578 X76223	Hs.295449	parvatbumin H.saplens MAL gene excn 4		3.00	2.47					
	103241	U84722	Hs.76206	Cadherin 5, VE-cadherin (vascular epithe			2.69					
85	103360	Y16791	Hs.73082	keratin; hair; acklic; 5							2.16	

	103496	O 02/080 Y09267	443 Hs.132821	flavin containing monocxygenase 2						PCT/	US02/1	597
	103496	Y10141	ns. 132021	"H.sapiens DAT1 gene, partial, VNTR"						3.27		0.07
	103561	NM_001843	Hs.143434	contactin 1			2.40					
5	103569 103575	NM_005512 Z26256	Hs.151641	glycoprotein A repetitions predominant "H.sapiens isoform 1 gene for L-type cal			2.99			4.18		
3	103627	Z48513		H.saplens XG mRNA (clone PEP6)						3.44		
	103767	BE244667	Hs.296155	CGI-100 protein							2.25	
	103850	AA187101 AA402801	Hs.213194 Hs.303276	Hypothetical protein MGC10895; sim to SR ESTs				46.55		3.05		
10	104078	AW732858	Hs.143067	ESTs						3.54		
	104352	BE219898	Hs.173135	dual-specificity tyroslne-(Y)-phosphoryl						3.16		
	104398	Al423930 Al904823	Hs.36790 Hs.31297	ESTs; Weakly similar to putative p150 [H ESTs	64.80							3.38
	1044/3	AW960427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC			2.47					3.30
15	104495	AW975687	Hs.292979	ESTs	28.60							
	104595	A1799603	Hs.271568	ESTs ESTs; Weakly similar to Slit-1 protein [6.00				3.42		
	104597	Al364504 AW969769	Hs.93967 Hs.105201	ESTs	34.00							
••	104686	AA010539	Hs.18912	ESTs		11.00						
20	104691	U29690 AI039243	Hs.37744 Hs.278585	ESTs; Beta-1-adrenergic receptor ESTs	56.80			60.40				
	104776	AA026349	H8.27 0000	ESTs	34.20			00.40				
	104825	AA035613	Hs.141883	ESTs			3.03					
25	104865	T79340 NM 016348	Hs.22575 Hs.10235	Homo sapiens cDNA: FLJ21042 fis, clone C ESTs	41.20							3.27
23	104942	R65998	Hs.285243	ESTs				40.00				
	105062	AW954355	Hs.36529	ESTs								3.20
	105101	H63202	Hs.38163 Hs.8364	ESTs ESTs	34.20							4.17
30	105173 105194	U54617 R06780	Hs.19800	ESTS		16.00						
	105226	R58958	Hs.26608	ESTs			2.34					
	105256	AA430650 BE245812	Hs.16529 Hs.8941	transmembrane 4 superfamily member (tehr FSTs			2.72 2.61					
	105647	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	33.60		2.01					
35	105789	AF106941	Hs.18142	arrestin; beta 2								3.59
	105817 105847	AA397825 AW964490	Hs.32241	synaptopodin ESTs				35.40		4.46		. "
	105894	AI904740	Hs.25691	calcitonin receptor-like receptor activi			3.43	•••••				
40	105999	BE268786	Hs.21543	ESTs		7.00						
40	106075 106178	AA045290 AL049935	Hs.25930 Hs.301763	ESTs KIAA0554 protein	34.80			42.60				
	106381	AB040916	Hs.24106	ESTs	04.00				12.00			
	106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2				96.40		3.69		
45	106536 106569	AA329648 R20909	Hs.23804 Hs.300741	ESTs sorcin				47.20				
45	106605	AW772298	Hs.21103	Homo saplens mRNA; cDNA DKFZp564B076 (fr				220.40				
	106842	AF124251	Hs.26054	novel SH2-containing protein 3 sporm associated antigen 6	39.20		2.55					
	105844	AA485055 AI983730	Hs.158213 Hs.26530	serum deprivation response (phosphalidy)	35.20		2.28					
50	106943	AW888222	Hs.9973	ESTs								4.28
	106954	AF128847 AA862496	Hs.204038 Hs.28482	ESTs ESTs					10.45			4.32
	107163	AF233588	Hs.27018	ESTS			2.57		10.10			
	107201	D20378	Hs.30731	EST						3.84		
55	107238 107376	D59362 U90545	Hs.330777 Hs.327179	EST solute carrier family 17 (sodium phospha		8.03 10.67						
	107530	Y13622	Hs.85087	latent transforming growth factor beta b			2.32					
	107688	AW082221	Hs.60536	ESTs				34.60				
60	107706 107723	AA015579 AA015967	Hs.29276	ESTs EST	28.40					3.29		
00	107727	AA149707	Hs.173091	DKFZP434K151 protein				80.80				
	107750	AA017291	Hs.60781	ESTs				51.40		3.14		
	107751 107873	AA017301 AK000520	Hs.235390 Hs.143811	ESTs ESTs		9.00				3.14		
65	107899	BE019261	Hs.83869	ESTs; Weakly similar to IIII ALU SUBFAMI						3.65		
	107994	AA036811	Hs.48469	ESTs				44.60 32.00				
	107997 108041	AL049176 AW204712	Hs.82223 Hs.61957	Human DNA sequence from clone 141H5 on c ESTs				30.80				
	106048	AI797341	Hs.165195	ESTs							4.75	
70	106338 108434	AA070773 AA078899		"zm53g11.s1 Stratagene fibroblast (#9372 "zm94b1.s1 Stratagene colon HT29 (#93722			2.33				2.92	
	108447	AA079126		"zm92a11.s1 Stratagene ovarian cancer (#						3.06		
	108480	AL133092	Hs.68055	ESTs				34.00				3.36
75	108499 108535	AA083103 R13949	Hs.226440	"zn1b12.s1 Stratagene hNT neuron (#93723 Homo sapiens clone 24881 mRNA sequence					19.00			3.30
15	108550	AA084867		"zn11f6.s1 Stratagene hNT neuron (#93723					12.00			
	109604	AA934589	Hs.49698	ESTs			2.33					5.82
	108625 108629	AW972330 AA102425	Hs.283022	ESTs *zn24c6.s1 Stratagene neuroepithelium NT							3.42	0.02
80	106655	AA099960		"zm65c6.s1 Stratagene fibroblast (#93721		7.00						
-	108756	AA127221	Hs.117037	Homo saplens mRNA; cDNA DKFZp564N1164 (f	28.80	6.05						
	108864	Al733852 AL138272	Hs.199957 Hs.62713	ESTs ESTs	28.80 32.80							
	108921	Al568801	Hs.71721	ESTs				57.80				
85	108967	AA142989	Hs.71730	ESTs	28.89							

	w	O 02/086	443							PCT/U	JS02/1	2476	
	109001	Al056548	Hs.72116	ESTs, Moderately similar to hedgehog-int			2.57						
	109003	AA147497	Hs.71825	ESTs		5.60					211		
	109004 109065	AA156235 AA161125	Hs.139077 Hs.252739	EST EST		5.60			10.00				
5	109250	H83784	Hs.62113	ESTs; Wealdy similar to PHOSPHATIDYLETHA					10.00		3.44		
-	109490	AA233416	Hs.139202	ESTs							2.92		
	109510	AI798863	Hs.87191 Hs.27214	ESTs ESTs		10.00	2.40						
	109578	F02208 F02695	Hs.311662	EST EST		10.00		40.80					
10	109613	H47315	Hs.27519	ESTs				54.40					
	109650	R31770	Hs.23540	ESTs	31.20	0.40							
	109682 109724	H18017 D59899	Hs.22869 Hs.127842	ESTs ESTs		8.40		29.40					
	109782	AB020644	Hs.14945	long tatty acyl-CoA synthetase 2 gene					8.00				
15	109833	R79864	Hs.29889	ESTs		10.00	6.49						
	109837	H00656 T64183	Hs.29792 Hs.282982	ESTs ESTs			0.43				2.75		
	109984	A1796320	Hs.10299	ESTs				107.00					
20	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 1B						3.48	2.22		
20	110271	H28985 AW874263	Hs.31330 Hs.32468	ESTs ESTs	44.20					3.40			
	110420	R93141	Hs.184261	ESTs				32.00					
	110578	T62507	Hs.11038	ESTs	28.40				20.00				
25	110634 110726	R98905 AW961818	Hs.35992 Hs.24379	ESTs potassium voltage-gated channel; shaker-					20.00			4.15	
23	110837	H03109	Hs.108920	ESTs: Wealdy similar to semaphorin F [H.				56.80					
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfami		5.33	3.13						
	110894 110971	R92356 Al760098	Hs.66881 Hs.21411	ESTs; Moderately similar to cytoplasmic ESTs		3.33		44.60					
30	111023	AV655386	Hs.7645	ESTs	32.40								
	111057	179639	Hs.14629	ESTs					17.14		4.58		
	111247 111330	AW058350 BE247767	Hs.16762 Hs.18166	Homo sapiens mRNA; cDNA DKFZp564B2062 (/ KIAA0870 protein							4.00	3.42	
	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap								3.91	
35	111442	AW449573	Hs.181003	ESTs				33.20 53.00					
	111737	H04607 AI741471	Hs.9218 Hs.23666	ESTs ESTs	46.20			55.00					
	111807	R33508	Hs.18827	ESTs		16.00				3.91			
40	111862 112045	R37472 Al372588	Hs.21559 Hs.8022	EST TU3A protein						3.91	2.74		
-10	112057	R43713	Hs.22945	EST							4.92		
	112214 112263	AW148652 R52393	Hs.167398 Hs.25917	ESTs ESTs			2.43		13.00				
	112314	AW206093	Hs.748	ESTs		9.00							
45 ·	112324	R55965	Hs.26479	limbic system-associated membrane protei			2.49		14.00				
	112362 112380	AW300887 H63010	Hs.26638 Hs.5740	ESTs; Weakly similar to CD20 receptor [H ESTs			2.34						
	112425	AA324998	Hs.321677	ESTs: Weakly similar to IIII ALU SUBFAM!		8.00				4.53			
50	112473 112492	R65993 N51620	Hs.279798 Hs.28694	pregnancy specific beta-1-glycoprotein 9 ESTs				29.80		4.53			
50	112541	AF038392	Hs.116674	ESTs						3.62			
	112620	R80552	Hs.29040	ESTs ESTs			2.37 2.26						
	112623 112867	AW373104 T03254	Hs.25094 Hs.167393	ESTS			2.20		12.00				
55	112894	T08188	Hs.3770	ESTS		6.50							
	112954	AA928953	Hs.6655	ESTs ESTs; Weakly similar to IIII ALU SUBFAMI		7.00						4.39	
	113029 113086	AW081710 AA346839	Hs.7369 Hs.209100	DKFZP434C171 protein								4.47	
	113140	T50405	Hs.175987	ESTs					10.00				
60	113252	NM_004469	Hs.11392 Hs.159367	c-fos induced growth factor (vascular en ESTs		14.00				3.72			
	113257 113394	AJ821378 T81473	Hs.177894	ESTS						3.60			
	113437	T85349	Hs.15923	EST	35.00								
65	113454	Al022166	Hs.16188	ESTs ESTs	39.60	6.00							
05	113502 113552	T89130 Al654223	Hs.16026	ESTs	00.00							3.88	
	113645	T95358	Hs.333181	ESTs							2.58		
	113691 113706	T96935 AA004693	Hs.17932 Hs.269192	EST .				38.20		3.09			
70	113883	U89281	Hs.11958	oxidative 3 alpha hydroxysterold dehydro			2.31			0.00			
	113924	BE178285	Hs.170056	Homo saplens mRNA; cDNA DKFZp586B0220 (f	30.40				13.00		_		
	114035 114058	W92798 AK002016	Hs.269181 Hs.114727	ESTs ESTs					13.00			5.00	
	114084	AA708035	Hs.12248	ESTs				40.60					
75	114121	H05785	Hs.25425	ESTs			2.31						
	114124	W57554 AW515443	Hs.125019 Hs.306117	Human lymphoid nuclear protein (LAF-4) Interleukin 13 receptor, alpha 1		7.00 6.00							
	114275	AA149707	Hs.173091	DKFZP434K151 protein				48.80					
80	114427	AA017176	Hs.33532	FSTs: Highly similar to Miz-1 protein IH					10.00	3.45			
80	114449 114452	AA020736 Al369275	Hs.243010	ze63b11.s1 Soares retina N2b4HR Homo sa ESTs, Moderately similar to RTCO_HUMAN G		14,00			10.00				
	114609	AA079505		zm97a5.s1 Stratagene colon HT29 (#93722				05.45		3.13			
	114648 114731	AA101056 BE094291	Hs.155651	"zn25b3.s1 Stratagene neuroepithellum NT Homo sapiens HNF-3beta mRNA for hepatocy				35.40				3.42	
85	114762	AA146979	Hs.288464	ESTs	33.00								

	w	O 02/08	5443							PCT/I	US02/1	2476	
	114776	AA151719	Hs.95834	ESTa	34.40								
	115009	AA251561	Hs.48689	ESTs	30.20								
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60								
5	115279	AW964897	Hs.290825	ESTs		6.00			12.00				
,	115302 115365	AL109719 AW976252	Hs.47578 Hs.268391	ESTs ESTs					12.00	3.32			
	115559	AL079707	Hs.207443	ESTs				48.00					
	115566	AJ142336	Hs.43977	ESTs				56.20					
10	115683	AF255910	Hs.54650	ESTs, Weakly similar to (define not ava	31.40			33.60					
10	115744 115819	AA418538 AA486620	Hs.43945 Hs.41135	ESTs; Highly similar to dJ1178H5.3 [H.sa Endomucin 2				74.40					
	115949	A1478427	Hs.43125	ESTs			3.18						
	115965	AA001732	Hs.173233	ESTs				388.80					
1.5	116035	AA621405	Hs.184664	ESTs .				33.20					
15	116049	AA454033	Hs.41644	ESTs				45.80		3.57			
	116081 116082	Al190071 AR029496	Hs.55278 Hs.59729	ESTs ESTs			3.06			3.37			
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) Interactin	50.60		-						
	116228	AI767947	Hs.50841	ESTs; Weakly similar to tuffelin [M.musc			3.85						
20	116250	N76712	Hs.44829	ESTs		6.00							
	116419 116617	Al613480 D80761	Hs.47152 Hs.45220	ESTs; Weakly similar to testicular tektil EST			2.27	30.00					
	116517	AB007979	Hs.45220 Hs.301281	tenascin R (restrictin; Janusin)	47.20		2.21						
	116835	N39230	Hs.38218	ESTs				41.20					
25	116970	AB023179	Hs.9059	KIAA0962 protein					11.00				
	117023	AW/070211	Hs.102415	ESTs	49,40			91.00					
	117027 117036	AW035208 H88908	Hs.130093 Hs.41192	ESTs EST	49.40			32.60					
	117110	AA160079	Hs.172932	ESTs .		8.67		02.00					
30	117209	W03011	Hs.306881	ESTs				30.60					
	117325	N23599	Hs.43396	ESTs					9.29				
	117454	N29569	Hs.44055	ESTs	44.00					3.19			
	117475 117543	N30205 RF219453	Hs.93740 Hs.42722	ESTs ESTs	44.00	16.00							
35	117567	AW444761	Hs.44565	ESTs		10.00			12.00				
55	117570	N48649	Hs.44583	ESTs					11.00				
	117600	N34963	Hs.44676	EST						3.74			
	117730	N45513	Hs.46608	ESTs		6.00 9.00							
40	117791 117929	N48325 N51075	Hs.93956 Hs.47191	EST ESTs		9.00		29.20					
70	117990	AA446167	Hs.47385	ESTS		8.00		20120					
	118224	N62275	Hs.48503	EST	31.40								
	118244	N62516	Hs.48556	ESTs	32.80		2.40						
45	118357 118446	AL109667	Hs.124154 Hs.269121	Homo sapiens mRNA full length insert cDN			2.40						
43	118445	N66361 N66399	Hs.49193	ESTs EST	30.80		2.20						
	118530	N67900	Hs.118446	ESTs						3.10			
	118549	N68163	Hs.322954	EST						3.41			
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty			3.94			3.58			
50	118862 118935	W17065 AI979247	Hs.54522 Hs.247043	ESTs KIAA0525 protein				33.00		3.30			
	118944	AI734233	Hs.226142	ESTs; Weakly similar to IIII ALU SUBFAMI				00.00	11.43				
	118995	N94591	Hs.323056	ESTs		14.00							
	119073	BE245360	Hs.279477	ERG-2/ERG-1; V-els avian erythroblastosi				52.60					
55	119268	T16335	Hs.65325	EST Accession not listed in Genbank	31.40					3.50			
	119514 119824	W37937 W74536	Hs.184	advanced glycosylation and product-speci			2.75			0.00			
	119831	AL117664	Hs.58419	DKFZP586L2024 protein								3.21	
	119861	W78816	Hs.49943	ESTs; Moderately similar to IIII ALU SUB				33.80					
60	119889	W84346 W86192	Hs.58671 Hs.58815	ESTs ESTs	29.00			30.03					
	119921 120082	W86192 H80286	Hs.40111	ESTs	23.00					3.80			
	120094	AAB11339	Hs.124049	FSTs		6.00							
	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)				36.60					
65	120378	AA223249	Hs.285728	ESTs		12.00							
	120404	AB023230-	Hs.96427	KIAA1013 protein	39.40				8.00				
	120504 120512	AA256837 N55761	Hs.194718	ESTs ESTs	33.00				0.00				
	120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa	00.00							4.18	
70	120777	AA287702	Hs.10031	KIAA0955 protein				46.60					
	121082	AA398722		ESTs	41.60			39.00					
	121191 121248	AA400205 AA400914	Hs.104447 Hs.97827	ESTs EST	41.00						5.08		
	121363	AJ287280	Hs.97933	ESTs					12.00				
75	121366	AI743515		ESTs					20.00				
	121483	A1660332	Hs.25274	ESTs; Moderately similar to putative sev				20.00		3.32			
	121518	AA412155		ESTs			2.29	30.20					
	121545 121622	AA412442 AA416931	Hs.98132 Hs.126065	ESTs ESTs		9.00	2.29						
80	121622	AA416556	Hs.98234	FSTs		5.40		34.80					
	121709	Al338247	Hs.98314	Homo saplens mRNA; cDNA DKFZp586L0120 (f	34.80								
	121730	A1140683	Hs.98328	ESTs	38.80								
	121740	AA421138	Hs.98334	EST Homo saplens mRNA for alpha integrin bin	38.20	7.00							
85	121772 121821	AJ590770 AL040235	Hs.110347 Hs.3346	Homo sapiens mikrika for alpha integrin oin ESTs	30.20							3.61	
00	121021												

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	121835	AB033030	Hs.300670	ESTs			2.34			PCI	USU2/1	24/6
	121841	AA427794	Hs.104864	FSTs			2.61					
	121885	AA934883	Hs.98467	ESTs							2.25	
5	121888	AA426429	Hs.98463	ESTs				** **			2.92	
3	121938	AA428659	Hs.98610	ESTs EST				46.80 31.40				
	121950 122030	AA429515 AA431310	Hs.98724	ESTs	34.40			31.40				
	122054	AA431725	Hs.98746	EST							3.58	
10	122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40							
10	122233	AA436455	Hs.98872 Hs.98890	EST EST	29.80			39.80				
	122253	AA436676 AA436703	Hs.104936	ESTs; Wealdy similar to hypothetical pro		9.00		43.00				
	122266	AA436840	Hs.98907	EST						3.60		
1.5	122285	AA436981	Hs.121602	EST	30.80					3.14		
15	122409 122485	AA446830 AA524547	Hs.99081 Hs.160318	ESTs phospholemman	30.80		2.65					
	122697	AA420683	Hs.98321	Homo saplens cDNA FLJ14103 fis, clone MA		15.00	2.00					
	122772	AW117452	Hs.99489	ESTs		6.67						
20	122831	AJ857570	Hs.5120	ESTs				32.20		3.37		
20	122913 123049	A1638774	Hs.105328 Hs.211869	ESTs FSTs				32.20 41.80				
	123049	BE047680 Al345569	Hs. 190046	ESTs	35.80			41.00				
	123136	AW451999	Hs.194024	ESTs	******						2.58	
0.5	123309	N52937	Hs.102679	ESTs				82.80	19.00			
25	123455	AA353113 AA609579	Hs.112497 Hs.112724	ESTs ESTs				82.80		3.95		
	123756	AA609971	Hs.112724	EST	35,40					3.50		
	123802	AA620448		Homo sapiens clone 24760 mRNA sequence	58,00							
	123837	Al807243	Hs.112893	ESTs				32.40				
30	123844 123936	AA938905 NM_004673	Hs.120017 Hs.241519	olfactory receptor, family 7; subfamily ESTs	29.00		2.63					
	123930	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR	23.00			70.60				
	124013	AI521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40							
25	124160	R40290	Hs.124685	ESTs					13.00	474		
35	124205	H77570	Hs.108135	ESTs			2.35			4.74		
	124226 124246	AA618527 H67680	Hs.190266 Hs.270962	ESTs ESTs			2.30	29.40				
	124348	AI796320	Hs.10299	ESTs		17.00						
40	124358	AW070211	Hs.102415	"yw35g11.s1 Morion Fetal Cochlea Homo sa			3.07			3.14		
40	124409 124442	AI814166 AW663632	Hs.107197 Hs.285625	ESTs TATA box binding protein (TBP)-associate			2.48			3.14		
	124442	N51413	Hs.109284	ESTs			2.40	30.80				
	124479	AB011130	Hs.127436	calcium channet; voltage-dependent; alph								6.03
4.5	124519	A1670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO			2.50					
45	124711 124866	NM_004657 AJ768289	Hs.26530 Hs.304389	serum deprivation response (phosphatidy) ESTs	59.20	8.00						
	124874	BE550182	Hs.127826	ESTS		0.00		37.60				
	125097	AW576389	Hs.335774	ESTs					10.00			
	125179	AW206468	Hs.103118	ESTs						3.12	2.79	
50	125200 125299	AW836591 T32982	Hs.103156 Hs.102720	ESTs ESTs				34.20			2.79	
	125299	AL110151	Hs.128797	DKFZP586D0824 protein	29.00			04.20				
	125810	H00083		aryl hydrocarbon receptor-Interacting pr	32.20							
55	126178	BE242256	Hs.2441	KIAA0022 gene product HUM525A058 Human placenta polyA+ (TFuli		12.00		33.60				
33	126303 126403	D78841 AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80			33.00				
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu				29.80				
	126773	AA648284	Hs.187584	ESTs	39.60							
60	127307	AW962712	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	28.80			34.40				
00	127462 127486	AA760776 AW002846	Hs.293977 Hs.105468	sa59h04.s1 NCL_CGAP_GCB1 Homo saplens c FSTs		9.00		34.40				
	127572	AA594027	Hs. 191788	ESTs			2.36					
	127609	X80031	Hs.530	ESTs				29.40				
65	127832	AW976035	Hs.292396	ESTs				37.20			4.42	
03	127898 128073	AA774725 AW340720	Hs.128970 Hs.125983	ESTs ESTs				38.40			4.42	
	128101	AA905730	Hs.128254	ESTs		7.33						
	128149	NM_012214	Hs.177576	mannosyl (alpha-1;3-)-glycoprotein beta-							2.58	
70	128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma) ESTs; Weakly similar to LRS (H.sapiens)			3.09	34.40				
70	128333 128364	W68800 N76462	Hs.12126 Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT		10.00		04.40				
	128426	AI265784	Hs.145197	ESTs							4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20							
75	128634	AA464918		ESTs; Moderately similar to IIII ALU SUB				41.60 87.00				
13	128687 128726	AW271273 Al311238	Hs.23767 Hs.104476	ESTs ESTs				01.00				4.02
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp					9.00			
	128833	W26667	Hs.184581	ESTs								3.76
80	128870	H39537	Hs.75309	eukaryotic translation elongation factor			2.66			3.10		
80	128878 128885	R25513 AF134803	Hs.10683 Hs.180141	ESTs cofilin 2 (muscle)					11.00	3.10		
	128998	W04245	Hs.107761	FSTs: Weakly similar to PUTATIVE RHO/RAC							3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi								3.68
85	129038	AW156903	Hs.108124	ribosomal protein L41 ESTs	34.60					3.17		
92	129098	AW580945	Hs.330466	Edis	34.00		-					

	337	A 02/08/	142							PCT/I	US02/1	2476
	129210	O 02/086 AL039940	Hs.202949	KIAA1102 protein						rein	0.302/1	4.09
	129210		Hs.237868	interleukin 7 receptor			2.29					
	129262	BE222198	Hs.109843	ESTs						3.30		4.05
5	129301 129331		Hs.330780 Hs.279772	Human cytochrome P450-IIB (hIIB3) mRNA; ESTs; Highly similar to CGI-38 protein [4.09
,	129381		Hs.110903	claudin 5 (transmembrane protein deteted			2.93					
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1				160.80				
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD ESTs; Weakly similar to collagen alpha 1					10.00	3.40		
10	129613 129782	AW978517 AW016932	Hs.172847 Hs.104105	EST		9.00				0.40		
10	129950	F07783	Hs.1369	decay accelerating factor for complement				87.80				
	129958	R27496	Hs.1378 Hs.274463	annexin A3 defensin; alpha 1; myeloid-related seque			272	44.60				
	129959 130160	AL036554 AA305688	Hs.267695	UDP-GalthetaGlcNAc beta 1:3-gatactosyltr				42.20				
15	130259	NM_000328	Hs.153614	retinitis plamentosa GTPase regulator			2.54					
	130273		Hs.153863	MAD (mothers against decapentaplegic; Dr DKFZP586G1219 protein				51.60		3.16		
	130312	AF056195 NM_001928	Hs.15430 Hs.155597	D component of complement (adipsin)								4.11
	130523	AA999702	Hs.214507	ESTs						4.77		
20	130799 130885	AB028945 NM_005883	Hs.12696 Hs.20912	ESTs adenomatous polyposis coli like		6.00				3.54		
	131002	AL050295	Hs.22039	KIAA0758 protein								3.50
	131012	AL039940	Hs.202949	KIAA1102 protein		20.00						
25	131031	NM_001650 N64328	Hs.288650 Hs.268744	aquaporin 4 ESTs; Moderately similar to KIAA0273 [H.	41.20			31.40				
25	131061 131066	AW169287	Hs.22588	ESTs				29.60				
	131082	AJ091121	Hs.246218	ESTs: Weakly similar to zinc finger prot					9.00			3.86
	131087	AF147709 AF033382	Hs.22824 Hs.23735	ESTs; Wealdy similar to p160 myb-binding potassium voltage-gated channel; subfami						3.14		3.00
30	131161	AA171388	Hs.184482	DKFZP586D0624 protein						3.80		
	131182	AJB24144	Hs.23912	ESTs			2.98					3.67
	131205	NM_003102		superoxide dismutase 3; extracellular ESTs			3.15					
	131277 131281	AA131466 AA251716	Hs.23767 Hs.25227	ESTS			0.10	32.20				
35	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma						6.40		3.44
	131285 131355	Al567943 R52804	Hs.25274 Hs.25956	ESTs; Moderately similar to putative sev DKFZP564D206 protein		8.00				6.40		
	131393	AW085781	Hs.26270	ESTs		10.00						
40	131461	AA992841	Hs.27263	butyrale response factor 2 (EGF-response	28.80						4.03	
40	131487 131517	F13036 AB037789	Hs.27373 Hs.263395	Homo saplens mRNA; cDNA DKFZp56401763 (f ESTs; Highly similar to semaphorin VIa [39.00						4.03	
	131545	AL137432	Hs.28564	ESTs	00.00				11.00			
	131583	AK000383	Hs.323092	ESTs; Wealdy similar to dual specificity			2.47		10.00			
45	131647 131675	AA359615 H15205	Hs.30089 Hs.30509	ESTs ESTs			2.47			3.06		
73	131676	Al126821	Hs.30514	ESTs	45.80							
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta			2.28					3.78
	131717 131756	X94630 AA443966	Hs.3107 Hs.31595	CD97 antigen ESTs				40.60				
50	131762	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi								3.67
	131821	AA017247 AB014533	Hs.164577 Hs.33010	ESTs KIAA0633 protein			2.87				3.48	
	131839 131861	AL096858	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	54.00							
~~	132015	Al418008	Hs.3731	ESTs				49.20 34.80				
55	132070 132242	BE622641 AA332697	Hs.38489 Hs.42721	ESTs ESTs			2.68	34.60				
	132334	AW080704	Hs.45033	lacrimal profine rich protein			4.68					
	132476	AL119844	Hs.49476	Homo saplens clone TUA8 Cri-du-chat regi	34.20		2.66					
60	132490	NM_001290 Al922968	Hs.4980 Hs.172510	UM binding domain 2 ESTs		13.00	2.00					
00	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture				30.60				
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin ligh						4.02 3.18		
	132652 132726	N41739 N52298	Hs.61260 Hs.55608	ESTs ESTs; Weakly similar to cDNA EST yk484g1					11.43	3.10		
65	133028	RS1604	Hs.300842	ESTs			2.37					
	133071	BE384932	Hs.64313	ESTs			2.27 2.63					
	133120 133129	NM_003278 AA428580	Hs.65424 Hs.65551	tetranectin (plasminogen-binding protein ESTs			2.03					5.49
	133147	AA026533	Hs.66	Interleukin 1 receptor-like 1			6.20					
70	133151	NM_014051	Hs.94896	ESTs				31.40		3.69		
	133213	AA903424 AW978439	Hs.6788 Hs.69504	ESTs ESTs				31.40	9.00			
	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famili	41.20							
75	133407	AF017987	Hs.7306	secreted frizzied-related protein 1 protocadherin 2 (cadherin-like 2)	50.20					3.72		
13	133535	AL134030 U41518	Hs.284180 Hs.74602	aquaporin 1 (channel-forming integral pr						3.72		3.35
	133656	BE149455	Hs.75415	Accession not listed in Genbank			2.65					
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma) ESTs				90.80		3.05		
80	133779	T58486 AF035718	Hs.222566 Hs.78061	transcription factor 21			2.92			•.••		
00	133985	L34657	Hs.78146	platelet/endothellal cell adhesion molec								3.45
	134000	AW175787 Al372588	Hs.334841 Hs.8022	selenium binding protein 1 TU3A protein			4.49					4.05
	134111 134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f							3.27	
85	134204	AI873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein (40.80				

		O 02/086								US02/12476
	134641 134677	Al092634 AA251363	Hs.156114 Hs.177711	protein tyrosine phosphatase; non-recept ESTs				32.20	3.76	
	134745	NM_000685		angiotensin receptor 1B		15.00				
-	134749	T28499	Hs.89485	carbonic anhydrase IV			3.05			
3	134786	T29618	Hs.89640	anglopoietin 1 receptor, TEK tyrosine ki				57.80		
	134825	U33749	Hs.197764	thyroid transcription factor 1						3.73
	134978 135010	AI829008 N50465	Hs.333383 Hs.92927	ficolin (collagen/fibringen domain-cont ESTs			2.52	31.60		
	135053	AW796190	Hs.93678	ESTs				31.00	3.21	
10	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80				U.Z.1	
10	135091	AA493650	Hs.94367	ESTs	20.00					4.24
	135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associate		8.00				
	135203	C15737	Hs.269386	ESTs					4.31	
	135236	AI636208	Hs.96901	ESTs	43.00					
15	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd						6.42
	135346	NM_000928	Hs.992	phospholipase A2; group iB (pancreas)			3.82			
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-			4.15			
	135387	NM_001972		elastase 2; neutrophil	37.20					
20	135388	W27965	Hs.99865	EST	38.80					
20	135402	L12398	Hs.99922	dopamine receptor D4					4.21	

TABLE 28 shows the accession numbers for those primeleys lacking uniquenel/Os for Table 2A. For each problems we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were complete using sequences derived from Genhank ESTs and mRVAs. These sequences were clustered based on sequence shalled using clustering and Alignment Tools (Double Twist, California). The Genhank accession numbers for sequences comprising each cluster are fasted in the "Accession" column.

Piery: Unique Eos probeet l'uniffer number Accession: Genérales en munter Piery CAT number: Accession: Genérales en munter 25 10847 3452_7 AA079126 108550 12073_1 AA05860 AA15913 108550 12732_1 AA05860 AA15913 108550 12752_1 AA05860 AA0	
Accession: Cerubank accession numbers	
Piery CAT number Accessions 35 108447 434527 108505 12702_1 AA079126 108505 12702_1 AA098987 AA084995 108505 12702_1 AA098987 AA0989895 108505 12702_1 AA0989897 AA0989897 108505 12702_1 AA0989897 108505 12702_1 AA0989897 108505 12702_1 AA098987 108505 12702_1 AA0989897 108505 12702_1 AA0989897 108505 12702_1 AA0989897 108505 12702_1 AA098987 108505 12702_1 AA09887	
35 108407 43452_7 AAU79126 AAU8487 AAB4995 AAU8487 AAB4995 AAU8487 AAB4995 AAU8487 AAB4995 AAU8497 AAU84995 AAU8497 AAU84995 AAU8497 AAU84995 AAU8497 AAU84995 AAU8497 AAU84995 AAU8497 AAU849	
35 108550 12703_1 AAB4867 AAB4968 108655 12752_1 108550 12752_1 108550 12752_1 108561 12752_1 108561 12752_1 108561 12752_1 108561 12752_1 108561 12752_1 1275	
35 108550 2073_1 AAB4867 AA08498 A10013 108555 12752_1 108555_1 108555_1 10855_1 1	
109565 127522_1 AA05980_A113013 102397 44371_1 Ut1898 125303 152593_1 107884 1797880 40 105627 2512_2 Z48513_248512 121366 29040_1 A745315_AA45817_AW276706	
102397 443711 U41998	
125303 1252503 1 07884 178880 1 125004 1 1550044 1 150005 R91002 2 1500 1 1550044 1 100005 R91002 2 1250 1 12500 1 125	
40 103627 2515_2 Z48513 Z48512 121366 280401_1 A1743515 AA405617 AW276706	
40 103627 2615_2 Z48513 Z48512 121366 280401_1 AI743515 AA405617 AW276706	
114609 116777_1 AA079505 AA079537	
115272 172113.1 AW015947 AA211890 AA279425	
108338 112186_1 AA070773 AA070774	
45 108434 114012.1 AA078899 AA078782 AA075788	
123802 genbank_AA620448 AA620448	
102310 NOT_FOUND_entrez_U33839 U33839	
102636 entrez_U67092_U67092	
104776 genbank_AA026349 AA026349	
50 120504 genbank AA256837 AA256837	
113502 genbank_T89130T89130	
108499 genbank_AA083103 AA083103	
101308 entrez_L41390 L41390	
108629 genbank_AA102425 AA102425	
55 103098 221_215 M86361 Z26593 X02850 D13070 AE000559 M17649 M87869 M87871 X61077 M16286 AF018169 X61079	359351 X60142 AF043169
103241 entrez_X76223 X76223	
103508 entrez_Y10141 Y10141	
103575 entrez_Z26256 Z26256	
119514 NOT_FOUND_entrez_W37937 W37937	
60 121082 genbank_AA398722 AA398722	
128634 AA464918_at AA464918	
105817 genbank AA397825 AA397825	
12f518 genbank_AA412f55 AA412166	
114449 genbank_AA020736 AA020736 6.5 114548 genbank_AA101056 AA101056	
121950 genbank_AA429515 AA429515	
107723 genbank_AA015967 AA015967	

PCT/US02/12476 WO 02/086443

Table 34 shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chrock non-matignant lung diseases such as throsts, emphysems, and bronchits. These genes were selected from 35580 probession in the Entul/Alfrendix Hald Generalia grang. Gene aupression data for each probession date from this analysis was expressed as exempts intently (All), a normalized value refloring the netable veries of mRMA expression.

5	Pkey: ExAcon: Unigenel	Exemp D: Uniger	olar Accession on ne number	identifier number number, Genbank accession number			
10	Unigene R1: R2:	80th or	ne gene title ercentile of AI f ercentile of AI f	for chronically diseased lung samples divided by the 9 for chronically diseased lung samples divided by the 9	Oth percentile Oth percentile	of Al for not of normal h	mal lung samples. ng samples, squamous cell carcinomas and
	R3:	adenor 70th po divideo	carcinomas ercentile of Al I I by the 90th po	for chronically diseased lung samples minus the 15th	percentile of A	d for all nor	nal lung, chronically diseased lung and turnor samples nas minus the 15th percentile of Al for all normal lung,
15		Carona	cany diseased i	long and tornor samples			
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2	R3
	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
20	135378	AW961818	Hs.24379	MUM2 protein			2.13
	135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
	135235	AW298244	Hs.293507	ESTs	12.40		
	135057	U90268	Hs.93810	cerebral cavemous malformations 1	11.67		
25	134951	BE305081	Hs.169358	hypothetical protein		8.00 8.20	
23	134799 134786	M36821 T29618	Hs.89690 Hs.89640	GRO3 oncogene TEK tyrosine kinase, endothelial (venous		0.20	
	134772	NM_000829	Hs.163697	glutamate receptor, ionotrophic, AMPA 4	29.80		
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
	134749	T28499	Hs.89485	carbonic anhydrase IV			2.07
30	134696	BE326276	Hs.8861	ESTs			
	134636	NM_005582	Hs.87205	lymphacyte antigen 64 (mouse) homolog, r	13.60		4.00
	134627	AI018768	Hs.12482	glyceronephosphale O-acyltransferase			1.92 1.92
	134622 134570	AW975159 U66615	Hs.293097 Hs.172280	ESTs, Wealdy similar to A55380 faciogeni SWI/SNF related, matrix associated, acti	13.20		1.02
35	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	10.2.5		1.78
55	134468	NM 001772	Hs.83731	CD33 antigen (gp67)		6.20	
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci			
	134343	D50683	Hs.82028	transforming growth factor, beta recepto			
40	134323	BE170651	Hs.8700	deleted in liver cancer 1			
40.	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1 complement component C1q receptor			
	134299 134253	AW580939 X52075	Hs.97199 Hs.80738	sialophorin (op.L115, leukosialin, CD43)	20.60		
	134182	D52059	Hs.7972	KIAA0871 protein	12.20		
	133985	L34657	Hs.78146	platelet/andothelial cell edhesion molec			
45	133978	AF035718	Hs.78061	transcription factor 21			
	133835	AI677897	Hs.76640	RGC32 protein			•
	133651 133633	Al301740 D21262	Hs.173381 Hs.75337	dihydropyrimidinase-like 2 nucleolar and colled-body phosphprotein	15.20		
	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	10120		
50	133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAVL			1.77
	133488	AA335295	Hs.74120	adipose specific 2			
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
	133337	AF085983	Hs.293676	ESTs		9.60	1,77
55	133200 133153	AB037715 AF070592	Hs.183639 Hs.66170	hypothetical protein FLJ10210 HSKM-B protein	30.60		i.ii
33	133130	AI128606	Hs.6557	zinc finger protein 161	22.60		
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-blnding protein			
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		
	132836	AB023177	Hs.29900	KIAA0960 protein			
60	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60		
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40	7.20	
	132548 132476	X12830 AL119844	Hs.193400 Hs.49476	interfeukin 6 receptor Homo saplens clone TUAS Cri-du-chat regi		4.76	
	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
65	132240	AB018324	Hs.42676	KIAA0781 protein	21,20		
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
	132199	AL041299	Hs. 165084	ESTs	15.20		1.76
	131751	T96555	Hs.31562	ESTs	27.80		1./6
70	131745	AI828559 NM_000246	Hs.31447 Hs.3076	ESTs, Moderately similar to A46010 X-II MHC class II transactivator	21.00	4.00	
70	131694 131686	NM_000246 NM_012296	Hs.30687	GRB2-associated binding protein 2		-1100	
	131676	Al126821	Hs.30514	ESTs		6.20	
	131629	Z45794	Hs.238809	ESTs	21.40		
	131589	C18825	Hs.29191	epithelial membrane protein 2			
75	131536	AA019201	Hs.269210	ESTs		9.40	
	131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59 4.48	
	131355 131253	R52804 R71802	Hs.25956 Hs.24853	DKFZP584D206 protein ESTs	15.00	4.40	
	131207	AF104266	Hs.24212	latrophilin			1.75
80	131156	AJ472209	Hs.323117	ESTs			1.84

ESTS
ESTS
KIAA1796 protein
guanine nucleotide blading protein (G pr
hypothetical protein DKFZp564L0864 simil

Hs.24212 Hs.323117 Hs.22588 Hs.268744 Hs.296261 Hs.21015 Hs.1898

131066 AW169287 131061 N64328 131053 AA348541 130895 AA641767 130762 D84371

85

3.54 1,93

16.60 12.00

		O 02/086	443				
	130657	AW337575	Hs.201591	ESTs			
	130655	AI831962	Hs.17409	cysteine-rich protein 1 (intestinal)			2.08
	130589 130562	AL110226 D50402	Hs.16441 Hs.182611	OKFZP434H204 protein			1,91
5	130552	R69743	Hs.116774	solute carrier family 11 (proton-coupled integrin, alpha 1		9.60	1.31
,	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60	5.50	
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr		6.60	
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator			1.91
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20		
10	129958 129898	R27496 Al672731	Hs.1378 Hs.13256	annexin A3 ESTs		5.05	
	129675	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60		
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	10.00		
	129626	F13272	Hs.111334	ferritin, light polypeptide			
15	129598	N30436	Hs.11556	Home sapiens cDNA FLJ12566 fis, clone NT	22,63		
	129593	Al338247	Hs.98314	Homo saplens mRNA; cDNA DKFZp586L0120 (f			
	129565 129527	X77777 AA769221	Hs.198726 Hs.270847	vasoactive intestinal peptide receptor 1 della-tubulin	39.20		2.53
	129402	W72062	Hs.11112	ESTs	35.20		2.11
20	129385	AA172106	Hs.110950	Rag C protein	15.20		
	129315	NM_014563	Hs.174038	soondyloeolohyseal dysplasia, late	12.40		
	129312	T97579	Hs.110334	ESTs, Weakly similar to 178885 serine/th	20.83		
	129240	AA361258	Hs.237868	Interleukin 7 receptor			1.95
25	129210 129122	AL039940 AW958473	Hs.202949 Hs.301957	KIAA1102 protein nudix (nucleoside diphosphate linked mol		4.20	
23	129057	N90866	Hs.276770	CDW52 anligen (CAMPATH-1 anligen)		4.20	
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3		5.20	
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2			
20	128789	AW368576	Hs.139851	caveolin 2			2.24
30	128778	AA504776	Hs.186709	ESTs, Weakly similar to 138022 hypothet	12.20 26.40		
	128766 128631	AW160432 R44238	Hs.296460 Hs.155546	craniofacial development protein 1 KIAA1080 protein; Golgi-associated, gamm	20.40		1.78
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH			2.51
	128609	NM 003616	Hs.102456	survival of motor neuron protein interac	16.00		
35	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80		
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s		4.00	
	128458 128061	H55884 AF150882	Hs.56340 Hs.186877	ESTs sodium channel, voltage-gated, type XII,	17.20		
	127968	AA830201	Hs.124347	ESTs	21.30		
40	127959	Al302471	Hs.124292	Homo saplens cDNA: FLJ23123 fis, clone L	21100		
	127944	AJ557081	Hs.262476	S-adanosylmethionine decarboxylase 1	10.60		
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40		
	127896	A1669586	Hs.222194	ESTS	14.00	7.00	
45	127859 127817	AA761802 AA836641	Hs.291559 Hs.163085	ESTs ESTs	14.00		
45	127742	AW293496	Hs.180138	ESTS	11.00		
	127628	AI240102	Hs.322430	NDRG family, member 4	11.10		
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture			
	127582	AA908954	Hs.130844	ESTs	19.60		
50	127543 127535	AK000787 AA568424	Hs.157392	Homo saplens cONA FL/20760 fis, clone CO ESTs	15.40 17.50		
	127404	Al379920	Hs.164450 Hs.270224	ESTS	14.60		
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40		
	127374	AA442797	Hs.312110	ESTs. Weakly similar to 138022 hypothet	14.60		
55	127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	21.00		
	127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN91_HUMAN ZINC	15.80		
	127307 127242	AW962712 AW390395	Hs.126712 Hs.181301	ESTs, Wealdy similar to AF191020 1 E2IG5 cathepsin S	22.60		
	127167	AA625690	Hs.190272	ESTs .	21.40		
60	127048	AA321948	Hs.293968	ESTs	41.20		
	126928	AA480902	Hs.137401	ESTs	11.00		
	126900	AF137386	Hs.12701	plasmolpin		5.60	1.78
	126852 126816	AA399961 AA248234		gb:zu68c01.r1 Soares_testis_NHT Homo sap gb:csg2228.seq.F Human fetal heart, Lamb	12.20	5.00	
65	126812	AB037860	Hs.173933	nuclear factor I/A	17.19		
0.5	126666	AA648886	Hs.151999	FSTs	13.57		
	126845	AA316181	Hs.81635	six transmembrane epithelial antigen of	15.40		
	126592	Al611153	Hs.6093	Homo saplens cDNA: FLJ22763 tis, clone K		4.67	
70	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00 16.77		
70	126433 126299	AA325606 AW979155	Hs.298275	gb:EST28707 Cerebellum II Homo seplens c	14.60		
	126299	AU049801	Hs.13649	amino acid transporter 2 Novel human gene mapping to chomosome 13	14.00	3.50	
	126182	AA721331	Hs.293771	ESTs	13.40		
	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20		
75	126142	H86281	Hs.40568	ESTs	14.00		
	126077	M78772	Hs.210836	ESTs	16.59		
	125994 125934	Al990529 AA193325	Hs.270799	ESTs hypothelical protein FLJ21901	17.40 13.00		
	125934	AW161885	Hs.32646 Hs.249034	ESTs	49.57		
80	125831	H04043		gb:yj45c03.r1 Soares placenta Nb2HP Homo			
	125731	R61771	Hs.26912	ESTs	13.20		
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20		
	125561	F18572	Hs.22978	ESTs, Wealdy similar to ALU4_HUMAN ALU S ESTs, Wealdy similar to I38022 hypotheti	12.60		
85	125552 125489	H09701 H49193	Hs.278366 Hs.124984	ESTs, Weakly similar to ISSU22 hypotheti ESTs, Moderately similar to ALU7_HUMAN A	12.60 33.40		
95	12,5403		. 4. 14.100	20.4			

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WU 02/086443	PC 1/USUZ/124/6

	125422	AA903229	Hs.153717	ESTs			1.80
	125331	AM22996	Hs.161378	ESTs	38.00 18.20		
	125309 125167	T12411 AL137640	Hs.183745 Hs.102541	hypothetical protein FLJ 13456 natrin 4	10.20		1.95
5	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to			1.84
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80		
	124711 124631	NM_004657 NM_014053	Hs.26530 Hs.270594	serum deprivation response (phosphatidy) FLVCR protein	23.20	10.60	
	124578	N68321	Hs.231500	EST	21.43		
10	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2			1.77
	124472	N52517	Hs.102670	EST	37.20		
	124438 124357	BE178536 N22401	Hs.11090	membrane-spanning 4-domains, subfamily A gb:yw37g07.s1 Morton Fetal Cochlea Homo	14.64		
	124306	AW973078	Hs.293039	ESTs		4.00	
15	124214	H58608	Hs.151323	ESTs			
	124097	AW298235	Hs.101689	ESTs ESTs		27.20	2.03
	123978 123972	T89832 T46848	Hs.170278 Hs.70337	immunoglobulin superfamily, member 4		6.00	200
	123961	AL050184	Hs.21610	DKFZP434B203 protein			1.79
20	123936	NM_004673	Hs.241519	angiopoletin-like 1		15.80	
	123802	AA620448	Hs.312447	gb:ae58c09.s1 Stratagene lung carcinoma FSTs		4.23 4.20	
	123734 123619	AA609861 AA602964	HS.312447	gb:ne97c02.s1 NCI_CGAP_Pr2 Homo saplens	33.60	4.20	
	123596	AA421130	Hs.112640	EST	10.93		
25	123476	AA384564	Hs.108829	ESTs	44.00		2.18
	123340	AA504264 AA489212	Hs.182937 Hs.105228	peptidylprolyl isomerase A (cyclophilin EST	11.20 14.20		
	123190 123136	AM451999	Hs.194024	ESTS		7.00	
	123073	AA485061	Hs. 105652	ESTs	31.20		
30	123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcri		4.80 5.00	
	122699 122679	AA456130 AAB11286	Hs.301721 Hs.192837	KIAA1255 protein ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40	5.00	
	122633	NM_001546	Hs.34853	Inhibitor of DNA blading 4, dominant neg			
	122553	AA451884	Hs. 190121	ESTs	40.00		
35	122544	AW973253	Hs.292689	ESTs	15.40		1.81
	122485 122211	AA524547 AA300900	Hs.160318 Hs.98849	FXYD domain-containing ion transport reg ESTs, Moderately similar to AF161511 1 H		12.10	1.01
	122127	AW207175	Hs.106771	ESTs			1.95
	122011	AA431082		gb:zw78a10.s1 Soares_testls_NHT Homo sap			1.89
40	121992	AI860775	Hs.98506	ESTs		3.60	2.01
	121989 121835	W56487 AB033030	Hs.193784 Hs.300670	Homo sapiens mRNA; cDNA DKFZp586K1922 (f KIAA1204 protein			1.85
	121726	AF241254	Hs.178098	angiotensin i converting enzyme (peptidy	12.43		
	121690	AV660305	Hs.110286	ESTs			1.82
45	121643 121633	AA640987 AA417011	Hs.193767 Hs.98175	ESTs EST	14.00		
	121622	AA416931	Hs.126065	ESTs	14.00	16.40	
	121497	AA412031	Hs.97901	EST	11.20		
50	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20		1.83
50	121314 121242	W07343 AA400857	Hs. 182538 Hs. 97509	phospholipid scramblase 4 ESTs	22.40		1.63
	121059	AA393283	113.31303	ob:zt74e03.r1 Soares_testis_NHT Homo sap	14.80		
	120934	AA226198		abanc26a07.s1 NCI_CGAP_Pr1 Homo septens	21.20		
55	120755	AA312934	Hs.190745	Homo saplens cDNA: FLJ21326 fis, clone gb:ob39a05.s1 NCI_CGAP_GCB1 Homo saplens	20.00		1.79
33	120637 120484	AA811804 AA253170	Hs.96473	FST NCI_CGAP_GCD1 Hollo sapitals	40.20		
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60	
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheli	16.80	4.73	
60	120132 120041	W57554 AA830882	Hs.125019 Hs.59368	ESTs ESTs		4.73	1.75
00	119996	W88996	Hs.59134	EST		7.20	
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20		
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78	
65	119824 119740	W74536 AW021407	Hs.184 Hs.21068	advanced glycosylation end product-speci hypothetical protein	20.20		
05	119271	AID61118	Hs.65328	Fanconi snemia, complementation group F	15.20		
	119221	C14322	Hs.250700	tryptase beta 1			
	119126	R45175	Hs.117183	ESTs	12.60		
70	119073 118928	BE245360 AA312799	Hs.279477 Hs.283689	ESTs activator of CREM in testis		10.00	
70	118901	AW292577	Hs.94445	ESTs		3.96	
	118661	AL137554	Hs.49927	nmtein kinase NYD-SP15		9.60	
	118607	Al377444	Hs.54245	ESTs, Weakly similar to \$65824 reverse t	10.40		1.90
75	118449 118416	AI813865 N66028	Hs.164478 Hs.49105	hypothetical protein FLJ21939 similar to FKBP-associated protein	16.20		1.30
15	118379	N64491	Hs.48990	FSTs		4.00	
	118329	N63520		cb:vy62/01.s1 Soares_multiple_sclerosis_		6.60	
	118320	N63451 AA497044	Hs.141600	ESTs. Weakly similar to alternatively s	17.60	3.80	
80	118253 118124	N56968	Hs.20887 Hs.46707	hypothetical protein FLJ10392 chromosomo 21 open reading frame 37	14.00		
00	118056	AB037746	Hs.42768	hypothetical protein DKFZp761O0113			1.86
	118032	N52802	Hs.47544	- FST		5.00 4.00	
	117840 117404	T26379 N39725	Hs.48802 Hs.15220	Homo saplens clone 23632 mRNA sequence zinc finger protein 106		4.00	1.90
85	117314	N32498	Hs.15220 Hs.42829	ESTs	14.20		

		U 02/080					
	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f			2.31
	116814	H50834		gb:yp66a10.s1 Soares fetal fiver spieen	20.20		
5	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
,	116766	AI608657	Hs.95097	ESTs	16.20	6.80	
	116712	AW901618 H10344	Hs.61935 Hs.49050	Homo sapiens mRNA; cDNA DKFZp761l071 (fr ESTs, Wealdy similar to A Chain A, Human	18.60	0.80	
	116707 116351	AL133623	Hs.82501	similar to mouse Xm1 / Dhm2 protein	19.40		
	116279	AU971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	19.40		
10	116166	AL039940	Hs.202949	KIAA1102 prolein			2.13
10	116152	AL040521	Hs.15220	zinc finger protein 106			1.75
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970			2.36
15	115955	AF263613	Hs.44198	intracellular membrane-associated calciu	18.20		
	115844	Al373062	Hs.332938	hypothetical protein MGC5370	18.57		
	115683	AF255910	Hs.54650	functional adhesion molecule 2		23.00	
	115673	AA406341	Hs.269908	Homo saplens cDNA FLJ11991 fis, clone HE	11.82		
	115672	Al889110	Hs.73251	ESTs	10.60		
20	115566	Al142336	Hs.43977	Human DNA sequence from clone RP11-196N1			1.76
	115313	AA808001	Hs.184411	albumin	25.20		
	115279	AW964897	Hs.290825	ESTs		8.00	
	115230	AA278300	Hs.124292	Homo saplens cDNA: FLJ23123 fis, clone L.			1.80
25	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
23	114999	BE246481	Hs.87856	ESTs	19.20		
	114930 114922	AA237022 AA235672	Hs.188717	ESTs ESTs		5.60 3.60	
	114837	BE244930	Hs.87491 Hs.166895	ESTS	43.70	3.00	
	114769	AA149060	Hs.296100	ESTS	11.00		
30	114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
50	114736	AJ610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A	14.00	4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71	4.20	
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALUS_HUMAN ALU S	20.40		
35	114452	Al369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5			2.09
	114357	R41677	Hs.6107	Homo saplans cDNA FLJ 14839 fis, clone OV	12.40		
	114251	H15261	Hs.21948	ESTs			2.00
	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
40	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo saplens cDNA FLJ13510 fis, clone PL			1.82
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN IIII			
	113606	NM_013343	Hs.278951	NAG-7 protein		2.00	2.15
45	113590	R49642	Hs.142447 Hs.268626	ESTs, Weakly similar to ALU1_HUMAN ALU S	32.00	3.60	
43	113560 113552	T91015 Al654223	Hs.16026	ESTs hypothetical protein FLJ23191	32.00		
	113532	AW152618	Hs.16757	ESTs			
	113502	T89130	110.10757	gh:ye12d01.s1 Stratagene lung (937210) H		8.35	
	113288	AI076B3B	Hs.12967	ESTs	12.40	0.00	
50	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	12.10	4.27	
	113238	R45467	Hs.189813	ESTs			
	113203	AA743563	Hs.10305	ESTs	21.20		
	113195	H83265	Hs.8881	ESTs, Weekly similar to S41044 chromosom			1.92
	113089	T40707	Hs.270862	ESTs	14.33		
55	113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti		12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
60	112794	R97018		gb:yq74b08.s1 Soares fetal liver spleen	26.60		
00	112691	R88708	Hs.220647	ESTs	15.33		
	112602 112366	AW004045 AF036318	Hs.203365 Hs.12533	ESTs Homo saplens clone 23705 mRNA sequence	15.60 15.40		
	112210	R49645	Hs.7004	ESTs	14.00		
	112064	AL049390	Hs.22689	Homo saplens mRNA; cDNA DKFZp58601318 [f	13.00		
65	111998	R42379	Hs.138283	ESTs	11.00		
05	111987	NM.015310	Hs.6763	KIAA0942 protein	22.40		
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	22.70		1.77
	111737	H04607	Hs.9218	ESTs			1.86
	111605	T91061	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00		
70	111510	R07856	Hs.16355	ESTs	11.02		
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr			1.88
	111280	AA373527	Hs.19385	CGL-58 nmleln	18.40		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp56482062 (f			
76	111232	A1247763	Hs.16928	ESTs	27.60		
75	110942	R63503	Hs.28419	ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-lingers and homeoboxes 1	24.71		0.40
	110837	H03109	Hs.108920	HTO18 protein	40.00		2.18
	110824	AI767183	Hs.26942	ESTs	12.20		1.75
80	110776	AB032417 H60869	Hs.19545	frizzied (Drosophila) homolog 4 ESTs	13.00		1.75
00	110576 118369	AK000768	Hs.37889 Hs.107872	hypothetical protein FLJ20761	10.00	5.60	
	110099	R44557	Hs.23748	ESTs		3.00	2.31
	109984	Al796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL			2.0.
	109958	AA001266	Hs.133521	ESTs	11.25		
			Hs.30484	ESTs			2.68
85	109893	AA884208					

		O 02/086					
	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to 138022 hypotheti			3.91
	109796	AI800515	Hs.12024	ESTs		17.20	
_	109688	R41900	Hs,22245	ESTs		9.60	
5	109548	H17800	Hs.7154	ESTs	22.80		
	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			1.89
	109523	AW193342	Hs.24144	ESTs		6.00	1.09
10	109472	AK001989	Hs.91165 Hs.48297	hypothetical protein DKFZP586C1620 protein	15.00	0.00	
10	109355	AA524525	Hs.131915		25.60		
	109260	AW978515	HS.131915	KIAA0863 protein gb:zn98g07.st Stratagene fetal retina 93	14.20		
	108663	AA128654 BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti	11.00		
	108573	AA086005	NS.232000	gh:zi84c04.s1 Stratagene colon (937204)	26.00		
15	108480	AL133092	Hs.68055	hypothetical protein DKFZp434l0428	20.00		
10	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str			1.83
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	ALD49990	Hs.51515	Homo saplens mRNA; cDNA DKFZp584G112 (fr		3.60	
	108087	AA045708	Hs.40545	ESTs	15.44		
20	108048	AI797341	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1			
	107922	BE153855	Hs.61460	le superfamily receptor LNIR	14.20		
25	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
	107666	AA010511	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292	BE166479	Hs.4789	Homo saplens serologically defined breas	32.00		
20	107230	AI034467	Hs.34650	ESTs	17.40		
30	107168	W57578	Hs.237955	RAB7, member RAS encogene family	10.43		
	107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
	107054	A1076459	Hs.15978	KIAA1272 protein	21.40		
	107029	AF264750 H93281	Hs.288971 Hs.10710	myeloid/lymphold or mixed-lineage teukem	35.80		
35	106999		Hs.204038	hypothetical protein Ft.J20417 Indolethylamine N-methyltransferase	30.60		1.76
33	106954 106870	AF128847 AI983730	Hs.26530	serum deprivation response (phosphatidy)			1.70
	106865	AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6	10.10	7.13	
	106820	NM 016831	· Hs.12592	period (Drosophila) homolog 3		7.00	
40	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
-10	106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL			2.05
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF Interact	12.60		
	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
45	106667	AW360847	Hs.16578	ESTs			
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			240
	106567	AW450408	Hs.86412	chromosome 9 open reading frame 5			1.78
	106562	AL031846	Hs.152151	plakophilin 4			1.76
50	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	23.20		2.19
50	106533	AL134708	Hs.145998	ESTs	15.20		
	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (Inhib	15.20		
	106490	AA404265	Hs.115537 Hs.42484	putative dipeptidase hypothetical protein FLJ10518	10.44		
	106474	BE383668	Hs.126083	ESTs	10.44	29.80	
55	106211 105986	AA428240 AB037722	Hs.8707	KIAA1301 protein		3.70	
33	105894	Al904740	Hs.25691	receptor (calcitonin) activity modifying			1.94
	105847	AW964490	Hs.32241	ESTs, Weakly similar to \$65657 alpha-1C-			1.75
	105803	AW747996	Hs.160999	ESTs. Moderately similar to A56194 throm			2.47
	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
60	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
	105688	AJ299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
	105101	H63202	Hs.38163	ESTs		8.30	
	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
65	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
	104969	A1670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903	AJ436323	Hs.31141	Homo saplens mRNA for KIAA1568 protein,	40.00	7.60	
	104896	AW015318	Hs.23165	ESTs	13.80		
70	104865	T79340	Hs.22575	Homo saplens cDNA: FLJ21042 fis, clone C FSTs			1.87
70	104825	AA035613	Hs.141883	DKFZP434B203 protein			1.93
	104781	AA099904 AA026349	Hs.21610	gb:zj99f01.s1 Soares_pregnant_uterus_NbH		10.20	1.00
	104776 104691	VAU26349 UZ9690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
	104667	Al239923	Hs.30098	ESTs		3.82	
75	104667	H58762	10,00000	gb:EST00057 HE6W Homo saplens cDNA clone		4.20	
,,	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ 10229 fis, clone HE	27.20		
	104392	AB002298	Hs.173035	KIAA0300 protein	2.00		1.91
	104212	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
	103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
80	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD			- 1.80
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496	Y09267	Hs.132821	flavin containing monocxygenase 2			
	103428	BE383507	Hs.78921	flavin containing monocxygenase 2 A kinase (PRKA) anchor protein 1	11.20		
85	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

	w	O 02/0864	143					PCT/US02/12476
	103295	X81479	Hs.2375	eaf-like module containing, mucin-like,		3.60		
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula				
	103100		Hs.184585	LIM domain only 2 (rhombolin-like 1)			1.76	
	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t			2.15	
5	102698	M18667	Hs.1867	progastricsin (pensinogen C)				
,	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00			
	102580	U60808	Hs.152981	CDP-diacylolycerol synthase (phosphatida	25.40			
	102417		Hs.153487	signal transducing adapter molecule (SH3	14.00			
	102363		Hs.198241	amine oxidase, copper containing 3 (vasc				
10	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86			
10	102283		Hs.83381	guanine nucleotide binding protein 11				
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1		7.40		
	102151		Hs.3132	steroidogenic acute regulatory protein	16.40			
	102151	127013	Hs.74101	solenn tyrosine kinase	15.40			
15	101842	M93221	Hs.75182	mannose receptor, C type 1	10.10			
13	101842		Hs. 153837	myeloid cell nuclear differentiation ant				
			Hs. 153837 Hs. 81256	S100 calcium-bloding protein A4 (calcium			1.78	
	101764			tachykinin, precursor 1 (substance K, su	18.80		1.70	
	101716	AF050658	Hs.2563		10.00		2.22	
20	101678	M62505	Hs.2161	complement component 5 receptor 1 (CSa I	504.80		2.22	
20	101447	M21305		gb:Human alpha satellite and satellite 3	004.00	31.00		
	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co		31.00	1.75	
	101348	AI738616	Hs.77348	hydroxyprosteglandin dehydrogenase 15-(N			1.75	
	101345	NM_005795	Hs. 152175	calcitonin receptor-like			2.24	
0.5	101336	NM_006732	Hs.75678	FBJ murine osleosarcoma viral oncogene h			2.24	
25	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4				
		L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00			
	101168		Hs.211569	G protein-coupled receptor kinase 5			2.01	
		NM_003243	Hs.79059	transforming growth factor, beta recepto				
30	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte		7.52		
	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38			
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte			1.91	
	100893		Hs.180789	S164 protein	15.40			
	100770			amyloid beta (A4) precursor protein (pro	11.20			
35	100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80			
	100555	M69181		gb:Human nonmuscle myosin heavy chain-B	33.00			
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20			
	100408	D86640	Hs.56045	are homology three (SH3) and cysteine ri		4.00		
		D83407	Hs.156007	Down syndrome critical region gene 1-lik		4.24		
40	100351			•		6.20		
	100299	D49493	Hs.2171	growth differentiation factor 10		21.20		
	100134	AA305746	Hs.49	macrophage scavenger receptor 1				
	100108	U09577	Hs.76873	hyaluronoglucosaminidase 2			1.79	
	100095	Z97171	Hs.78454	myocilin, trabecular meshwork inducible		5.40		
45	100066				11.29			

TABLE 39 shows the accession numbers for those primaterys leading uniquealD's for Table 34. For each probeset we have listed the gone cluster number from which the objecticities were designed. Gene clusters were compiled using sequences derived from Genbenk ESTs and mRNAs. These sequences were clustered based on sequences of semilarly using Caustring and Alignment Tools (Double's list, California). The Genbenk accession numbers for sequences comprising each cluster are listed in the "Accession" column.

55	Accessio	n: Genbank a	ccession num	nbers
60	Pkey	CAT number	Accession	s
	123619	371681_1	AA602964	AA609200
	126433	127143 1	AA325606	AA099517 N89423
	125831	1522905_1	H04043 D	60988 D60337
	126816	122973 1	AA248234	AA090985
65	126852	136135 1	AA399961	AA128347
	121059	273450_1	AA393283	AA398628
	120637		AAB11804	AA809404 AA286907 AW977624
		76172	AA431082	
	120934		AA226198	AA226513 AA383773
70	123802	genbank_AA6	20448	AA620448
	116814	genbank_H508	334	H50834
	118329		20	N63520
	104404	H58762 at	H58762	
	104776	genbank AA0:	26349	AA026349
75	113502		30T89130	
	101262	entrez_L35854	L35854	
	108573			AA086005
	101447	entrez_M2130	5 M21305	
	124357	genbank_N224	101	N22401
80	108781	genbank AA1	28654	AA128654
	112794	genbank R976	18	R97018
	100351	entrez D6415	B D64158	
	100555	6gr_HT2245	M69181 N	AB1 105 U51039
85				

Pkey; Unique Eos probesel Identifier number CAT number: Gene cluster number

55

Table 44 shows 22 (pore sup-regulated in samples from patients treated with chemoflurary) or radiotherapy. These genets were selected from 59590 probesets on the Scalkflymark Hu30 Genechip array. Cone expression data for each probeset obtained from this enalysis was expressed as average Intensity (AI), a normalized value reflecting the neither level of mRN4 expression.

Plezy: Unique Eos probesel identifier number
Exboan: Exemple Accession number, Genbank accession number
UniquentEl: UniquentEl
Uniqu 5

• •	R1:	average of	Al for samples	s from patients treated with chemotherapy or radioliner	ipy aivided
10				to to the way	R1
	Pkey	ExAcen	UnigenelD	Unigene Title	KI
	400440	NM 001269	Hs.84746	chromosome condensation 1	27.20
	100113		Hs.78183	aldo-keto reductase family 1, member C3	20.60
15	100187 100210	D17793 D26361	Hs.3104	KIAA0042 gene product	20.40
13	100210	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
	100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
	100438	AA013051	Hs.91417	topolsomerase (DNA) II binding protein	23.50
	100877	X80821	Hs.27973	KIAAD874 protein	35.56
20	100893	BE245294	Hs.180789	S164 protein	43.40
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
	101447	M21305		gb:Human alpha satellite and satellite 3	193.60
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
~ ~	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80 78.60
25	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris entigen	162.20
	101809 101879	M86849 AA176374	Hs.323733 Hs.243886	gap junction protein, beta 2, 26kD (conn nuclear autoantigenic sperm protein (his	50.00
	101915	AF207881	Hs.155185	cytosofic ovarian carcinoma antigen 1	26.00
	101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
30	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
50	102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
	102052	NM_002202	Hs.505	ISL1 transcription factor, LIMhomeodoma	51.20
	102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
	102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
35	102610	U65011	Hs.30743	preferentially expressed antigen in mala	110.60
	102829	NM_006183	Hs.80962	neurotensin -	116.80 2.30
	103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	181.40
	103036	M13509	Hs.83169 Hs.296323	matrix metalloproteinase 1 (Interstitia) serum/glucocorticoid regulated kinase	49.20
40	103507 103587	AJ000512 BE270266	Hs.82128	5T4 oncofetat trophoblast glycoprotein	86.60
70	104560	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
	104896	AW015318	Hs.23165	ESTs	29.40
	105038	AW503733	Hs.9414	KIAA1488 protein	21.50
	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
45	105510	Z42047	Hs.283978	Homo saplens PRO2751 mRNA, complete cds	20.20
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
	106073	AL157441	Hs.17834	downstream neighbor of SON	25.40 32.00
	106205	AW965058	Hs.111583	ESTs, Weakly similar to 138022 hypotheti	40.60
50	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (ESTs	59.80
30	106533	AL134708	Hs.145998 Hs.105421	ESTA	43.40
	106575 106654	AW970602 AW075485	Hs.286049	phosphoserine aminotransferase	50.80
	106851	Al458623	115.200043	gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	53.40
	106995	AB023139	Hs.37892	KIAA0922 protein	20.88
55	107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20
	107922	BE153855	Hs.61460	lg superfamily receptor LNIR	49.00
	108609	BE409857	Hs.69499	hypothetical protein	19.67 48.17
C O	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17 59.20
60	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabidnes	28.60
	109260	AW978515 AK001355	Hs.131915 Hs.279610	KIAA0863 protein hypothetical protein FLJ10493	22.80
	109292	AW975746	Hs.188662	KIAA1702 protein	
	109384	AA219172	Hs.86849	FSTs	21.00
65	109415	U80736	Hs.110828	trinucleotide repeat containing 9	31.60
	109445	AA232103	Hs.189915	ESTs	24.20
	109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
	109633	AW003785	Hs.170267	ESTs	20.40
70	109786	AI989482	Hs.146288	kinesin family member 13A	19.60
70 ·	109958	AA001266	Hs.133521	ES7s	24.00 28.40
	110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi zinc-fingers and homeoboxes 1	36.00
	110924 111084	AW058463 H44186	Hs.12940 Hs.15456	PDZ domain containing 1	61.20
	111132	AB037807	Hs.83293	hypothetical protein	24.60
75	111229	AW389845	Hs.110855	ESTs	27.20
, 5	111337	AA837396	Hs.263925	LIS1-Interacting protein NUDE1, rat homo	48.00
	111987	NM_015310	Hs.6763	KIAA0942 protein	37.80
	112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
80	112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	28.40
	112871	AL110216	Hs.12285	ESTs, Weakly similar to 155214 salivary	47.64 22.00
	112897	AW206453	Hs.3782	ESTs	65.00
	112973	AB033023	Hs.318127	hypothetical protein FLJ10201 Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
85	112992 113073	AL157425 N39342	Hs.133315 Hs.103042	microtubule-associated protein 18	55.40
03	1130/3	1403042	na.103042	undergrand-grandenes brown to	

	w	O 02/086	143		
	113494	T91451	Hs.86538	ESTs	22,80
	113560 113849	T91015 AA457211	Hs.268626 Hs.8858	ESTs bromodomain adjacent to zinc finger doma	51.80
_	113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	28.20
5	114339 114365	AA782845 H42169	Hs.22790 Hs.18653	ESTs	20.20 21.00
	114455	H37908	Hs.16003 Hs.271616	hypothetical protein FLJ14627 ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
10	114824 114837	AA960961 BE244930	Hs.305953 Hs.166895	zinc finger protein 83 (HPF1) ESTs	27.20 30.20
10	114837	AW956931	Hs.179662	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084 115291	BE383668 BE545072	Hs.42484 Hs.122579	hypothetical protein FLJ10518 hypothetical protein FLJ10461	28.86 38.00
15	115313	AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909 116090	AW872527 AJ591147	Hs.59761 Hs.61232	ESTs, Weakly similar to DAP1_HUMAN DEATH ESTs	27.77 20.80
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
20	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099 117881	H93699 AF161470	Hs.260622	gb:yv16a11.s1 Soares fetal liver spleen butyrate-induced transcript 1	21.60 49.40
	118091	AW005054	Hs.47883	ESTs. Weakly similar to KCC1 HUMAN CALCI	22.40
25	118138	AA374756	Hs.93560	Homo saplens mRNA for KIAA1771 protein,	22.00
23	118720 118873	N73515 Al824009	Hs.44577	gb:za49d07.s1 Soares fetal liver spleen ESTs	20.00 19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro DKFZP586B0319 prolein	33.00 31.00
30	119940 120268	AL050097 AI807264	Hs.272531 Hs.205442	ESTe Waskly elmilar to T34036 hynotheli	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA826434 AA398209	Hs.1619 Hs.97587	achaete-scute complex (Drosophila) homol EST	95.40 105.20
	121054	AW976570	Hs.97387	ESTs	38.80
35	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335 122612	AA443258 AA974832	Hs.241551 Hs.128708	chloride channel, calcium activated, fam ESTs	30.80 19.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
40	123440	A1733692	Hs.112488	ESTs EST	23.17 23.00
40	123596 123619	AA421130 AA602964	Hs.112640	gb:ne97c02.s1 NCI_CGAP_Pr2 Homo sapiens	28.80
	124006	Al147155	Hs.270016	ESTs .	77.60
	124169 124281	BE079334 Al333756	Hs.271630 Hs.111801	ESTs arsenate resistance protein ARS2	22.20 42.20
45	124472	N52517	Hs.102670	EST PORT AND A	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631 124839	NM_014053 R55784	Hs.270594 Hs.140942	FLVCR protein ESTs	30.40 21.20
	125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
50	125321	TB6652	Hs.178294	ESTs	27.00 23.80
	125535 125646	NM_013243 AA628962	Hs.22215 Hs.75209	secretogranin III protein kinase (cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo saplens cDNA: FLJ21663 fis, clone C	21.20
55	125724 125847	AL360190 AW161885	Hs.295978 Hs.249034	Homo sapiens mRNA full length Insert cDN ESTs	48.80 31.00
33	125934	AA 193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299 126395	AW979155 Al468004	Hs.298275 Hs.278956	amino acki transporter 2 hypothetical protein FLJ12929	21.80 71.00
60	126433	AA325606		gb:EST28707 Cerebellum II Homo saplens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80 23.10
	126538 126666	AB030656 AA648886	Hs.17377 Hs.151999	coronin, actin-binding protein, 1C ESTs	36.00
	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
65	126872	AW450979	11- 000000	gb:UI-H-BI3-ala-a-12-0-UI.s1 NCL_CGAP_Su	46.29 22.80
	127046 127431	AA321948 AW771958	Hs.293968 Hs.175437	ESTs ESTs, Moderately similar to PC4259 femi	30.00
	127489	AA550250	Hs.272076	ESTs	20.80
70	127521 127742	AW297206 AW293496	Hs.164018 Hs.180138	ESTs ESTs	25.20 28.00
70	127742	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672	Hs.123304	ESTs	20.54
	127968 127987	AA830201 Al022103	Hs.124347 Hs.124511	ESTs ESTs	28.20 19.60
75	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40 53.80
	128777 128949	AI878918 AA009647	Hs.10526 Hs.8850	cysteine and glycine-rich protein 2 a disintegrin and metalloproteinase doma	23.00
	129168	Al132988	Hs.109052	chromosome 14 open reading frame 2	37.60
80	129404	Al267700	Hs.317584	ESTs	28.60 40.80
	129527 129574	AA769221 AA026815	Hs.270847 Hs.11463	delta-lubulin UMP-CMP kinase	31.20
	129598	N30436	Hs.11556	Homo saplens cDNA FLJ12566 fis, clone NT	29.60
85	129785 129970	H19006 AV655806	Hs.184780 Hs.296198	ESTs chromosome 12 open reading frame 4	72.20 22.20
05	129970	VAR02000	1197530139	CHONOCHIO IZ OPONICAGUNY NAME 4	22.20

WO 02/086443 PCT/US02/12476 Hs. 173655 methylenetetrahydrofolate dehydrogenase Hs. 173028 a disintegrin and metalloproteinase doma Hs. 155637 protein kinase, DNA-cafvaled, catalyfic Hs. 180059 Home sapiens cDNA FLJ20653 fis, chone KA Hs. 1574 bacutoviral IAP repeat containing 5 (sur Hs. 1574 glutamine-Inuctose-6-phosphate iransamin 130149 AW067805 29.60 Z48579 U63630 27.60 28.36 130199 130441 130466 130482 130617 20.20 W19744 5 22.40 AW409701 19.60 M00516 19.40 130703 R77776 Hs.18103 ESTB - cadherin 13, H-cadherin (heart) UDP glycosyltransferase 1 family, polype CCAAT/enhancer birding protein (C/EBP), chromogranin B (secretogranin 1) E1A binding protein SUAAB648 protein 130732 AW890487 Hs.63984 Hs.284239 Hs.2227 110.00 130867 NM 001072 10 AI879165 25.20 131028 40.60 AL035461 Hs.2281 131086 NM_001429 131284 Hs.25272 21.00 131775 AB014548 BE383676 Hs.31921 KIAAUS48 protein Rho guanina nudeotide exchange factor (replication factor C (activator 1) 4 (37 Homo saptens cDNA: FLJ22373 fis, clone H karyopherin alpha 3 (Importin alpha 4) ESTs 33.40 He 334 131860 BE383676 NM_002916 NM_001196 NM_002267 AA310393 15 131945 Hs.35120 Hs.315689 20.40 132040 29.40 132084 He 3886 Hs.190044 Hs.4859 32.40 132389 EST's Cycle L anis-69 both on the property of the Cycle L anis-69 both one prophogenetic protein 7 (osteopenic power of the Cycle L anis-69 both one prophogenetic protein pro AA152106 cyclin L ania-6a 27 40 132437 20 75.60 132550 AW969253 Hs.170195 31.36 Hs.5338 Hs.5398 132617 AF037335 AU076916 132632 132672 W27721 Hs.54697 23.40 AA025480 Hs.292812 61.20 132742 25 22.33 132771 Y10275 He 56407 133070 U92649 Hs.64311 133153 AF070592 Hs.66170 30.00

AB011155 NM_005025 NM_014781 134032 35 31.60 134125 Hs.50421 30.60 Hs.79428 134158 U15174 23.40 Hs.8172 134321 BF538082 49.20 134367 AA339449 Hs.82285 134570 U66615 NM_006482 AA448542 Hs. 172280 20.20 40 Hs.173135 Hs.251677 134753 135002 135029 37.60 H58818 Hs.187579 53.40 31.60 135047 AL134197 Hs.93597 135345 X53655

Hs.66744 Hs.286145 Hs.71573

Hs.75113

Hs.75426

Hs.170290

He 78580

Hs.99171

TABLE 48 shows the accession numbers for those primekeys lacking uniquealD's for Table 4A. For each probeset we have listed the gene cluster number from which the disponsibilities were designed. Gene clusters were complete using expansions derived from Genbank ESTs and nRPMs. These sequences were destanted based on seque intelliging the complete general control of the complete general properties and disponse and duster are lated to the complete general properties. The Genbank access numbers for expensions comprehenging and duster are lated in the 50

33 80 51 60

82.00

69.33

33.20

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

55

133181 X91662 AA449015

133282 30

133592 AV652066 133658 AA319146

133865

45

70

A1400220 133350

	Pkey	CAT number	Accessions
60	123619 126433 126872	371681_1 127143_1 142696_1	ALBIZORIA ALBIZORO ANZISSORIA AUGISTO TINBACZI ANKIGOTO JA AL (1955) ANTISORIA ANTISORIA ANGINI ANGINI SER ELEBANTA ANGINOSA ANGINOSA ANTISORIA BEDITIZE BEDITIZED BEDITIZET BEDITIZES BEDITIZES BEDITIZES BEDITIZES BEDITIZES
65	106851 118720 120515 117099 101447 123130	322947_1 genbank_N7351 genbank_AA258 321871_1 entrez_M21305 genbank_AA487	A458623 AA3S3709 AA485409 R22065 AA485570 5 N73515 N73515 S S S S S S S S S S S S S S S S S S

WU U2/U86443
PCT/US02/12476
Table 54 shows 600 geners up-regulated in squarmost cell carcinoma or adennocarcinoma lang lumors relative to normal lang and chronically diseased lung. These geners were secticed from 5000 protected on the EcolAfymetrix Hu30 Genechip array. Gane expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value relitecting the relative level of mRNA expression.

	5	Pkev:	Unique Eos probeset identifier number
		ExAcon:	Exemplar Accession number, Genbank accession number
		UnigenelD:	Unigene number
		Unigene Title:	Unigene gene title
		R1:	70th percentile of Al for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of Al for normal and chronically
- 1	0		diseased lung samples.
		R2:	80th percentile of All adenocarcinoma lung tumor samples divided by the 90th percentile of All for normal and chronically diseased lung samples.
		R3:	80th percentile of Al squamous cell carcinoma lung tumor samples divided by the 90th percentile of Al for normal and chronically diseased lung samples.
		R4:	80th percentile of Al adenocarchoma lung tumor samples divided by the 80th percentile of Al for squamous cell carchoma lung tumor samples.
	_	R5:	70th percentile of Al for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of Al for all normal lung, chronically
- 1	5		diseased lung and tumor samples divided by 90th percentile of Al for normal and chronically diseased lung samples minus the 15th percentile of Al for all
			normal lung, chronically diseased lung and lumor samples

20	Pkey	ExAcon	UnigeneID	Unigene Title	RI	R2	R3	R4	R5
20	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037			AFFX controt: GAPDH					5.75
	100071	A28102		Human GABAa receptor alpha-3 subunit		8.00			
25	100114	X02308	Hs.82962	thymidylate synthetase					5.71
23	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
	100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetythydrola	5.07				
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product					3.79
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	
	100486	T19006	Hs.10842	RAN, member RAS oncogene family					5.49
40	100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs.99949	protectin-induced protein				14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid				9.30	
45	100629	AA015693	Hs.21291	mitogen-activated protein kinase kinase				20.60	
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k			-1-00	10.00	
	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leuxem			24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			7.99
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1		40.00			7.55
	100867	U14622		gb:Human transketclase-like protein gene		10.20 8.00			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			5.16
	100906	AU076916	Hs.5398	guanine monphosphate synthetase	2.57				3.10
55	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.51				4.69
	101045	J05614		gb:Human proliferating cell nuclear anti					4.19
	101061	NM_000175	Hs.180532	glucose phosphate isomerase potassium voltage-gated channel, Shab-re		12.91			
	101071		Hs.84244 Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
60	101124	L10343 U82671	Hs.36980	melanoma antigen, family A, 2	3.50				
OU	101175	BE262521	Hs.73798	macrophage migration inhibitory factor (0.00				5.69
	101181	1.24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08				
	101210	L29301	Hs.2353	colold receptor, my 1			6.40		
	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
65	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (7.90
03	101233		Hs.878	sorbital dehydrogenase					4.45
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				
	101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase					4.17
	101346	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
70	101369	NM_000892	Hs.1901	kalikrain B, plasma (Fletcher factor) 1				12.80	
, 0	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small proline-rich protein 1B (comilin)					7.90
	101448	NM. 000424	Hs. 195850	keralin 5 (epidermolysis bullosa simplex	8.31				
	101462	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
75	101466	BE262660	Hs.170197	glutamic-oxeloacetic transaminase 2, mit					4.01
,,,	101484		Hs.20315	Interferon-induced protein with tetratri				12.00	
	101502			gb:Human parathyroid hormone-related pro	10.50				
	101505	AA307680	Hs,75692	asparagine synthelase					4.46
	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
80	101535	X57152	Hs.99853	fibrillarin					4.65
	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663		Hs.2178	H2B histone family, member Q	5.59				
	101664		Hs.121017	H2A histone family, member A	7.00				
85	101669		Hs.80409	growth errest and DNA-damage-inducible,		7.60			

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	101695	M69136	Hs.135626	chymase 1, mast cell	4.79					
	101724	L11690	Hs.620	bullous pemphigold antigen 1 (230/240kD)	15.21					
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	55.50					
~	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino					4.10	
5	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant				18.57		
	101804	M86699	Hs.169840	TTK protein kinase	4.50 140.00					
	101809 101833	M86849 AU076442	Hs.323733 Hs.117938	gap junction protein, beta 2, 26kD (conn collagen, type XVII, alpha 1	2.56					
	101842	M93221	Hs.75182	mannose receptor, C type 1	2.00			12.80		
10	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor				12.00	5.88	
	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min		7.80				
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1					4.35	
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)			7.40			
	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4					5.12	
15	102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,				12.00		
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20					
	102154	U17760	Hs.75517	laminin, beta 3 (niceln (125kD), kalinin	2.62					
	102193	AL036335	Hs.313 Hs.301613	secreted phosphoprotein 1 (asteopontin,	5.85				6.18	
20	102217 102224	AA829978 NM_002810	Hs.148495	JTV1 gene proteasome (prosome, macropain) 26S subu					4.49	
LU	102234	AW163390	Hs.278554	heterochromatin-like protein 1					5.80	
	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50					
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)					5.15	
	102330	BE298063	Hs.77254	chromobox homoton 1 (Drosophila HP1 beta					4.17	
25	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro				9.33		
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87					
	102368	U39817	Hs.36820	Eloom syndrome	15.91					
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma			19.20	44.00		
30	102404 102537	NM_005429	Hs.79141	vascular endothellal growth factor C RAB27A, member RAS oncogene family				14.00 12.00		
30	102537	U57094 AU077228	Hs.50477 Hs.77256	enhancer of zeste (Drosophila) homolog 2				12.00	4.57	
	102501	AI435128	Hs.181369	ubiquitin fusion degradation 1-like					3.98	
	102610	U65011	Hs.30743	preferentially expressed antigen in meta	77.50					
	102623	AW249285	Hs.37110	metanoma antigen, family A, 9	12.50					
35	102642	AA205847	Hs.23016	G protein-coupled receptor			22.00			
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00				
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein				12.80		
	102669	U71207	Hs.29279 Hs.29287	eyes absent (Drosophila) homolog 2	6.50 8.50					
40	102672 102687	U72066 NM 007019	Hs.29207 Hs.93002	retinoblastoma-binding protein 8 ublguitin carrier protein E2-C	0.30				9.24	
40	102696	BE540274	Hs.239	forthead box M1					5.54	
	102768	U82321	113.200	gb:Homo sapiens clone 14.99 mRNA sequenc		6.60				
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e					3.78	
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat					4.26	
45	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H			14.40			
	102829	NM_006183	Hs.80962	neurotensin	8.00					
	102888	Al346201	Hs.76118	ubiquilin carboxyl-terminal esterase t.1					5.50	
	102892	BE440042	Hs.83326 Hs.80342	maintx metalloproteinase 3 (stromelysin keralin 15	4.64		6.70			
50	102913 102935	NM_002275 BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.93					
50	102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.50			11.40		
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)					7.26	
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01					
	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90					
55	103038	AA926960	Hs.334883	CDC28 protein kinase 1					8.79	
	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin					4.27	
	103099	Al693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro		9.80				
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05					
60	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	3.07				5.62	
00	103185 103192	NM_005825 M22440	Hs.74368 Hs.170009	transmembrane protein (63kO), endoplasmi transforming growth factor, alpha		7.40			3.02	
	103223	BE275607	Hs.1700	chaperonin containing TCP1, subunit 3 (g		7.40			4.70	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o			100.00		4.10	
	103316	X83301	Hs.324728	SMA5				9.80		
65	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71					
	103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00					
	103385	NM_007069	Hs.37189	similar to rat HREV107				11.00		
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93					
70	103404	BE394784	Hs.78596	proteasome (prosome, macropaln) subunit,					5.15	
70	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr				04.40	3.98	
	103446	X98834	Hs.79971	sal (Drosophila)-like 2		13.00		21.40		
	103476 103477	Y07701 AJ011812	Hs.293007 Hs.119018	aminopeptidase puromycin sensitive transcription factor NRF		13.00	6.40			
	103477	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02		0.40			
75	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50					
,,,	103558	BE616547	Hs.2785	keratin 17	6.41					
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp					3.84	
	103587	BE270266	Hs.82128	5T4 oncotetal trophoblast glycoprotein	78.50					
	103594	Al368680	Hs.816	SRY (sex determining region Y)-box 2	6.51					
80	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50					
	103768	AF086009		gb:Homo saplens full length insert cDNA					4.48	
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468		8.00				
	103847	AF219946	Hs.102237	tubby super-family protein		10.40		45.00		
0.5	103913	AW967500	Hs.133543	ESTs				15.60		

	104150	O 02/086	443 Hs.331633	hypothetical protein DKFZp566N034				26.00	PCT/	US02/12476
	104257	BE560621	Hs.9222	estrogen receptor blading site associate		6.80		20.00		
	104261	AW248364	Hs.5409	RNA polymerase I subunit					3.98	
~	104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein		6.80				
5	104415 104558	BE410992	Hs.258730 Hs.88959	heme-regulated initiation factor 2-alpha		10.29				
	104550	R56678 AW373062	Hs.83623	hypothetical protein MGC4816 nuclear receptor subfamily 1, group 1, m	4.21			15.79		
	104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H				17.40		
10	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	6.40					
10	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr				40.00	6.55	
	104754 104758	AJ206234 BE560269	Hs.155924 Hs.7010	cAMP responsive element modulator NPD002 protein				10.00	4.47	
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87				4.41	
	105011	BE091926	Hs.16244	mitotic spindle coiled-coll related prot	3.83					
15	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86					
	105026 105076	AA809485 AJ598252	Hs.124219 Hs.37810	hypothetical protein FLJ12934 hypothetical protein MGC14833		11.00			5.01	
	105132	AA148164	Hs.247280	HBV associated factor					3.99	
	105143	AI368836	Hs.24808	ESTs, Weakly similar to 138022 hypotheti			11.00			
20	105158	AW976357	Hs.234545	hypothetical protein NUF2R		16.00				
	105175	AA305384 AA328102	Hs.25740 Hs.24641	ERO1 (S. cerevisiae)-like cytoskeleton associated protein 2	4.32 3.00					
	105264	AA227934	715.2404 I	gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi	3.00			10.00		
	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69					
25	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8				9.20		
	105460 105667	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,	4.12		7.80			
	105067	AA767526 BE246502	Hs.22030 Hs.9598	paired box gene 5 (B-cell lineage specif sema domain, immunoglobulin domain (lg),	4.12 3.82					
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	0.01		27.00			
30	105848	AW954064	Hs.24951	ESTs			7.60			
	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha					4.14	
	106019 106069	AF221993 BE566623	Hs.46743 Hs.29899	McKusick-Kaufman syndrome ESTs, Weakly similar to G02075 transcrip			16.80 23.40			
	106073	AL157441	Hs.17834	downstream neighbor of SON	9.50		23.40			
35	106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00					
	106159	AK001301	Hs.3487	hypothetical protein FLJ10439					3.95	
	106220 106260	D61329 Al097144	Hs.32196 Hs.5250	mitochondrial ribosomal protein L36 ESTs, Weakly similar to ALU1_HUMAN ALU S			13.20		6.04	
	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso			13.20		5.02	
40	106307	AA436174	Hs.37751	ESTs. Weakly similar to putative p 150 f		6.60				
	106318	AA025610	Hs.9805	cleavage and polyadenylation specific to					5.04	
	106341 106440	AF191020 AA449563	Hs.5243 Hs.151393	hypothetical protein, estradiol-induced glutamate-cysteine ligase, catalytic sub			13.80		7.25	
	106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75		13.00			
45	106586	AA243837	Hs.57787	ESTs				10.84		
	106605	AW772298	Hs.21103	Homo sapians mRNA; cDNA DKFZp564B076 (fr				45.60		
	106654 106785	AW075485 Y15227	Hs.286049 Hs.20149	phosphoserine aminotransferase deleted in lymphocytic teukemia, 1	28.00 3.00					
_	106813	C05766	Hs.181022	CGI-07 protein	3.00		11.40			
50	106895	AK001826	Hs.25245	hypothetical protein FLJ11269			6.00			
	106913	AI219346	Hs.86178	M-phase phosphoprotein 9		6.56			4.00	
	106919 107054	AW043637 A1076459	Hs.21766 Hs.15978	ESTs, Weakly similar to ALU5_HUMAN ALU S KIAA1272 protein				34.80	4.27	
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71			04.00		
55	107098	AI823593	Hs.27688	ESTs				24.80		
	107104	AU076640	Hs.16243	nucleolar protein 1 (120kD)	0.00				7.05	
	107129 107198	AC004770 AV657225	Hs.4756 Hs.9846	flap structure-specific endonuclease 1 KIAA1040 protein	2.60	19.20				
	107203	D20426	Hs.41639	programmed cell death 2		7.60				
60	107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50					
	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71					
	107318 107518	T74445 X57152	Hs.5957 Hs.99853	Homo sapiens clone 24416 mRNA sequence fibrillarin			8.71		4.33	
	107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)					4.00 .	
65	107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603838, mRNA,		10.80				
	107851	AA022953	Hs.61172	EST			8.00			
	107901 107922	L42612 BE153855	Hs.335952 Hs.61460	keratin 6B Ig superfamily receptor LNIR	3.40 2.88					
	107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50					
70	108015	AW298357	Hs.49927	protein kinase NYD-SP15				23.40		
	108056	AA043675	Hs.62633	ESTs				12.80		
	·108075 108187	AJ867370 BE245374	Hs.139709 Hs.27842	hypothetical protein FLJ12572 hypothetical protein FLJ11210		7.00		12.80		
	108298	N31256	Hs.161623	ESTs		6.60				
75	108305	AA071391		gb:zm61e06.r1 Stratagene fibroblast (937				11.80		
	108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer				11.80		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428		6.40		20.80		
	108554	AA084948 AA086005		gb:zn13b09.s1 Stratagene hNT neuron (937 gb:zl84c04.s1 Stratagene colon (937204)		0.40		25.40		
80	108584	AA088326	Hs.120905	Homo saplens cDNA FLJ11448 fis, clone HE		9.60				
	108597	AK000292	Hs.278732	hypothetical protein FLJ20285				14.60		
	108695 108699	AB029000	Hs.70823 Hs.70832	KIAA1077 protein ESTs	3.00			10.00		
	108699	AA121514 AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c			11.00	10.00		

	11/	O 02/086	442						PCT/US02/12476	
	108810				8.50				PC 1/0502/124/0	•
	108810	AW295647 AA130884	Hs.71331 Hs.270501	hypothetical protein MGC5350 ESTs, Moderately similar to ALU2_HUMAN	8.50	7.40				
	108857	AK001468	Hs.62180	ančlin (Drosophila Scraps homolog), act	4.00	7.40				
	108860	AA133334	Hs.129911	ESTs	6.09					
5	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.00					
	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69					
	109121	BE389387	Hs.49767	NAOH dehydrogenase (ubiquinone) Fe-S pro					4.53	
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	10.58					
10	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00				
10	109415 109418	U80736 AIB66946	Hs.110826	trinucleotide repeat containing 9 FSTs		51.40		11.00		
	109418	AA232265	Hs.161707 Hs.295232	ESTs, Moderately similar to A46010 X-II			17.60	11.00		
	109454	AW967069	Hs.211556	hypothetical protein MGC5487			9.49			
	109543	AA564994	Hs. 222851	ESTs .		12.67	0.40			
15	109648	H17800	Hs.7154	ESTs				10.40		
	109680	AB037734	Hs.4993	KIAA1313 protein			33.20			
	109700	FD9609		gb:HSC33H092 normalized infant brain cDN				16.00		
	109704	AI743880	Hs.12876	ESTs			11.00			
20	109792	R49625		gb:yg61f03.s1 Soares infant brain 1NIB H				12.60		
20	109981 109998	BE546208 AL042201	Hs.26090 Hs.21273	hypothelical protein FLJ20272 transcription factor NYD-sp10	4.00	7.80				
	110039	H11938	Hs.21273	histone acelyltransferase		7.00				
	110156	AA581322	Hs.4213	hypothetical protein MGC16207		7.00			4.24	
	110500	AA907723	Hs.36962	ESTs	4.50					
25	110551	AW450381	Hs.14529	ESTs		8.60				
	110561	AA379597	Hs.5199	HSPC150 amtein similar to ubiquitin-con	3.06					
	110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to		6.80				
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		6.80	8.80			
30	110916	BE178102 N52980	Hs.24349 Hs.83765	ESTs ditydrofolate reductase		6.80		16.80		
50	111337	AA837396	Hs.263925	US1-Interacting protein NUDE1, rat homo	2.54			10.00		
	111434	R01608	Hs.142736	ESTs				9.80		
	111439	Al476429	Hs.19238	ESTs				10.40		
20	111540	U82670	Hs.9786	zinc finger protein 275			15.40			
35	111597	R11499 T80581	Hs.189716	ESTs		6.80		9.20		į.
	111895 111929	AF027208	Hs.12723 Hs.112360	Homo sapiens clone 25153 mRNA sequence prominin (mouse)-like 1		0.00		14.67		
	112054	R43590	113.112.000	gb:yc85g02.s1 Soares Infant brain 1NiB H		10,80				
	112210	R49645	Hs.7004	ESTs				10.20		
40	112244	AB029000	Hs.70823	KIAA1077 protein	2.99					
	112382	R59904		gbryh07g12.s1 Soares infant brain 1NIB H		6.60	7.10			
	112392 112442	R60763 AA280174	Hs.193274 Hs.285681	ESTs, Moderately similar to 157588 HSret Williams-Beuren syndrome chromosome regi	3.00		7.10			
	112539	R70318	Hs.339730	ESTs	0.00			37.20		
45	112772	AI992283	Hs.35437	ESTs, Moderately similar to 138026 MLN 6				14.60		
	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin					4.83	
	112935	R71449	Hs.268760	ESTs	2.73			12.00		
	112970 112973	AA694010 AB033023	Hs.6932 Hs.318127	Homo sapians clone 23809 mRNA sequence hypothetical protein FLJ10201	11.50			12.00		
50	112992	AL157425	Hs.133315	Homo saplens mRNA; cDNA DKFZp761J1324 (f	11.00		10.89			
	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00					
	113073	N39342	Hs.103042	microlubule-associated protein 1B			15.31			
	113078	T40444	Hs.118354	CAT56 protein		7.00		41.20		
55	113238 113591	R45467 T91881	Hs.189813 Hs.200597	ESTs KIAA0563 gene product				9.40		
55	113702	T97307	H5.200357	gb:ye53h05.s1 Soares fetal liver spleen	25.00			3.40		
	113844	A/369275	Hs.243010	Homo saptens cDNA FLJ14445 fis, clone HE	20.00			13.91		
	113984	R96696	Hs.35598	ESTs		7.80				
	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (1		7.20				
60	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42					
	114208 114251	AL049466 H15261	Hs.7859 Hs.21948	ESTs			6.74	33.20		
	114285	R44338	Hs.21946	ESTs ESTs				13.20		
	114313	H18456	Hs.27946	ESTs				10.00		
65	114339	AA782845	Hs.22790	ESTs		7.80				
	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f					4.14	
	114560	A1452469	Hs.165221	ESTs				9.80		
	114699 114767	AA127386 AI859865	Hs.154443	gb:zn90d09.r1 Stratagene lung carcinoma minichromosome maintenance deficient (S	3.21	7.60				
70	114793	AA158245	F10.104440	gb:zo76c03.s1 Stratagene pancreas (93720	3.21		6.00			
,,,	114833	AI417215	Hs.87159	hypothetical protein FLJ12577				11.40		
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31	
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3					4.03	•
75	115097	AA256213	Hs.72010	ESTs				35.40		
13	115113 115123	AA256460 AA256841	Hs.236894	gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sepl ESTs, Highly similar to S02392 alpha-2-m				15.20	4.19	
	115123	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol				12.40		
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00					
	115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00				
80	115414	AA662240	Hs.283099	AF15q14 protein	3.25					
	115522	BE614387	Hs.333893	o-Myc target JPO1	3.68 10.50					
	115536 115566	AK001468 AI142336	Hs.62180 Hs.43977	antilin (Drosophila Scraps homolog), act Human DNA sequence from clone RP11-196N1	10.50			24.40		
	115645	AI142336 AI207410	Hs.69280	Homo saplens, clone IMAGE:3636299, mRNA,	4.17			24,40		
85	115648	AW016811	Hs.234478	Homo saplens cDNA: FLJ22648 fis, clone H			6.00			

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	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81				1 € 17 € 502/12470
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14				
	115793	AA424883	Hs.70333	hypothetical protein MGC10753				11.80	
5	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL			27.40	9.71	
•	115892 115906	AA291377 Al767756	Hs.50831 Hs.82302	ESTs Homo sagiens cDNA FLJ14814 fis, clone NT	2.53		27.40		
	115909	AW872527	Hs.59761	ESTs. Weakly similar to DAP1_HUMAN DEATH	11.82				
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970				34.29	2.00
10	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g ESTs, Wealthy similar to T08599 probable	3.00				8.23
10	115985 116090	AA447709 Al591147	Hs.268115 Hs.61232	ESTs, Weakly similar to 100599 probable	5.17				
	116096	AA682382	Hs.59982	ESTs			8.20		
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60			
15	116157	BE439838	Hs.44298 Hs.67776	mitochondrial ribosomal protein S17 ESTs, Weakly similar to T22341 hypotheti					5.82 4.08
13	116190 116278	AI949095 NM_003686	Hs.47504	exonuclease 1	9.50				4.00
	116335	AK001100	Hs.41690	desmocollin 3	3.67				
	116496	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00		12.60	
20	116503	AI925316	Hs.212617 Hs.92127	ESTs ESTs			32.00	12.00	
20	116674 116929	AI768015 AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp		7.60	32.00		
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F		9.80			
	116993	AJ417023	Hs.40478	ESTs				10.20 15.20	
25	117079 117317	H92325 Al263517	Hs.43322	gb:ys85f05.s1 Soares retina N2b4HR Homo ESTs				13.40	
23	117326	N23629	Hs.241420	Homo saplens mRNA for KIAA1756 protein,				20.60	
	117396	W20128	Hs.296039	ESTs				10.60	
	117412	N32536	Hs.42645	ESTs				16.00	
30	117519 117693	N32528 AW179019	Hs.146286 Hs.112110	kinesin family member 13A mitochondrial ribosomal protein L42				9.11	4.01
30	117721	N46100	Hs.93939	EST				19.80	4.01
	117881	AF181470	Hs.260622	butyrate-induced transcript 1	2.71				
	117903	AA768283	Hs.47111	ESTs				17.80	4.17
35	117992 118013	Al015709 Al674126	Hs.172089 Hs.94031	Homo sapiens mRNA; cDNA DKFZp586I2022 (f ESTs				10.60	4.17
33	118017	AIR13444	Hs.42197	ESTs			8.82		
	118186	N22886	Hs.42380	ESTs		7.00			
	118325	AI868065	Hs.166184	Intersectin 2			6.14	13.80	
40	118367 118368	N64269 N64339	Hs.48946 Hs.48956	EST gap junction protein, beta 6 (connexin 3	3.14		0.14		
70	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3			12.40		
	118709	AA232970	Hs.293774	ESTs				12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f hypothetical protein FLJ11808	4.50 3.22				
45	119027 119052	AF086161 R10889	Hs.114611	gb:yf38d02.s1 Soares fatal liver spleen	3.22	9.60			
73	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome			6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593				10.80 9.44	
	119243 119490	T12603 AA195276	Hs.263858	gb:CHR90123 Chromosome 9 exon II Homo sa ESTs, Moderately similar to B34087 hypot				11.80	
50	119499	AI918906	Hs.55080	ESTs			14.80		
-	119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas		12.60			
	119780	NM_016625	Hs.191381	hypothetical protein	17.00 13.50				
	119845 119941	W79123 AA699485	Hs.58561 Hs.58896	G protein-coupled receptor 87 ESTs	10.50	8.00			
55	119994	AA642402	Hs.59142	ESTs	7.73				
	120102	W67353	Hs.170218	KIAA0251 protein	2.91		39.60		
	120104 120294	AK000123 AK000059	Hs.180479 Hs.153881	hypothetical protein FLJ20118 Homo sapiens NY-REN-62 antigen mRNA, par	2.91		8.20		
	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73				
60	120599	AA804448	Hs.104463	ESTs		7.00			
	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos gb:zs59a06.s1 NCI_CGAP_GCB1 Homo saplens		9,40		10.00	
	120715 120621	AA292700 Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein		5.40		13.80	
	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol		9.00			
65	120880	AA360240	Hs.97019	EST		16.60			
	120983	AA398209	Hs.97587	EST nucleoportn 50kD			27.66 20.80		
	121034 121121	AL389951 AA399371	Hs.271623 Hs.189095	similar to SALL1 (sai (Drosophila)-like		22,80	20.00		
	121313	AA402713	Hs.97872	ESTs				10.00	
70	121369	AW450737	Hs.128791	CGI-09 protein	25.71				5.42
	121376 - 121476	AA448103 AA412311	Hs.187958 Hs.97903	solute carrier family 6 (neurotransmitte ESTs		8.30			3.42
	121509	AA868939	Hs.97888	ESTs		8.59			
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50				
75	121753	AK000552	Hs.323518	WD repeat domain 5	7.00			10.40	
	121838 121857	AA425680 BE387162	Hs.98441* Hs.280858	ESTs ESTs, Highly similar to A35661 DNA excis	6.00			13.40	
	121991	AA430058	Hs.98649	EST				12.20	
00	122089	AW016543	Hs.98682	hypothetical protein FKSG32			8.60		
80	122105	AW241685	Hs.98699	ESTs			6.14	10.40	
	122163 122318	AA435702 AA429743	Hs.98829	EST gb:zv60b05.rl Soares_testis_NHT Hamo sap				18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50				
06	122338	AA443311	Hs.98998	ESTs ESTs, Weakly similar to S47073 finger pr	4.80	8.00			
85	122414	Al313473	Hs.99087	EO19, STORRY SERIES EO O-STOVO MINES PE		0.00			

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	122512	AF053305	Hs.98658	budding uninhibited by benzlmidazoles 1			8.80			1/0502/124/0
	122516.	AA449352	Hs.99217	ESTs				9.40		
	122702	A1220089	Hs.99439	ESTs .		9.20		10.40		
5	122852 122925	A\580056 A\7268962	Hs.98992 Hs.111335	ESTs ESTs		6.80		10.40		
-	123005	AW369771	Hs.52620	integrin, beta 8			12.60			
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro			0.00		5.35	
	123160 123315	AA486687 AA496369	Hs.284235	ESTs, Weakly similar to 138022 hypotheti gb:zv37d10.s1 Soares overy tumor NbHOT H			6.06 12.40			
10	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po			11.80			
	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein		12.00				
	123518 123519	AL035414 AW015887	Hs.21068 Hs.112574	hypothetical protein ESTs		12.20	13.00			
	123614	AK000492	Hs.98806	hypothetical protein		12.20	7.80			
15	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L				10.60		
	123673 123727	BE550112 AI083986	Hs.158549 Hs.282977	ESTs, Weakly similar to T2D3_HUMAN TRANS hypothetical protein FLJ13490	23.00	7.00				
	123727	AA609839	HS.202311	gb:ae62f01.s1 Stratagene lung carcinoma		7.00	9.80			
	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50					
20	123900	AA621223	Hs.112953	EST	97.00			12.80		
	124006 124069	A/147155 BE387335	Hs.270016 Hs.283713	ESTs, Wealdy similar to S64054 hypotheti	3.02					
	124069	AF134160	Hs.7327	claudin 1	0.02		27.80			
0.5	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha				35.80		
25	124273 124297	AA457211 AL080215	Hs.8858	bromodomain adjacent to zinc finger doma Homo sapiens mRNA; cDNA DKFZp586J0323 (f		7.20		11.00		
	124297	AW963221	Hs.102301	ab:EST375294 MAGE resequences, MAGH Homo				16.00		
	124676	Al360119.com	pHs.181013	phosphoglycerate mutase 1 (brain)					6.08	
30	124874 124904	BE550182 AK000483	Hs.127826	RalGEF-like protein 3, mouse homolog KIAA1682 protein		9.40		21.00		
50	124969	A1650360	Hs.93872 Hs.100256	ESTs		5.40		10:80		
	125000	T58615	Hs.110640	ESTs				9.80		
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypotheti		7.60 6.59				
35	125266 125299	W90022 T32982	Hs.186809 Hs.102720	ESTs, Highly similar to LCT2_HUMAN LEUKO ESTs		6.59		9.57		
33	125356	AI057052	Hs. 133554	ESTs, Weakly similar to Z195_HUMAN ZINC				14.00		
	125370	AA256743	Hs.134158	Homo saplens, Similar to KIAA0092 gene p			8.20			
	125418 125433	AA777690 AL162066	Hs.188501 Hs.54320	ESTs hypothetical protein DKFZp762D096		21.40		13.20		
40	125437	A1609449	Hs.140197	ESTs		6.98				
	125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F		8.80				
	125711	AA305800 BE174587	Hs.5672	hypothetical protein AF140225				11.20	4.31	
	125756 125757	AI274906	Hs.289721 Hs.166835	growth arrest specific transcript 5 ESTs, Highly similar to 1814460A p53-ass				15.60	4.31	
45	125769	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.20					
	125839	AW836261	Hs.337717	ESTs ESTs	2.65	8.20				
	125850 125875	W85858 H14480	Hs.99804	gb:ym18b09.r1 Soares infant brain 1NIB H	2.00	7.40				•
	125924	BE272506	Hs.82109	syndecan 1					4.23	
50	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein				10.60	3.98	
	126034 126327	H60340 AA432266	Hs.44648	gb:yr39b04.r1 Soares fetal liver spleen ESTs		11.60		10.00		
	126345	N49713	163.77070	gb:yv23f06.s1 Soares fetal liver spieen		6.67				
	126435	AW614529	Hs.285847	CGI-19 protein				10.60		
55	126487 126521	AA283809 AJ475110	Hs.184601 Hs.203933	solute carrier family 7 (cationic amino ESTs		6.60			4.38	
	126522	W31912	15.203533	gb:zc76d03.s1 Pancreatic Islet Homo sapi		0.00		14.80		
	126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g					4.01	
60	126567 126605	AA058394 AA676910	Hs.57887	ESTs, Wealdy similar to KIAA0758 protein gb:zj65h07.s1 Soares_fetal_liver_spleen_			7.80	11.60		
00	126627	AA497044	Hs.20887	hypothetical protein FLJ10392				14.60		
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00					
	126737	AW976516	Hs.283707	Homo sapiens cBNA: FLJ21354 fis, clone C	2.92					
65	126795 126802	AW975076 AW805510	Hs.172589 Hs.97056	nuctear phosphoprotein similar to S. cer hypothetical protein FLJ21634	7.50	11.60				
05	126892	AF121856	Hs.284291	sorting nexin 6	3.50					
	126928	AA480902	Hs.137401	ESTS				22.83 11.80		
	126979 126986	AA210954 Al279892	Hs.46801	gb:zq89h10.r1 Stratagene hNT neuron (937 sorting nexin 14				11.60		
70	126992	A/809521	160.40001	gb;wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s				20.80		
	127066	R25066		gb:yg42c07.r1 Soares Infant brain 1NIB H				27.60		
	127099	AA347668 AAR30233	Hs.293585	gb:EST54026 Fetal heart II Homo saptens ESTs				21.60 11.20		
	127139 127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10			11.20		
75	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76					
	127225	AA315933	Hs.120879	ESTs	1100			16.80		
	127313 127444	AK002014 AW978474	Hs.47546 Hs.7560	Homo sapiens cDNA FLJ11458 fis, cione HE Homo sapiens mRNA for KIAA1729 protein,	14.00			13.60		
	127500	AW971353	Hs.162115	ESTs		11.20				
80	127524	AI243596	Hs.94830	ESTs. Moderately similar to T03094 A-kin			7.80			
	127540	N45572	Hs.105362	Homo saplens, clone MGC:18257, mRNA, com	3.53			13.80		
	127599 127609	AA613204 X80031	Hs.150399 Hs.530	ESTs collagen, type IV, alpha 3 (Goodpasture				28.00		
	127662	W80755	Hs.8294	KIAA0196 gene product				19.80		
85	127668	Al343257	Hs.139993	ESTs				11.20		

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	127746	Al239495	Hs.120189	ESTs				14.18	
	127812 127817	AA741368 AA836641	Hs.291434 Hs.163085	ESTs ESTs	4.50			24.60	
	127959	AI302471	Hs. 124292	Homo sapiens cDNA: FLJ23123 fis, clone L				9.20	
5	127960	AI613226	Hs.41569	ohosobalidic acid ohosobalase type 2A				16.83	
	127969 128015	F06498 Z21169	Hs.93748 Hs.334659	Homo sapiens cDNA FLJ14676 fis, clone NT hypothetical protein MGC14139		13.60			
	128027	AI433721	Hs.164153	ESTs		1.00		37.40	
10	128077	AI310330	Hs.128720	ESTs				9.60	
10	128168	NM_006147	Hs.11801	interferon regulatory factor 6 GM2 ganglioside activator protein	19.00			9.24	
	128226 128305	A1284940 A1954968	Hs.289082 Hs.279009	matrix Gla protein	13.00			10.40	
	128341	AA191420	Hs.185030	ESTs		9.00			
1.5	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul		12.60			4.30
15	128539 128568	R46163 H12912	Hs.258618 Hs.274691	ESTs adenylate kinase 3		12.00			4.56
	128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9				10.00	
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2			16.80		4.48
20	128781 128796	N71826 AJ000152	Hs.105465 Hs.105924	small nuclear ribonucleoprolein polypept defensin, beta 2		8.12			4,40
20	128920	AA622037	Hs.166468	programmed cell death 5					4.62
	128924	BE279383	Hs.26557	plakophilin 3		12.60			4.04
	128971 129008	H05132 AL079648	Hs.107510 Hs.301088	ESTs ESTs		8.80			
25	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu					6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59		0.07		
	129105 129189	Al769160 AB023179	Hs.108681 Hs.9059	Homo sapiens brain tumor associated prot KIAA0962 protein		8.00	6.67		
	129229	AF013758	Hs.109643	polyadenytate binding protein-interactin	4.00	0.00			
30	129241	Al878857	Hs.109706	hematological and neurological expressed					4.06
	129300	W94197	Hs.110165	ribosomal protein L26 homolog ESTs	2.55 18.00				
	129404 129457	AI267700 X61959	Hs.317584 Hs.207776	aspartylglucosaminidase	6.50				
	129466	L42583	Hs.334309	keratin 6A	12.94				
35	129494	Al148976	Hs.112062	ESTs				11.00	4.46
	129605 129641	AF061812 Al911527	Hs.115947 Hs.11805	keratin 16 (focal non-epidermolytic palm ESTs				12.00	4.40
	129665	AW163331	Hs.118778	KDFL (Lvs.Asn-Glu-Leu) andoplasmic retic					4.70
40	129703	BE388665	Hs.179999	Homo sapians, clone IMAGE:345/003, mRNA					4.02 5.71
40	129720 129748	AA156214 M16707	Hs.12152 Hs.123053	APMCF1 protein H4 histone, family 2	3.50				3.71
	129890	Al868872	Hs.282804	hypothetical protein FLJ22704					4.21
	129896	BE295568	Hs.13225	UDP-Gat:betaGlcNAc beta 1,4- galactosytt	2.56				4.03
45	129945 130010	BE514376 AA301116	Hs.165998 Hs.142838	PAI-1 mRNA-binding protein nucleotar phosphoprotein Nopp34			7.00		4.03
43	130026	T40480	Hs.332112	EST		6.40	1.00		
	130080	X14850	Hs.147097	H2A histone family, member X					4.65
	130149 130285	AW067805 AA063546	Hs.172665 Hs.75981	methylenetetrahydrofolato dehydrogenase ubiquitin specific protease 14 (IRNA-gua	2.74		7.40		
50	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic					3.91
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87			9.60	
	130500	AB007913 U89995	Hs.158291 Hs.159234	KIAA0444 protein forkhead box E1 (thyroid transcription f			13.40	9.60	
	130524 130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)			8.20		
55	130553	AF062649	Hs.252587	pituitary tumor-transforming 1					6.06
	130567 130577	AA383092 M69241	Hs.1608 Hs.162	replication protein A3 (14kD) insufin-like growth factor binding prote	3.04		7.00		
	130577	M69241 BE003064	Hs.162 Hs.1695	matrix metalloproteinase 12 (macrophage	3.87				
	130648	A1458165	Hs.17296	hypothetical protein MGC2376				16.20	
60	130697	1.29472	Hs.1802	major histocompatibility complex, class				17.80	5.23
	130744 130800	H59696 Al187292	Hs.18747 Hs.19574	POP7 (processing of precursor, S. cerev) hypothetical protein MGC5469					4.43
	130867	NM_001072	Hs.284239	LIDP ofvoosyltransferase 1 family, polype	16.84				
	130869	J03626	Hs.2057 ·	uridine monophosphale synthetase (orotat				9.60	4.92
65	130925 130994	ÁF093419 W17044	Hs.169378 Hs.327337	multiple POZ domain protein ESTs		12.40		9.00	
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	10.21				
	131031	NM_001650	Hs.288650	enuenorin 4				9.80 9.60	
70	131041 131058	T15767 W28545	Hs.22452 Hs.101514	Homo saplens mRNA for KIAA1737 protein, hypothetical protein FLJ10342				17.00	
70	131090	AI143139	Hs.2288	vislala like 1	2.74				
	131112	H15302	Hs.168950	Homo saplens mRNA; cDNA DKFZp566A1046 (f			8.80		
	131148	AW953575 BE280074	Hs.303125 Hs.23960	p53-induced protein PIGPC1 cyclin B1	3.12 3.07				
75	131185 131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07				
,,,	131219	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.87				
	131257	AW339037	Hs.24908	ESTs			19.20	14.67	
	131375 131460	AW293165 NM_003729	Hs.143134 Hs.27076	ESTs RNA 3'-terminal phosphate cyclase	3.50		13.20		
80	131476	AJ521663	Hs.334644	hypothetical protein FLJ14668	15.00				
	131510	BE245374	Hs.27842	hypothetical protein FLJ11210			7.80		
	131646 131786	BE302464 BE000971	Hs.30057 Hs.306083	MRS2 (S. cerevisiae)-like, magnesium hom Novel human gene mapping to chomosome 22	2.65		7.00		
	131786	AB014533	Hs.33010	KIAA0633 protein				35.20	
85	131843	AA192315	Hs.184062	putative Rab5-interacting protein					4.11

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	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00				101/05	02/124/0
	131885	BE502341	Hs.3402	ESTs	6.48					
	131921	AA456093	Hs.34720	ESTs			8.40			
5	131945 131958	NM_002916 NM_014062	Hs.35120 Hs.3566	replication factor C (activator 1) 4 (37 ART-4 protein	56.00				3.82	
,	131965	W79283	Hs.35962	ESTs	3.03				0.01	
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80				
	132040 132109	NM_001196 AW190902	Hs.315689 Hs.40098	Homo sapiens cDNA: FLJ22373 fis, clone H cysteine knot superfamily 1, BMP antagon	3.30 21.00					
10	132114	NM_006152	Hs.40202	lymphold-restricted membrane protein	21.00	8.40				
	132162	AA315805	Hs.94560	desmogtein 2					12.25	
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70					
	132180	NM_004460 AW961231	Hs.418 Hs.16773	fibroblast activation protein, alpha Homo saplens clone TCCCIA00427 mRNA sequ	3.83					
15	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A				13.20		
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50					
	132277 132328	AK001745 NM_014787	Hs.184628 Hs.44896	hypothetical protein FLJ 10883 DnaJ (Hsp40) homolog, subfamily B, membe	4.50			9.20		
	132326	AK001680	Hs.30488	DKFZP434F091 protein				19.80		
20	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALUS_HUMAN A			8.60			
	132528 132543	T78736 BE568452	Hs.50758 Hs.5101	SMC4 (structural maintenance of chromoso protein regulator of cytokinesis 1	4.38		27.40			
	132544	L19778	Hs.5101	H2A histone family, member P	4.30	7.00				
	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64					
25	132552	BE621985	Hs.296922	thiopurine S-methyltransferase			6.60	15.83		
	132581 132617	AK000631 AF037335	Hs.52256 Hs.5338	hypothetical protein FLJ20624 carbonic anhydrase XII	4.95		6.60			
	132638	Al798870	Hs.54277	DNA segment on chromosome X (unique) 992		8.20				
••	132653	Z15008	Hs.54451	taminin, gamma 2 (nicetn (100kD), kalini	4.38					
30	132669 132710	W38586 W74001	Hs.293981 Hs.55279	guantne nucleolide binding protein (G pr serine (or cysteine) proteinase inhibito	4.60				4.36	
	132771	Y10275	Hs.56407	phosphoserine phosphalase	3.71					
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,				9.48		
35	132833 132892	U78525 AW834050	Hs.57783	eukaryotic translation initiation factor				12.00	5.83	
33	132992	BE613337	Hs.9973 Hs.234896	geminin	3.09			12.00		
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT					3.87	
	132952 132990	AA576635	Hs.6153 Hs.334334	CGI-48 protein transcription factor AP-2 alpha (activat	3.50 6.18					
40	132994	X77343 AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19					
	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96					
	133050	X73424 BE244588	Hs.63788 Hs.6456	propionyl Coenzyme A carboxylase, beta p chaperonin containing TCP1, subunit 2 (b	2.55				4.00	
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso					8.96	
45	133134	AF198620	Hs.65648	RNA binding motif protein 8A				10.80	4.28	
	133155 133181	M58583 X91662	Hs.662 Hs.66744	cerebellin 1 precursor twist (Orosophila) homolog (acrocephalos	3.00			10.80		
	133204	BE267696	Hs.254105	enolase 1, (alpha)					4.63	
50	133412	U41493	Hs.73112	guantne nucleotide binding protein (G pr	2.85	12.50				
30	133421 133451	AF134160 AW970026	Hs.7327 Hs.73818	claudin 1 ubiquinol-cytochrome c reductase hinge p	2.00				4.66	
	133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept		6.80				
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14				4,55	
55	133506 133615	BE562958 M62843	Hs.74346 Hs.75236	hypothetical protein MGC14353 ELAV (embryonic lethal, abnormal vision,				17.80	4.00	
	133627	NM_002047	Hs.75280	glycyl-IRNA synthetase					4.85	
	133649	U25849 NM_006925	Hs.75393 Hs.166975	acid phosphatase 1, soluble splicing factor, erginine/serine-rich 5				14.00	6.34	
	133749	L20852	Hs.10018	solute carrier family 20 (phosphale tran			6.11	14.00		
60	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+, poly (ADP-					4.91	
	133865 133946	AB011155	Hs.170290	discs, large (Drosophila) homolog 6 NIPSNAP, C. elegans, homolog 1	3.07				4.60	
	133946	AJ001258 N55540	Hs.173878 Hs.78026	ESTs, Weakly similar to similar to ankyr				13.00	4.00	
	134047	BE262529	Hs.78771	phosphoglycerate kinase 1					3.85	
65	134098 134107	BE513171 NM 005629	Hs.79086 Hs.187958	mitochondrial riposomal protein 1.3 solute carrier family 6 (neurotransmitte	2.56		8.20			
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			0.20		4.08	
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00					
70	134160	T98152	Hs.79432	fibrillin 2 (congenital contractural ara Homo sapiens cDNA: FLJ23602 fis, clone L			24.60		6.71	
70	134168 134185	AA398908 AA285136	Hs.181634 Hs.301914	neuronal specific transcription factor D				14.74	0.71	
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40				
	134272 134276	X76040 BE083936	Hs.278614 Hs.80976	protease, serine, 15 antigen identified by monoclonal antibod	4.50	9.00				
75	134276	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m		0.00		16.40		
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.80					
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68				3.84	
	134423	H53497 AA279661	Hs.83006 Hs.83753	CGI-139 protein small nuclear ribonucleoprotein polypept					5.81	
80	134470	X54942	Hs.83758	CDC28 protein kinase 2					4.21	
	134498 134502	AW246273 BE148534	Hs.84131 Hs.84168	threonyl-IRNA synthetase UV-B repressed sequence, HUR 7		13.60			7.30	
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase				9.70		
85	134548	N95406	Hs.333495	Deloted in split-hand/split-foot 1 regio	6.00				4.63	
63	134654	AK001741	Hs.8739	hypothetical protein FLJ 10879	0.00					

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	134724	AF045239	Hs.321576	ring finger protein 22				12.00	
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00				
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone			25.20		
_	134806	AD001528	Hs.89718	spermine synthase					4.58
5	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle					4.79
	134859	D26488	Hs.90315	KIAA0007 protein			6.20		
	134891	R51083	Hs.90787	ESTs			7.40		
	134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00				
	134993	BE409809	Hs.301005	purine-rich element binding protein B					4.43
10	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50				
	135080	AI761180	Hs.94211	red1 (required for cell differentiation,	5.00				
	135103	NM 003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00			
	135145	AW014729	Hs.95262	nuclear factor related to kappa 8 bindin					4.01
	135184	U13222	Hs.96028	forkhead box D1			7.00		
15	135242	Al583187	Hs.9700	cyclin E1	13.50				
	135286	AW023482	Hs.97849	ESTs	6.46				
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80			
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00				
	135371	NM_006025	Hs.997	protesse, serine, 22	8.00				
20	135393	L11244	Hs.99886	complement component 4-binding protein,	0.00			14.60	

TABLE 58 shows the accession numbers for those primekeys lacking unigeneitD's for Table 54. For each probeset we have listed the gene cluster number from which the oligonaccedates were designed. Gene clusters were complied using sequences derived from Centanik ESTs and mRNAs. These sequences were clustered based on sequestrating using collegering and Alignment Tools (Drouble Twick Colater and Estate). The Centralia recognism numbers for exquences comprising solution are lated in the

25

85

Pkey: Unique Eos probesat identifier number CAT number: Gene cluster number Accession: Genbank accession numbers 30 Pkey CAT number Accessions 117079 1621717 1 H92325 T97125 35 AW963221 AA344870 AA344871 H93331 12430 242183_1 M26958 18202_-6 754958_1 101502 R49625 F10674 109792 1598157_1 44641_1 1653833_1 126034 H60340 N9163 102768 1182321 H66077 40 N49713 N49819 W03810 126345 127066 1703458_1 R25066 R20144 R20145 Z43845 244301_1 127099 AA347668 AW956810 Z44271 F07065 F07064 R13506 T12603 T12604 119243 1774795 1 H14480 N98295 125875 1566433 1 45 112054 1538292 1 R43590 F10439 126979 171411_1 AA210954 AA211007 AIR09521 H12174 742556 126993 880855 1 122318 292419 1 AA429743 AA442754 114699 135322 1 AA127386 R15644 AA127404 50 AA 158245 AA 158235 114702 150742 1 108305 111550_1 AA071391 AA069892 AA069891 AA075211 AA075245 AA075126 AA074946 U14622 108393 113411_1 tigr_HT4586 U14622 genbank_AA609839 genbank_F09609 F09609 123731 AA609839 55 109700 120715 genbank_AA292700 AA292700 genbank_T97307 T97307 genbank_AA256460 112705 AA256460 115113 genbank_AA2b460 enfrez_J05614 Jf genbank_AA084948 genbank_AA086005 149538_1 R 101045 60 108554 AA084948 AAGRAGGS 119052 R10889 R108 126522 416020_1 NASTIGIS I NATTIRESS ANTERISES WIRBOOM
WENDER SANDOTION SERVICE AND SERVICE AN 126605 439280 1 AA676910 AA778853 AA778865 W86800 65 46922 1 103768 70 75 80 ABBESTS I BOATE AND ISSUE AND HE STATE OF THE STATE OF TH

AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281 AZ09340 N56174 N68374 AA191088 AW247691 AA249013 AA093111 AA972536 AW29394 AA375893 T12139 W28186 AW243849 AJ286239 AA843996 W15250 A1188286 AW2486J78 R15836

genbank_W45552 W45552 119599 5 genbank_R59904 R59904 genbank_AA227934 112282 AA227934 105264 entrez_A28102 A28102 714071 1 AAA0623 100071 AAA96369 AAA966A6 123315

> AW958439 W91892 Hs.38613 ESTs

AA481788 H61037 Hs.190150

AB023179 Hs.9059

H98675 AF088019 117179

AA287747 Hs.173012

AA923278 Hs 290905

AW207555 He 97093

115722

116261

116830

117757

118283 80 118384 AF217525 Hs.49002

118657 A102210E Hs.49902 ECT.

120328 AB023230 Hs.96427

120404 120524 AA261852

120688

75

85

Hs.59600

He 269034 FSTe.

Hs.46732 EST

ECT.

ESTs

ESTs

ESTs, Weakly similar to ALU2_HUMAN ALU KIAA0962 prolein

ESTs, Weakly similar to A46010 X-linked Down syndrome cell adhesion molecule

ESTs, Weakly similar to protease [H.sap! KIAA 1013 protein

Homo seriens cONA: FLJ23004 fis, done L

10 Table 6A ahows 99 genes up-regulated nonsmokers with lung cancer relative to emokers with lung cancer. These genes were selected from \$5500 problems on the ExplAPymarkh Hu33 Genuchip entry. Cene expression data for each problems of bottom from this analysis was expressed as everage fatterably (AI), a normalized value reflecting the national level of MINN expression.

Piery: Unique Gos probeset Identifier number
Exchange: Exchange Computer Accession number, Cembrate accession number
Uniquest 15ths.

Rt: Rt: Rs: excepted A for samples from non-smokers with adenocarcinoma divided by the 90th percentile of All for samples from annotans with adenocarcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with a quamous coll carcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with aquamous coll carcinoma divided by the 90th percentile of All for samples from annotans with a quamous coll carcinoma divided by the 90th percentile of All for samples from annotans with a quamous coll carcinoma divided by the 90th percentile of All for samples from annotance and annotance annot 15 20 R1 מם Pkov Evacen UnigenelD Unigene Title fatty acid binding protein 4, adipocyte pre-T/NK cell associated protein thyroid hormone receptor interactor 11 thyroid hormone receptor interactor 8 \$100 calcium-binding protein A7 (psorias 25 RF379727 Hs.83213 3.64 100971 Hs.280 Hs.85092 15.00 L17330 101174 10129 Y12490 12.00 AA001021 AA586894 101304 Hs.6685 Hs.112408 2.68 101806 gb:beta-pot=DNA polymerase beta (axon a UDP glycosytransferase 8 (UDP-galactose a disintegrin and metalloproteinase doma gb:Human clone 143789 defective mariner 211 30 S82472 101972 7.50 Hs.158540 102274 U30930 NM_003816 Hs.2442 102394 13.50 102832 1192015 Hs.161640 tyrosine aminotransferase gb:H.saplens mRNA for ligase fike protei 9.50 103010 X52509 250 35 103439 X98266 gort-speens mixed for igase me prove activin A receptor, type I lacrimal proline rich protein doublecortin and Call kinase-like 1 nuclear receptor subfamily 1, group I, m ESTs, Weakly similar to ALUI_HUMAN ALU Hs.150402 9.00 103563 102911 304 AJ076795 Hs.45033 103857 104239 AB002367 Hs.21355 13 50 12.68 104590 AW373062 He 83623 40 16.50 104907 AA055829 Hs.196701 Hs.296244 SNARE protein 2.17 BE514788 106131 Hs.30643 7.00 ESTe H47233 KIAA1134 protein 106872 Hs.18282 Hs.32501 TECOOT 2 38 AA156238 106060 **FSTs** Homo saplens mRNA; cDNA DKFZp43401572 (f ESTs, Weakly similar to KIAA0758 protei gb:zm26c06.s1 Stratagene pancreas (93720 9 50 45 106971 Z43846 Hs.194478 2.95 AA035375 AA100796 Lie 57897 16 60 108562 MD-2 protein 13.00 108599 AB018549 Hs.69328 ESTs, Weakly similar to T26845 hypotheti 2 40 BE219231 Hs.292653 7.00 50 109247 AA314907 R44607 Hs 85950 **FSTs** 5.00 100630 He 22672 FSTs. Homo sapiens mRNA; cDNA DKFZp434M082 (fr 12 50 110193 Al004874 Hs.310764 16.50 H24458 Hs.32085 FST ESTs, Highly similar to type II CALM/AF1 three-PDZ containing protein similar to 110644 D04207 He 268989 55 AW274992 Hs.72249 17.00 T79639 ESTs 16.50 111057 Wolf-Hirschhorn syndrome candidate 1 AF071594 Hs.110457 3 00 Hs.26026 ESTe 112291 R53972 2.79 4.50 Z43784 Hs.75893 ankyrin 3, node of Ranvier (ankyrin G) 112956 ESTs
hypothetical protein FLJ14827
microtubule-associated protein 18
pmtein tyrosine phosphatase, receptor t 60 Hs.7246 T23699 BE564162 Hs.250820 N30342 113073 He 103042 AK001335 3 82 Hs.31137 113074 T48011 Hs.8764 EST 113121 hypothetical protein FLJ11362 65 113125 AA968672 AA703095 He 8929 2.65 113757 Hs.18631 ESTe ES1s
hypothetical protein FLJ23293 similar to
chromosome 12 open reading frame 2
nuclear receptor subfamily 1, group 1, m
Homo saptens mRNA; cDNA DKFZp564N1063 (113848 113884 W52854 Hs.27099 6.00 6.00 AI333076 Hs.28529 Hs.83623 Hs.236443 W17056 70 7.00 114875 114987 115460 AA235609 AA251016 Hs.87808 EST

9.00

2.68

2.39

3 57

9.50

8 50

7.50

7 50

16.50

7.00

	W	O 02/086	443				PCT/US02/12476
	121558	AA412497		gb:zi95g12.s1 Soares_testis_NHT Homo sap		2.95	
	121676	H56037	Hs.108146	ESTs	10.00		
	121936	AJ024600	Hs.98612	ESTs	15.00		
	121938	AA428659	Hs.98610	ESTs	14.00		
- 5	122177	AA435789	Hs.98833	EST	8.93		
-	123442	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.04		
	123551	AA608837	110.111100	gb;af03h12.s1 Soares testis NHT Homo sap	11.50		
	123756	AA609971	Hs.112795	EST	11.00		
	123861	AA620840		gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50	
10	124371	N24924	Hs.188601	ESTs	6.50		
10	127477	BE328720	Hs.280651	ESTs		4.33	
	127591	Al190540	Hs.131092	ESTS		3.02	
	128252	AA455924	Hs. 192228	ESTs	7.00		
	128426	AI265784	Hs.145197	ESTs		2.08	
15	128925	R87419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT		2.11	
13	128945	Al990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00		
	129105	Al769160	Hs.108681	Homo saplens brain tumor associated pro!	15.50		
	129235	AW977238	Hs.126084	KIAA1055 protein	10.00	4.25	
	129506	AB020684	Hs.11217	KIAA0877 protein	6.50		
20	129595	U09550	Hs.1154	oviductal givcoprotein 1, 120kD (mucin 9	0.00	10.00	
20	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00	10.00	
	130340	D82326	Hs.239106	solule carrier family 3 (cysfine, dibasi	11.50		
	131220	AB023194	Hs.300855	KIAA0977 protein	17.50		
	131430	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.10		
25	132114	NM_006152		lymphold-restricted membrane protein	0.10	6.15	
23	132458	AA935315	Hs.48965	Homo saplens cDNA: FLJ21693 fis, clone C		5.58	
	132647	NM 006927		significant series e 48 (beta-galactosidase	7.50	0.00	
	132655	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	7.00	2.53	
	132682	Al077500	Hs.54900	serologically defined colon cancer antig		2.50	
30	132747	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein		2.83	
50	132812	R50333	Hs.92186	Leman colled-coil protein		3.82	
	133337	AF085983	Hs.293676	ESTs		5.00	
	133876	AL134908	Hs.771	phosphorylase, glycogen; liver (Hers dis		3.00	
	134119	AW157837	Hs.79226	fasciculation and elongation protein zet		2.06	
35	134464	AA302983	Hs.239720	CCR4-NOT transcription complex, subunit		2.27	
-	134542	M14156	Hs.85112	Insulin-like growth factor 1 (somalomedi		11.50	
	135002	AA448542	Hs.251677	G antinen 78	87.00	11.00	
	135302	AA203555	Hs.98288	Homo sapiens cDNA FLJ14903 fis, clone PL	UU	6.50	
	133305	A4203355	HS.30200	numu sapienis cum rus 14903 lis, ciolis PL		0.00	

50	Unique Eos probeset identifier number Gene duster number Genbank accession numbers

36375.1 AA100756 AF020599 AA074529 AA075946 AA100849 AA085347 AA126309 AA079311 AA078323 AA065274
35330.1 X926259 M1124
Depthark AA6030340
Depthark AA603040
Depthark AA603040
Depthark A2603040
Depthark A260304
Depthark A260304
Depthark A260304
Depthark A260304
Depthark A260304
Depthark A260304
AA12637
AA12637 103439 123551 123861 102832 101972

126020 H79863

126547 U47732

R38438

85

Hs.114243 ESTs

Ha.182575

Hs.84072

transmembrane 4 superfamily member 3 solute carrier family 15 (H+/peptide tra

Table 74 shows 89 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 9900 probesets on the Eocl/Affymetrix Hud3 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 10 naminama Pkey ExAcon UnicenelD Unicene Title RI R2 aldo-keto reductase family 1, member C3 neuroblastoma (nerve tissue) protein calcitonin/calcitonin-related polypeptid 15 D17793 He 78183 164 10 100187 Hs.18551 100380 D82343 77.40 100576 X00356 Hs.37058 fatty acid blinding protein 4, adipocyte (NONE) 102 40 100971 RF370727 Hs.83213 463 80 672.00 1010/6 V01160 20 AW970254 Charol-Leyden crystal protein melanoma antigen, family A, 2 homeo box A5 66.00 Hs.36980 101175 U82671 77.20 62.80 101497 WASTER Hs.37034 homeo box A5
H28 histone family, member Q
complement component 4-binding protein,
dopa decarboxylase (aromalic L-arrino ac)
gbHERVK10HUMMTV revene transcriptase
sialyttransferase NM .003528 78.00 Hs 2178 101663 101677 NM_000715 186.20 Hs.1012 25 101745 Hs. 150403 80.08 577583 99.20 101941 NM DOGASE Hs.288215 103.10 102125 sidyltransferase retinoic acid receptor responder (tazaro macrophage stimulating 1 (hopatocyte gro hepatocyte nuclear factor 3, sipha dual specificity phosphatase 4 eyes absent (Drosophila) homolog 2 symplakir, Hunlingtin interacting protei neurolansin 102242 U27185 Hs.82547 67 On U37055 Hs.278657 Hs.299867 71.60 30 102360 1330840 69 70 102457 NM 001394 He 2359 153.00 102669 U71207 Hs.29279 65.70 AL079646 Hs.107019 58 80 102796 102829 NM 006183 Hs.80962 268.80 35 103207 X72790 neurotensm gb:Human endogenous retrovirus mRNA for alcohol dehydrogenase 7 (class IV), mu o casein, alpha gb:H.saplens DNA for endogenous retrovir 70.00 Hs.389 Hs.3155 103242 X76342 212.10 103260 X78416 130.70 64 60 103351 XB9211 104212 AB00229 Hs.173035 KIAA0300 protein 40 cell adhesion molecule with homology to solute carrier family 4, sodium bicarbon 104252 Hs.210863 63.80 AF002246 104258 AF007216 Hs.5462 Hs.9879 Hs.5250 94 40 FSTs 68.20 105024 AA126311 Al097144 ESTs, Weakly similar to ALU1_HUMAN ALU S ES1s, Weakly elimitar to ALU1_HOMAN ALU S glutamate-cysteline ligase, catalytic sub pt-601118016F1 NIH_MGC_17 Homo sapiens c Homo sapiens mRNA; cDNA DKFZpS648076 (fr hypothetical protein AF301222 106440 106566 AA449563 Hs.151393 71 10 45 BF298210 73 20 106605 106614 106654 AW772298 AA648459 AW075485 He 21103 83.80 Hs.335951 62.30 hypothetical protein AF-301222 phosphoserino aminotransferase hypothetical protein FLJ20417 ESTs, Moderately similar to 2109260A B c hypothetical protein MGC5350 Hs.286049 202.40 89.60 66.40 106996 H93281 Hs.10710 Hs.193540 50 108700 AA121518 108810 108857 109597 AW295647 Hs.71331 hypothetical protein MGC5330 anillin (Drosophila Scraps homolog), act 95 50 AK001468 Hs.62180 63.40 ESTs 85.00 AA989362 T65568 AI743860 Hs.293780 Hs.12860 Hs.12876 ESTa 55 109704 FSTs 60.60 76.40 110942 R63603 Hs.28419 **ESTs** 74.60 111722 R23924 Hs.23596 EST ESTs, Moderately similar to A46010 X-II Homo sapiens mRNA; cDNA DKFZp761J1324 (f microtubule-associated protein 1B Hs.293147 EA RO 112891 T03927 112992 AL157425 Hs.133315 76.70 60 113073 N39342 Hs.103042 Hs.21948 120 20 114251 H15261 ESTs 127.20 ESTS . Weatly similar to DAP1_HUMAN DEATH 115230 AA278300 Hs.124292 174.00 115291 BE545072 Hs.122579 91 00 66.40 115815 AW905328 Hs.180842 Hs.59761 65 115909 226 60 AWB72527 ESTs, Weakly similar to DAP1_HUMAN DEA hypothetical protein FLI/3093 hypothetical protein FLI/2093 hypothetical protein DKFZp434H247 gbrHUMGS0284B Human adult lung 3' direct gbryz33g08.s1 Morton Fetal Cochlea Homo 115965 AA001732 Hs.173233 82.80 116107 AI 133916 Hs.172572 361.60 D20508 D45652 69 00 116552 Hs.164649 116571 64.20 70 118466 N66741 63.50 120484 AA253170 AA398209 Hs.96473 81 60 He 97587 EST AL389951 nucleoporin 50kD 121034 Hs.271623 121423 AW973352 **ESTs** 64.40 75 122553 Hs.190121 60.40 major histocompatibility complex, class gb:ab19f02.s1 Stratagene lung (937210) H 188 60 122946 A1718702 Hs.308026 80.20 123130 AA487200 Hs.102670 124472 N52517 71.00 124526 125489 N62098 Hs.293185 ESTs, Weakly similar to JC7328 amino aci 104 90 80 ESTs, Moderately similar to ALU7_HUMAN A Hs.124984 Hs.26912 H49193 72.00 125731 ESTs 69.90 R61771 125747 NM_002884 Hs.865 RAP1A, member of RAS oncogene family 69.00 62.40

62.80

60.10

	w	O 02/086	443				PCT/US02/12476
	127472	AA761378	Hs.192013	ESTs	70.20		
	127610	AA960867	Hs. 150271	ESTs, Highly similar to unnamed protein	64.00		
	127742	AW293496	Hs.180138	ESTs	85.20		
	127987	AI022103	Hs.124511	ESTs	96.60		
5	128233	AW889132	Hs.11916	ribokinasa		78.90	
-	128420	AA650274	Hs.41296	Ebronectin leucine rich transmembrane p		106.90	
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80		
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53	
	129215	AB040930	Hs.126085	KIAA1497 protein	64.20		
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80		
10	130385	AW067800	Hs. 155223	stanniocalcin 2		139.60	
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60	
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40		
	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20		
15	131775	AB014548	Hs.31921	KIAA0648 protein	97.80		
13	132240	AB018324	Hs. 42676	KIAA0781 protein		71.00	
	132856	NM 001448	Hs.58367	glypican 4		88.40	
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20		
	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30	
20	133818	Al110684	Hs.7645	fibrinogen, B beta polypeptide	341.00		
20	134264	AF149297	Hs.8087	NAG-5 protein		64.30	
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53	
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00		
	134395	AA456539	Hs.8262	hysosomal-associated membrane protein 2		75.80	
25	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30	
23	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40		
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40		
	100003	74007120	110011				

TABLE 78 shows the accession numbers for those primeterys lacking uniquenel'De for Table 7A. For each probesed we have failed the gene cluster number from which the object-recipient services of the primeters of 30

35 Pkey: Unique Ecs probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

CAT number Accessions 40

103207

A72/99
BE298210 AB72315 AW086480 BE298417 AA459821 AA502537 BE287124 R14963 AA085210 AW274273 A333594 A308742 A1039688
A885056 AA76470 A787690 A885299 A398381 AW928224 AW340136 A7865956 AA452390 A31310815 A4464951
E52
D4582
D4582
D4582 106566

A188509 genbank_046562 genbank_N66741 entrez_K01160 K01160 entrez_X77583 \$77583 entrez_X89211 X89211 genbank_AA487200 116571 118466 101046 101941 103351 45

123130 AA487200 50

The Baltons 17/9 gains either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body fissues. Circulately diseased lung samples represent chronic non-malignant lung diseases such as Birosis, emphysema, and broad-hills. These genes were selected from 39/94 probests on the EcoloMymodist NatiC Genecity array. Cone expression data for each probeset obtained from hits analysis was expressed as everage intensity (Al), a normalized value reflecting the nistbler between of mRVM expression.

5

Play: Unique Eos probeast Identifier number
EbAcon: Essengial Accession number, Gerbank accession number
Unique Accession number, Gerbank accession number
Unique Title Linguis pera Bible
Rt: 70th personitie of Al for Inng Iumos dividad by 90th personitie of Al for normal lung
Rt: 70th personities of Al for Inng Iumos dividad by 90th personities of Al for normal lung 10

	Pkey	ExAcon	UnigeneiD	Unigene Title	R1	R2
15	300097	AJ916973	Hs.213603	ESTs	5.46	4.69
	300117	AW189787	Hs.147474	ESTs	0.58	0.56
	300197	AI686661	Hs.218286	ESTs	4.26	6.44
	300201	AI308300		gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
	300225	AI989963	Hs.197505	ESTs	1.68	1.75
20	300247	AW274682	Hs.161394	ESTs	1.08	2.28
	300256	Al469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00
	300337	AI707881	Hs.202090	ESTs	5.80	9.09
	300362	Z42308		gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
~ ~	300374	Al859947	Hs.314158	ESTs	2.99	4.38
25	300387	AW270150	Hs.254516	ESTs	1.50	2:53
	300440	AJ421541	Hs.146164	ESTs	3.98	5.25
	300441	R10367	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18 0.43	6.80 0.62
	300449	A1362967	Hs.132221	hypothetical protein FLJ12401	0.45	0.83
20	300469	AW135830	Hs.233955	hypothetical protein FLJ20401	4.10	9.75
30	300552	X85711	Hs.21838	hypothetical protein FLJ11191 gb:ab37d01_1 Stratagene HeLa cell s3 93	4.60	12.60
	300627	W27363	D- 40000		2.91	5.86
	300630	AW118822	Hs.128757	ESTs hypothetical protein FLJ23393	1.00	0.92
	300716	AI216113	Hs.126280	KIAA1542 protein	1.82	1.71
35	300738	AI623332	Hs.130541	KIAA1527 protein	4.48	8.22
33	300777	AA235361	Hs.96840	ESTs	1.29	1.18
	300790 300832	AI492471 - AI688147	Hs.188270 Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56
	300832	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34
	300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70	2.81
40	300878	AW449802	Hs.285901	Hamo sapiens cDNA FLJ20428 fis, clone KA	4.56	7.91
70	300897	A1890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23	1.58
	300926	AA504860	16.12/004	gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
	300960	AI041019	Hs.152454	ESTs	2.74	4.46
	300961	AW204069	Hs.312716	ESTs, Wealdy similar to unnamed protein	1.00	1.00
45	300962	AA593373	Hs.293744	ESTs	1.46	1,51
	300967	AA565209	Hs.269439	ESTs	0.39	1.30
	300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08
	300988	AJ927208	Hs.208952	ESTs	0.16	0.37
	301050	AW136973	Hs.288516	ESTs, Wealdy similar to S69890 mitogen !	3.23	1.94
50	301098	AA677570	Hs.185918	ESTs	6.76	14.28
	301157	AA729905	Hs.231916	ESTs	3.16	8.85
	301162	AI142118	Hs.129004	ESTs	1.68	7.18
	301170	AA737594	Hs.247606	ESTs	4.40	6.42
	301192	AI808751	Hs.121188	ESTs	6.38 4.35	11.59 7.78
55	301193	AA758115	Hs.128350	ESTs, Wealty similar to JC5423 2-hydroxy	1.56	1.61
	301267	AW297762	Hs.255690	ESTs	2.19	1.78
	301281	AA843986	Hs.190586	ESTs	0.76	0.76
	301341	AJ819198	Hs.208229	ESTs ESTs	1.00	1.81
60	301382	AA912839	Hs.163369 Hs.126830	ESTS	1.48	1.51
OU	301407	AW450466	Hs.159955	ESTS	0.51	1.48
	301452	AA975688	Hs.254655	Untitled	2.40	5.02
	301483 301494	AW272467 Al678034	Hs.131099	ESTs	2.79	3.41
	301521	AI733621	Hs.133011	zinc finger protein 117 (HPF9)	0.67	0.67
65	301521	AI077462	Hs.134084	ESTs	2.52	3.76
05	301580	Al878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92
	301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70
	301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
	301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78
70	301799	AA384252	Hs.286132	D15F37 (pseudogene)	6.93	7.04
	301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76
	301822	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.58	1.36
	301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00	1.00
	301868	T71508	Hs.13861	ESTs. Weakly similar to pH sensitive max	2.88	6.49
75	301882	178054		gb:yc97g09.r1 Soares infant brain 1NIB H	2.28	3.80
	301905	Al991127	Hs.117202	ESTs	1.00	1.00
	301948	AA344647	Hs.116724	aldo-kato reductase family 1, member B11	5.28	2.28
	301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48
	302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42
80	302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25
	302041	NM_001501	Hs.129715	gonadotropin-releasing hormone 2	0.71	0.99
	302072	AJ238381	Hs.132576	paired box gene 9	1.60	1.71
	302094	AJ286176	Hs.6786	ESTs	0.52	1.20
0.5	302095	AW044300	Hs.137506	Homo saplens BAC clone RP11-120J2 from 7	2.75	4.93
85	302148	AW269618	Hs.23244	ESTs	3.04	3.87

	w	O 02/086	5443			
	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal:belaGlcNAc beta 1,4- galactosylt	0.52 2.76	0.94 3.65
5	302206	Al937193	Hs.41143	phosphoinosliide-specific phospholipase killer cell lectin-like receptor subfami	1.00	1.00
د	302209	AF047445 AL049987	Hs.159297 Hs.166361	Homo sapiens mRNA; cDNA DKFZp584F112 (fr	1.68	1.50
	302235 302290	AL117607	Hs.175563	Homo saplens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
10	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CO3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
	302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
15	302432	AL080068	Hs.272534	Homo saplens mRNA; cDNA DKFZp564J062 (fr	2.44	6.77
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:a-1,3-D-mannosid	4.18 1.85	5.64 0.92
	302455	AA356923	Hs.240770 Hs.6335	nuclear cap binding protoin subunit 2, 2 SWI/SNF related, matrix associated, acti	2.04	2.13
20	302472 302476	AA317451 AF182294	Hs.241578	US snRNA-associated Sm-like protein LSm8	1.44	1.89
20	302489	780660	Hs.230424	Homo saplens cDNA FLJ13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	FSTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 8 (connexin 3	5.34	2.68
	302566	AA085996	Hs.248572	hypothelical protein FLJ22965	1.00	1.21
25	302630	AB029488	Hs.272100	SMS3 protein	0,52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophlia, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
20	302655	AJ227892	Hs.146274	ESTs	1.00 2.97	4.32 0.93
30	302656	AW293005	Hs.70704	Homo saplens, clone IMAGE:2823731, mRNA, S164 protein	0.80	0.95
	302668	AA580691 H65022	Hs.180789	gb:yu66g11.r1 Welzmann Olfactory Epithel	1.68	5.04
	302679 302680	AW192334	Hs.38218	ESTs	2,70	7.98
	302697	AJ001408	110.002.10	gb:Homo saplens mRNA for Immunoglobulin	4.25	8.13
35	302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12069		gb:Homo saplens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38 4.68
40	302771	H98476	Hs.42522	ESTs gb:Homo sapiens mRNA for immunoglobulin	2.94 3.49	6.31
	302789 302795	AJ245067 AJ245313	Hs,272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250	110.212000	gb:H.sapiens mRNA for variable region of	1,13	0.77
	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
45	302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940		gb:H.sapiens rearranged ig heavy chain (1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
	302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	0.53 2.45	0.67 2.62
50	302977	AW263124	Hs.315111	hypothetical protein FLJ12894 Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
30	303006	AF078950 AF090405	Hs.24139	gb:Homo sapiens clone 2A1 scFV anithody	1.41	1.86
	303011 303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprotyl Isomerase (cyclophilin)-l	0.72	0.76
	303077	AF163305	110.21000	gb:H.sapiens T-cell receptor mRNA	1.17	3.90
55	303090	AA443259	Hs.146286	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08 1.83
60	303131	AW081061	Hs.103180 Hs.233936	DC2 protein	2.02 1.32	3.95
60	303195	AA082211 AA082298	Hs.59710	myosin, fight polypeptide, regulatory, n ESTs	0.77	0.53
	303196	AA581439	Hs.152328	ESTs	0.24	0.63
	303216 303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
	303234	AA132255	Hs.143951	ESTs	2.28	3.17
65	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
05	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo saciens done 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
	303467	AA398801	Hs.323397	ESTs	4.54	9.65
70	303506	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09 1.00	0.04 1.72
	303552 303598	AA359799 AA382814	Hs.224662	ESTs, Weakly similar to unnamed protein ob:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
75	303756	AI738488	Hs.115838	ESTs	1.08	1.43
	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyocherin (Importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
	303946	AW474196	Hs.306637	Homo sanians cDNA FLJ12363 fis, clone MA	5.06	11.86
80	303978	AW513315			5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06 2.35
	303990 303998	AW515465 AW516449		gb:xta71a11.x1 NCI_CGAP_Kid8 Homo sapiens gb:xt68f05.x1 NCI_CGAP_Ut2 Homo sapiens	1.15	9.35
	303998	AW516611		ob-yo/70h11 v1 N/2 CGAP Ov39 Homo sapiens	4.85	6.28
85	304006	AW517947		gb:xp70b11.x1 NCI_CGAP_Ov39 Homo sapiens gb:xl66h02.x1 NCI_CGAP_Ut2 Homo sapiens	3.21	4.07

	w	O 02/08	6443			
	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB21B7 Fetal brain, Stratagene Homo s	2.15 5.88	3.55 11,80
5	304026. 304028	T03160 T03266		gb:FB26F2 Fetal brain, Stratagene Homo s gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
,	304028	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
	304046	T54803	NS.244021	gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		9b:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
10	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		qb:vi87q02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares infant brain 1NIB H	1.00	2.76
	304155	H68696		gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
1.5	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34 11.03
15	304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W rlbosomal protein, large, P0	6.47 1.34	1.16
	304267	AA064862 AA069711	Hs.73742	vimentin	3.40	5.40
	304270 304287	AA079286	Hs.297753 Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
	304267	AA179868	115.70400	gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
20	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430	AA347682		gb:EST54044 Fetal heart II Homo saplens	1.00	1.00
	304456	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares overy tumor NbHOT H	2.18	1.15
~-	304526	AA476427		cb:zx02c05.s1 Soares total fetus_Nb2HF8_	5.38	14,11
25	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibito	0.55 1.95	1.20 2.10
	304607 304640	AA513322 AA524440	11- 444004	gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo saplen femilin, light polypeptide	2.10	2.83
	304650	AA524440 AA527489	Hs.111334 Hs.3463	ribosamai protein S23	3.33	12.82
30	304735	AA576453	NS.3463	gb:nm75h11.s1 NCI_CGAP_Co9 Homo saplens	1.33	0.88
50	304760	AA580401		gb:nn13g09.s1 NCI_CGAP_Co12 Homo saplens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
	304921	AA603092	Hs.297753	vimentin	2.47	4.24
35	304966	AA613893	Hs.282435	ESTs .	6.78	11.66
	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305018	AA626876		gb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCI_CGAP_Pr24 Homo saplens	5.68 1.48	11.59 1,37
40	305111	AA644187	Hs.303405	ESTs gb:nt01g08.s1 NCI_CGAP_Lym3 Homo saplens	1.76	4.61
	305148 305159	AA654070 AA659166	Hs.275668	EST, Weakly similar to EF10_HUMAN ELONG	1.00	2.15
	305199	AA665955	NS.270000	gb:ag57d12.s1 Gessler Wilms turnor Homo s	5.31	8.14
	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
45	305235	AA670480	7.2.1.00 0	gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201		gb:z]44f07.s1 Soares_fetal_fiver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
	305394	AA720942	Hs.300697	Immunoglobulin heavy constant gamma 3 (G	1.16 5.86	0.68 9.87
50	305413 305447	AA724659 AA737856		gb:al10f08.s1 Soares_parathyroid_tumor_N gb:nx10c08.s1 NCL_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
	305528	AA769156	110,000012	gb:nz12e05.s1 NCI_CGAP_GCB1 Homo saplens	6.44	9.10
55	305612	AA782347	Hs.272572	hemodobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyrold_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal amtein S18	7.57	10.20
	305637	AA806124		gb:on29a12.s1 NCI_CGAP_Pr25 Homo saplens	4.78	12.42
	305639	AA806138		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo saplens gb:oe29c12.s1 NCI_CGAP_Pr25 Homo saplens gb:nw31e04.s1 NCI_CGAP_GC80 Homo saplens4	0.89	0.70
60	305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GCB0 Homo sapiens4	4,91	8.71 9.40
	305690	AA813477	11. 70740	gb:al67a05.s1 Soares_testis_NHT Homo sap ribosomal protein, large, P0	0.19	0.81
	305726	AA828156	Hs.73742	gb:of34a02.s1 NCI_CGAP_Kid6 Homo sapiens	5.12	9.29
	305728 305759	AA828209 AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
65	305792	AA845256		gb:ak84a08.s1 Barstead spleen HPLR82 Hom	2.34	4.25
05	305864	AA864374	Hs.73742	elbocomal protein Jama PO	0.30	1.40
	305901	AA872968	115.70742	gb:oh63h08.s1 NCI_CGAP_Kid5 Horno saplens gb:nx21h02.s1 NCI_CGAP_GC3 Horno saplens	2.10	5.21
	305910	AA875981		ab:nx21h02.s1 NCI_CGAP_GC3 Homo saplens	0.32	1.01
	306015	AA897116		gb:am08b07.s1 Soares_NFL_1_GBC_S1 Homo s1	.56	1.12
70	306017	AA897221	Hs.109058	riboscmal protein S6 kinase, 90kD, polyp	5.21	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Home s	7.38	20.69
	306065	AA906725	•	gb:xk78g02.s1 NCI_CGAP_GC4 Homo sapiens gb:xk85h11.s1 NCI_CGAP_Kid3 Homo sapiens	7.19 6.50	13.48 9.13
75	306104	AA910956		gb:ok85h11.s1 NCI_CGAP_RX03 Homo sapiens gb:og21e07.s1 NCI_CGAP_PNS1 Homo sapiens	4.21	9.13 5.25
13	306109 306148	AA911861 AA917409	Hs.288036	IDNA legantenthrophornhala transferse	2.20	2.70
	306242	AA932805	113.200030	tRNA isopentanybyrophosphate transferas gb:oo60g04.s1 NCI_CGAP_Lu5 Homo sapiens gb:oi53h05.s1 NCI_CGAP_HN3 Homo sapiens	2.84	5.35
	306288	AA936900		obxi53h05.s1 NCI CGAP_HN3 Homo saplens	1.60	1.12
	306325	AA953072	Hs.210546	Interleukin 21 receptor	1.65	2.26
80	306353	AA961382	Hs.275865	ribosomat protein S18	3.78	6.32
	306375	AA968650	Hs.276018	EST. Moderately similar to JC4662 ribos	4.30	5.74
	306396	AA970223		nb:nn09d05 s1 NCL CGAP Kid6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
0.5	306442	AA976899		gb:oq35e09.s1 NCI_CGAP_GC4 Homo sapiens gb:oq72e12.s1 NCI_CGAP_Kid6 Homo saplens	4.67	7.44
85	306446	AA977348		go:oq/2e12s1 NCI_CGAP_Not Homo sapiens	3.92	6.27

	WO 02/086443										
	306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77					
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72 1.00	5.37 1.00					
	306510	AA988546		gb:or84d07.s1 NCI_CGAP_Lu5 Homo sapiens	6.61	10.91					
5	306555	AA994304 AA994530	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R gb:ou57e08.s1 NCI_CGAP_Br2 Homo saptens	16.20	31.83					
,	306557 306572	AA995686		gb:0057606.51 NCL_CGAP_BIZ HORR Septemb	2.51	6.52					
	306582	AA996248		gb:os25c12.s1 NCI_CGAP_Kid5 Homo sapiens gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13					
	306598	Al000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68					
	306605	Al000497	Hs.119500	ribosomal protein, large P2	1.96	8.60					
10	306656	AJ004024		gb:ou11b07x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45					
	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28					
	306686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60 1.19					
	306702	AI022565	Hs.307670	EST	1.47	2.83					
15	306728 306751	AI027359	Hs.272572	hemoglobin, alpha 2 gb:ow70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21					
13	306767	AI032589 AI038963	Hs.249118	ESTs	3.33	6.06					
	306892	A1092465	110.240110	gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46					
	306897	AI093967		gh:ga33c06.s1 Soares NhHMPu, S1 Horno sapi	2.12	2.85					
	306956	AJ125111		gb:em66/03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52					
20	306958	AJ125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56					
	307035	Al142774	Hs.119122	ribosomai protein L13a	2.00	4.70					
	307041	Al144243		gb:qb85b12x1 Soares_fetal_heart_NbHH19W	9.12	12.56					
	307091	Al167439		gb:ax70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88 3.55	8.52 6.44					
25	307181	Al189251 Al205798	Hs.111334	gb:qc99g06.x1 Soares_pregnant_uterus_NbH ferritin, light polypeptide	2.46	465					
2.5	307297 307317	A1208303	Hs.147333	EST EST	5.64	10.13					
	307327	Al214142	Hs.246381	CD68 antigen	3.18	5.15					
	307382	Al223158	Hs.147885	ESTs	2.02	3.73					
	307410	Al241715	Hs.77039	ribosomal protein S3A	0.72	0.48					
30	307415	Al242118		gbxh92b02x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51					
	307423	Al243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44					
	307426	AI243364		gbxh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18 1.00	7.67 1.00					
	307517	Al275055		gb:q172d03.x1 Soares_NhHMPu_S1 Homo sapi gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20					
35	307551 307561	Al281556 Al282207		gbxp65a12x1 Soares_fetal_lung_NbHL19W	4.74	15.51					
33	307608	AJ290295		gb:cm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19					
	307657	Al306428	Hs.298262	ribosomal protein S19	1.76	2.44					
	307691	Al318285		ob-th/17h01 x1 NCL CGAP Ox37 Homo sanians	1.59	1.31					
	307701	AI318583	Hs.276672	EST, Wealthy similar to RL6_HUMAN 60S RI	1.90	2.13					
40	307718	A1333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99					
	307730	Al336092		gb:qt43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99					
	307760	Al342387		gb:qt27107.x1 Soares_pregnant_uterus_NbH	1.00	1.00					
	307764	Al342731		gbct/27(07.x1 Soess, pregream, Literus, NoH pbco26607.x1 NCI, CGAP Lust Homo septems gbct/95607.x1 NCI, CGAP, Co16 Homo septems gbct/95607.x1 NCI, CGAP, CG4 Homo septems gbct/95607.x1 NCI, CGAP, GC4 Homo septems gbct/95607.x1 NCI, CGAP, GC4 Homo septems gbct/95607.x1 NCI, CGAP, CG4 Homo septems gbct/95607.x1 NCI, CGAP, CG14 Homo septems gbct/95607.x1 NCI, CGAP, CG	4.52 1.42	12.58 1.00					
45	307783	Al347274 Al350556		gbtc05d02x1 NC_CGAP_C016 Home septens	6.57	9.61					
43	307798 307807	AI350556 AI351799		gbxt1809x1 NCL CGAP_GCA Home seriors	3.38	7.68					
	307808	Al351826		nhyt09n03 v1 NCL CGAP GC4 Homo saniens	0.33	0.86					
	307820	Al355761		obmt94a11.x1 NCI. CGAP. Co14 Homo sapiens	7.94	21.57					
	307830	Al358722	Hs.276737		2.05	3.32					
50	307852	Al365541		gb:rg208g05.x1 NCI_CGAP_CLL1 Homo sapiens gb:rg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21					
	307902	AI380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo saplens	3.13	4.99					
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00 5.86	3.01 12.64					
	308002	AI435240	Hs.283442	ESTs gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83					
55	308011 308023	Al439473 Al452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88					
23	308041	A3458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06					
	308059	AJ468938	Hs.276877	EST, Wealthy similar to RL10_HUMAN 60S R	1.80	1.98					
	308085	AJ474135	Hs.181165	eukarvotic translation elongation factor	3.38	4.14					
	308101	AI475950	Hs.181165	aukaryotic translation elongation factor	1.30	3.87					
60	308106	AJ476803		gb:tj77e12.x1 Scares_NSF_F8_9W_OT_PA_P_S2	.38	8.72					
	308122	AI480123	Hs.309411	EST gb:tn93d08.x1 NCI_CGAP_Ut2 Homo sapiens	2.70 0.66	3.86 1.33					
	308154 308171	Al500600 Al523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86					
	308211	AI557029	Hs.278572	anaplastic lymphoma kinase (KI-1)	2.43	2.14					
65	308213	Al557041	110-210012	nh:PT2 1 12 E04.r tumor2 Homo saplens cD	3.34	3.79					
05	308216	AI557135		gb:PT2.1_12_E04.r tumor2 Homo saplens cD gb:PT2.1_13_H06.r tumor2 Homo saplens cD	4.61	4.78					
	308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo saplens cD	4.87	7.94					
	308271	Al567844	Hs.252259	ribosomal protein S3	2.40	6.35					
	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33					
70	308362	Al613519	Hs.105749	KIAA0553 protein	1.24	1.41					
	308413	Al636253	Hs.196511	ESTs	3.16	4.82					
	308450	A1650860	Hs.96840	KIAA1527 protein EST, Moderately similar to 138055 myosi	1.79 4.87	2.68 8.27					
	308464 308588	AI672425 AI718299	Hs.277117	gb:as51g12.x1 Barstoad aorta HPLRB6 Homo	3.90	5.64					
75	308599	AI719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	5.12					
, ,	308615	Al738593	Hs.101774		3.11	2.36					
	308643	Al745040		gb:tr19a12x1 NCL_CGAP_Ov23 Homo sapiens gb:wt09c10x1 NCL_CGAP_CLL1 Homo sapiens	3.98	3.69					
	308673	A1760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sepiens	0.82	0.99					
	308697	AI767143		gb.wi97a07.x1 NCl_CGAP_Kid12 Homo sapien	2.76	5.59					
80	308762	AI807405	Hs.259408	CQTe	3.17	6.30					
	308778	AI811109	II- Man	gb.tr04c11.x1 NCL_CGAP_Ov23 Homo saplens	1.00 2.94	1.00 5.15					
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor gbwk52c01.x1 NCI_CGAP_Pr22 Homo saplens	4.41	8.34					
	308808 308823	AI818289 AI824118	Hs.217493	gb.wk52c01.X1 NCI_CGAP_F122 Holido sapisilis sanexin A2	1.85	1.92					
85	308875	AIB32332	110.211433	gb:at48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80					

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268886 ARS3340 ARS5000 ARS50		308879	O 02/084 AI832763	5443 Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
308989 ABS8845 ABS92024 BL1777 phothophishiphish		308886		FS.70000	nh:st76d10.x1 Barstead colon HPLRB7 Home		
\$ 386934 AR55027 Hs.177 phosphatiphronized glycan, clase H 4.14		308898	AI858845		gb:wi32d10.x1 NCI_CGAP_Ut1 Homo saplens	2.45	3.44
200915 AB19756 H.20027 September	-		AI865023	Hs.177	phosphatidylinositol glycan, class H		6.76
200915 AB19756 H.20027 September	5	308966	AI870704		gb:w/47h01.x1 NCI_CGAP_UTI Homo sapiens	7.15	11.00
200915 AB19756 H.20027 September		308979			nh:tn39f01.x1 NCI_CGAP_Ut1 Home sadens		
100		309051	AI911975		gb;wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	
1997 1997	10		AI917366	Hs.78202	SWI/SNF related, matrix associated, act		
200722 ARCHITICATE	10			Hs.119598			
15 309164 ABST761				HS.200804	nh-wn95a11.x1 NCI CGAP Kid11 Home saplen	1.00	2.92
Section		309128	AI928816	Hs.180842	obosomal orolein I 13	1.38	5.55
2009.00 AMISSIZE Ha.299469 EST E					gb:wp84b09.x1 NCI_CGAP_Brn25 Homo saplen	2.43	
2003939 AM0014823 AM014824	15			Un 200426	gb:wxt63g05.x1 NCI_CGAP_Br18 Home sapiens		
2009.000.000.000.000.000.000.000.000.000		309200		115.200420	chayn66c06 x1 NCL CGAP GC6 Homo sapiens	4.36	9.43
2-98 3-11		309303	AW004823		gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
208459 AMP117965 Ha.58114	20	309411		Hs.244144	EST	4.30	7.14
2-98 309479 AVM 35225 H-278771 1	20	309437			tubuhn, alpha, ubiquidus keratin 18	2.49	
209999 AM150807 His 1957 His 297871		309476	AW129368	10.00114	ch:ve14h05.v1 NCL CGAP Ut4 Homo saniens	2.08	6.60
255 309552 AM192004 H. 1-277816 septiment of the property of t		309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
2006025 AMP192004 Hz.275816 Series (or equilibril) problemate hibbit 4.46 12.00 Series (or equilibril) problemate hibbit 4.46 Series (or equilibril) problemate hibbit 4.46 Series (or equilibril) problemate hibbit 4.46 Series (or equilibril) 4.46 Se	20			Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	
309915	23			D- 207681	gb:xg33e10.X1 NCI_CGAP_UTI Homo saparts earing (or cycleina) proteinate inhibit		12.06
309875 AMV27214 1418/3505 157 AMV27724 1418/3505 157 AMV27724 1418/3505 157 AMV27724 157 AMV27818 157 AMV27724 157 AMV27818 157 AMV27724 157 AMV27818 157 AMV27724 157 AMV27818 157 AMV2788 157		309641	AW194230	Hs.253100	FCT Moderately similar to GHHU to gamm	1.47	1.39
309893 AW723921 Hs. 181357 309893 AW723916 Hs. 181357 30979 AW728916 Hs. 181357 30993 AW728916 Hs. 181357 30993 AW728916 Hs. 181357 30993 AW738916 Hs. 181357 30993 AW73917 40 30993 AW73918 Hs. 181357 30993 AW73917 Hs. 181357 30993 AW7391		309675		Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	16.20
309700 AW341717 th. 179617 blufult, belas polypapidds 1.41 1.25 1	20			Hs.181357	iaminin receptor 1 (67kD, ribosomal prot		
309773	30				mannosidase, aipna, class ZA, mumou Z	1 41	1.25
309783 AV727366 1.5 1.		309747	AW264889	113.173001	cb:xn36b02.x1 NCI CGAP Lu28 Homo sapiens	5.00	8.35
300783 AM7278401 Ha.284799 S00783 AM7278401 Ha.284799 S00783 AM7278401 Ha.284799 S00783 AM728974 Ha.300897 AM728974 Ha.48030		309769	AW272346		gb:xs13c10.x1 NCI_CGAP_Kid11 Homo sapien	5.76	11.90
309799	25	309782	AW275156				
1.00 1.00	33			Hs.254/98	champshot vt NCL CGAP Ov39 Homo sanions	1.68	1.44
1.00 1.00		309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
\$\frac{9.09529}{2.09589}		309903	AW339071	Hs.300697		1.05	1.18
\$30986 AM-44911 16.2871379 Physiolegist growth Mic-Colds (1987,29549116 (pt. 1989) 1.000 1	40				gb:hd05g08.x1 Soares_NFL_1_GBU_S1 Home s	2.30	13.71
\$30986 AM-44911 16.2871379 Physiolegist growth Mic-Colds (1987,29549116 (pt. 1989) 1.000 1	40		AW341683		mhhd13d01.x1 Soares NFL T GBC S1 Homo s	1,20	12.70
\$30986 AM-44911 16.2871379 Physiolegist growth Mic-Colds (1987,29549116 (pt. 1989) 1.000 1			AW341936		gb:hb73f10.x1 NCI_CGAP_Ut2 Homo sapiens		18.29
45 310098 AM98941 AM98942 Am99942		309964	AW449111		hypothetical protein MGC3265	1.99	3.07
310098 AMS994H H-161954 EST6 0.31 0.76	15	310002	A1439096		Homo sapiens mKNA; CUNA UKF-Zp304F116 (if	1.51	1 22
310109 A733094 h. 148333 ESTe 2.65 5.85	43		AVV 130022 AI685841	Hs.161354	ESTs. Weally sitting to 040010 promot	0.31	0.76
Signature		310109	AJ203094	Hs.148633	ESTs	2.06	5.83
				Hs.147253			
310146 A0086914 In-197422 ESTs 9.50 15.3	50			HS.223790		1.00	2.71
310193 ARCRES III H-147562 EST6 2.85 4.18 31025 ARCRES III H-147562 EST6 3.26 4.18 31026 ARCRES III H-147572 III H-147573 III H-147572	50	310146	AJ206614	Hs.197422	ESTs	9.50	15.31
		310193		Hs.147562		2.85	4.18
STOCK ADDRESS ADDRES		310255				3.28	4.40
310275 AV2102 https://dx.dx.dx.dx.dx.dx.dx.dx.dx.dx.dx.dx.dx.d	55			Hs.74170		0.26	0.86
310208	55	310275	AJ242102	Hs.213636	ESTs	5.43	8.19
130333 AR353200 16,145402 ESTe 1.17 1.91				Hs.156055		3.15	
\$\frac{3}{3}\frac{3}\frac{3}\frac{3}{3}\frac{3}{3}\frac{3}{3}\frac{3}{3}\frac{3}{3}\fr		310290		HS.149103		1.17	1.91
310365 A/35392 ht.166151 ESTs 5.56 7.79 310443 A/9119019 ht.166231 ESTs 2.20 15.35 310444 A/9119652 ht.166231 ESTs 2.20 15.35 31047 A/914961 ht.17073 ESTs 3.39 8.19 31047 A/914961 ht.17073 ESTs 3.39 8.19 31047 A/914961 ht.17073 ESTs 3.39 8.19 31047 A/914961 ht.17073 ESTs 3.30 7.81 31047 A/914961 ht.17073 ESTs 3.30 7.33 31047 A/914961 ht.17073 ESTs 3.30 7.33 31047 A/914961 ht.17073 ESTs 3.30 7.33 31047 A/914961 ht.190724 ESTs 3.30 7.33 31047 A/914961 ht.190724 ESTs 3.30 7.33 31047 A/914961 ht.190724 ESTs 3.30 8.19 310648 A/914767 ht.190724 ESTs 3.30 8.19 310649 A/914978 ht.190724 ESTs 3.30 8.19 310724 A/914964 ht.190725 ESTs 3.30 8.19 310724 A/914964 ht.190725 ESTs 3.30 8.49 310724 A/914964 ht.190725 ESTs 3.30 8.49 310724 A/914964 ht.190725 ESTs 3.30 8.40 8.40 8.30 8.30 8.40 8.40 8.30 8.30 8.40 8.40 8.30 8.30 8.40 8.40 8.30 8.30 8.40 8.40 8.30 8.30 8.40 8.40 8.30 8.30 8.40 8.40 8.30 8.30 8.40 8.40 8.30 8.30 8.30 8.40 8.40 8.30 8.30 8.30 8.40 8.40 8.30 8.30 8.40 8.40 8.30 8.30 8.30 8.40 8.40 8.30 8.30 8.30 8.40 8.30 8.30 8.30 8.30 8.30 8.30 8.30 8.3	60		AI261340	Hs.145517	ESTs	4.81	9.95
31044		310385	AJ263392	Hs.156151	ESTs	5.96	7.79
31046 AZESTIS 14,148226 EST6 2,19 3,85						2.90	
\$\frac{55}{310648} \qquad \qquad \qqqq \qqq \qqqq \qqq \qqqq \qqq \qqqq \qqqqq \qqqq \qqqqq \qqqqqq		310444				2.18	3.85
310477 A984980 H, 1171073 EST6 1.00 1.00 310512 A7827560 H, 1502772 EST8 H, Highly similar to AC004836 t simil 3.07 2.14 310514 A811454 H, 150772 EST8 H, Highly similar to AC004836 t simil 3.07 2.14 310564 A812567 H, 1502724 EST8 EST8 2.39 4.08 310564 A812567 H, 159102 EST8 2.39 310564 A814577 H, 159102 EST8 2.39 310564 A814577 EST8 2.30 310565 A814578 H, 150372 EST8 2.30 310565 A814568 H, 150372 EST8 2.30 310565 A814568 H, 150372 EST8 2.30 310724 A814640 H, 150737 EST8 2.30 310724 A814640 H, 150739 EST8 2.30 310725 A815650 H, 150739 EST8 3.30 310726 A815650 H, 150739 EST8 3.30 310726 A815650 H, 150739 EST8 3.30 310864 A875799 H, 150779 EST8 3.40 310864 A875799 H, 150779 EST8 3.51 310867 EST8 3.51 310868 A875789 H, 150779 EST8 3.51 310868 A875	65	310468		Hs.196398	ESTs	3.39	5.19
310514 A881145 Ha.190724 ESTe L.190 STe Highly similar to AC004636 t simil 3.30 7.33 3.00 3.00 7.33 3.00 7.33 3.00 7.33 3.00 7.33 3.00 7.33 3.00 7.33 3.00 7.33 3.00 7.33 3.00 7.33 3.		310477	AJ948801	Hs.171073	ESTs		1.00
310524 AM052270 14.12496 ESTA, Highly similar to AC004836 1 simil 0.72 1.44							
		310514			ESTs. Highly similar to AC004836 1 simil	0.72	1.44
310508 AR92224 15.199102 ESTs 5.60 6.48	70	310547	AI302654	Hs.208024	ESTs	3.26	3.46
316624 A351594		310584	AI653007	Hs.158304			4.08
310536 AB14737 Hs.164175 EST6 1.55 1.77 5310546 AB47262 1.65672 EST6 1.65072 EST6 1.76 1.70 5310546 AB472124 1.615727 EST6 1.60 1.20 5310714 AB14646 1.615726 EST6 1.76 3.51 5310714 AB14646 1.615726 EST6 1.76 3.51 5310734 AB16650 1.615726 EST6 1.60 3.51 5310734 AB76766 1.615726 EST6 1.60 3.51 531084 AB76767 1.617726 EST6 2.24 1.60 531085 AB767174 1.617726 EST6 2.25 1.60 531085 AB767174 1.617726 EST6 2.25 1.60 531085 AB767174 1.617726 EST6 2.25 1.60 531085 AB767174 1.61732 EST6 2.55 5		310608		Hs.196102			
75 310648 A347969 hs.159672 ESTe 310954 A158470 hs.159672 ESTe 310954 A158470 hs.15772 hs.157		310636		Hs.164175		1.85	1.71
310505 AM21214 Hs.157757 ESTs 4.82 6.27 310714 AM19446 Hs.157852 ESTs 1.76 3.51 310722 AB98031 Hs.157862 ESTs 1.14 6.85 310722 AB98031 Hs.157289 ESTs 1.14 6.85 310726 AB195501 Hs.157295 ESTs 1.476 7.37 310744 AD576796 Hs.167172 ESTs 4.76 7.37 310848 AM59554 Hs.167182 ESTs 2.24 1.99 310881 AM2951714 Hs.21703 ESTs 1.00 2.33 310881 AM2951714 Hs.167382 ESTs 1.00 2.33	75	310648	AI347863	Hs.156672	ESTA	0.17	
310714 AM14464 Extra Estra 1.76 2.51 3.51		310694		Hs.157752		5.40 4.82	13.22
310772 A098903 14:157289 EST's 6.46 50.3 01076 A098903 14:157289 EST's 8.46 53.3 01076 A098903 14:15729 EST's 8.476 7.37 310764 A0787909 14:167172 EST's 4.76 7.37 31088 A098954 14:161286 EST's 2.64 1.99 310881 A09891714 14:221703 EST's 1.00 2.33 108884 A021677 14:161332 EST's 6.37 5.99 40.37 5.99		310695			ESTs		3.51
80 310756 AS16660 ht.158707 ESTs 8.46 13.0 310764 ASTS709 ht.167172 ESTs 4.78 7.7 310846 AMSS54 ht.167172 ESTs 2.0 6.3 310846 AMSS54 ht.167280 ESTs 2.0 6.3 310851 AMSS717 ht.261332 ESTs 5.37 7.34			AI989803	Hs.157289	ESTs	1.14	6.85
310948 AH59554 Ha.161286 EST6 2.84 1.95 310951 AW291714 Ha.221703 EST5 1.00 2.33 310984 AH21677 Ha.161332 EST5 6.37 7.94	80	310756	AI916560	Hs.158707			
310851 AW291714 Hs.221703 ESTs 1.00 2.32 310854 AM21677 Hs.161332 ESTs 6.37 7.94				Hs.167172		2.70	1.37
310854 AH21677 Hs 161332 ESTs 6.37 7.94		310848	AM291714	Hs.161286	ESTs.		2.32
85 310858 AI871000 Hs.161330 ESTs 6.07 9.84		310854	AJ421677	Hs.161332		6.37	7.94
	85	310858	AI871000	Hs.161330	ESTs	6.07	9.84

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	310864	Al924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63 16.68
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A ESTs	7.07 1.00	1.00
5	310922 310955	AW195634 AI560210	Hs.170401 Hs.263912	ESTS ESTS	10.08	17.66
,	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AI521830	Hs.171050	ESTs	3.08	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
10	311034	AI564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44 6.04	14.19
10	311074 311134	AW290922 AI990849	Hs.199848 Hs.196971	ESTs ESTs	3.54	6.96
	311174	AW450552	Hs.205457	periaxin	0.65	0.95
	311187	AI638374	Hs.224189	ESTs	2.46	2.78
	311220	A1656040	Hs.196532	ESTs	1.10	2.52
15	311230	A1989808	Hs.197663	ESTs	1.41 2.18	1.75 2.11
	311236	AI653378	Hs.197674 Hs.200266	ESTs ESTs	0.63	5.11
	311242 311258	AW016812 Al671221	Hs.199887	ESTs	1.00	1.41
	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
20	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.96	6.70
	311351	AI682303	Hs.201274	ESTs	4.77 2.80	9.38 6.06
	311390 311405	AW392997 AW290961	Hs.202280 Hs.201815	ESTs ESTs	3.80	11.68
25	311409	A1698839	NS.201013	gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94
23	311420	Al936291	Hs.209867	ESTs	5.30	12.56
	311443	AI791521	Hs.192206	ESTs	4.39	6.09
	311467	Al934909	Hs.175377	ESTs	1.00 2.76	1.04 5.61
30	311479	AI933672	Hs.211399	ESTs	2.50	5.73
30	311488 311495	R57390 AW300077	Hs.301064 Hs.221358	arfaptin 1 ESTs .	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
	311537	AI805121	Hs.211828	ESTs	3.69	5.85 - 1.34
35	311543	AI681360	Hs.201259	ESTs POM (POM121 rat homolog) and ZP3 fusion	1.73 3.31	6.12
	31 1551	AW449774 AI819230	Hs.296380 Hs.211238	interleukin-1 homolog 1	1.00	1.00
	311557 311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
40	311563	AJ922143	Hs.211334	ESTs	2.39	3.32
	311586	AI827834	Hs.211227	ESTs .	2.47 1.00	3.85 1.00
	311616	AW450675 AI924307	Hs.212709 Hs.213464	ESTs ESTs	4.16	6.74
	311621 311635	Al928456	Hs.213081	ESTS	2.17	3.76
45	311668	AW193674	Hs.240044	ESTs	2.60	3.12
	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96 8.83
	311700	R49601	Hs.171495	retinoic acid receptor, beta ESTs, Weakly similar to CKG_HUMAN VOLTA	6.28 5.00	8.17
50	311714 311735	AW131785 AW294416	Hs.246831 Hs.144687	Homo saplens cDNA FLJ12981 fis, clone NT	0.96	0.72
50	311743	T99079	Hs.191194	ESTA	1.00	1.95
	311783	AJ682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AI056769	Hs.133512	ESTs	1.34	3.97 13.3
55	311799	AA780791	Hs.14014 Hs 254325	ESTs, Weakly similar to KIAA0973 protein	8.52 3.58	3.91
33	311819 311823	AW265275 AI069422	Hs.131297	ESTS	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
	311896	AW206447		gb:UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su	1.66	1.13
60	311910	N28365	Hs.22579	Homo saplens clone CDABP0036 mRNA sequen	1.66 0.42	2.30 2.63
	311923 311933	T60843 Al597963	Hs.189679 Hs.118726	ESTs ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
	311960	AW440133	Hs.189690	ESTs	3.87	6.62
65	31 1967	Al382726	Hs.182434	ESTs	5.80	8.14
	311975	AAB04374	Hs.272203	Homo sepiens cDNA FLJ20843 fis, clone AD	0.98 0.12	3.26 1.39
	312005	178450	Hs.13941 Hs.284450	ESTs ESTs	3.78	4.92
	312028 312046	T78886 AJ580018	Hs.268591	ESTS	4.11	7.32
70	312040	T83748	Hs.268594	ESTs	2.36	3.08
70	312064	AA576713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTs	0.68 3.06	0.85 4.48
75	312094	Z78390	11. 449400	gb:HSZ78390 Human fetal brain S. Meier-E zinc finger protein 148 (pHZ-52)	4.52	9.70
13	312097 312118	Al352096 TR5332	Hs.112180 Hs.178294	FSTs	2.40	2.60
	312118	AI052609	Hs.17631	Homo saplens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89855	Hs.195648	ESTs	0.67	1.03
	312175	AA953383	Hs.127554	ESTs	5.85	10.6
80	312179		Hs.269864	ESTs	2.41 0.24	3.32 0.89
	312201 312207	Al928365 H90213	Hs.91139 Hs.191330	solute carrier family 1 (neuronal/epithe	2.20	4.55
	312207		ris.191330	gb:za55a07.s1 Soares fetal liver spleen	4.28	11.1
	312252	Al128388	Hs.143655	ESTs	1.64	1.57
85	312304	AA491949	Hs.269392	ESTs	0.12	2.47

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	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein ESTs	5.78 0.44	4.46 1.74
	312321 312331	R66210 AA825512	Hs.186937 Hs.289101	glucose regulated protein, 58kD	3.73	5.96
5	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363	Al675558	Hs.181867	ESTs	10.08	16.73
	312375	AJ375098 R52089	Hs.172405	cell division cycle 27 ESTs	2.78 1.00	3.71 1.00
	312376 312389	A3863140	Hs.172717	nhrtz43h12 x1 NCI CGAP Bm52 Horno sapien	2.37	3.98
10	312437	AA995028		gb:RC4-8T0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	Al051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451 312458	R59989 A1167637	Hs.176539 Hs.146924	ESTs ESTs	4.96 1.11	10.04
	312507	A1167637 A1168177	Hs.143653	ESTs	5.89	8.24
15	312520	Al742591	Hs.205392	ESTs	3.30	8.92
	312548	AJ566228	Hs.159426	hypothetical protein PRO2121	1.38 0.40	1.65 0.77
	312564 312583	H21520	Hs.35088 Hs.124141	ESTs ESTs	0.40	0.94
	312599	Al193122 Al865073	Hs.125720	ESTs	3.75	5.29
20	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38 0.98	1.13 2.03
	312666 312689	AJ240582 AW450461	Hs.214678 Hs.203965	ESTs	0.90	0.61
	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Wealdy similar to unnamed protein	4.20 2.67	6.23 3.15
	312893 312902	AI016204 AW292797	Hs.172922 Hs.130316	ESTs ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
	312925	N90868	Hs.271695	ESTs	2.50	4.25
30	312936	Al681581	Hs. 121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30 0.60	4.80 1.05
	312978 312980	N24887 AA497043	Hs.292500 Hs.115685	ESTs ESTs	3.12	3.60
	312984	N25871	Hs.177337	ESTs	2.03	2.13
35	313000	Al147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520 AJ419290	Hs.170504 Hs.149990	ESTs ESTs, Weakly similar to unnamed protein	0.96 6.48	1.39 13.20
	313039 313049	AW293055	Hs.119357	ESTs	6.44	10.73
	313056	Al651930	Hs.135684	ESTs	1.51	2.04
40	313058	D81015	Hs.125382	ESTs	0.25 8.56	1.50 11.60
	313070 313097	Al422023 Al676164	Hs.161338 Hs.204339	ESTs ESTs	3.72	4.56
	313130	AW449171	Hs,168677	ESTs	3.28	5.06
	313136	N59284	Hs.288010	ESTs	0.49	1.36
45	313153	A1240838 N74077	Hs.132750 Hs.197043	ESTs ESTs	6.36 0.30	5.52 0.66
	313210 313236	N/40// AW238169	Hs.197043 Hs.83513	ESTS, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00	3.87
	313265	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	0.74 0.23	2.06 1.30
50	313267	A1770008	Hs.129583 Hs.159650	ESTs ESTs	6.68	9.57
	313275 313290	AI027604 AI753247	Hs.199630 Hs.29643	Homo sapiens cDNA FLJ 13103 fis, clone NT	1.34	1.07
	313292	Al362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
	313325	AJ420611	Hs.127832	ESTs	1.20 4.02	2.27 5.33
55	313357 313393	AW074848 AI674685	Hs.201501 Hs.200141	ESTs ESTs	1.36	2.84
	313393	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	Al241540	Hs.132933	ESTs	6.57	15.07
	313417	AA741151	Hs.137323	ESTs	0.63	3.01 4.70
60	313457 313499	AA576052 Al261390	Hs.193223 Hs.146065	Hamo sapiens cDNA FLJ11646 fis, clone HE KIAA1345 protein	2.78 0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313556	AA628517	Hs.118502	ESTs	0.23	0.70
	313569	AJ273419	Hs.135146	hypothetical protein FLJ13984	1.88 0.73	1.00 2.27
65	313570 313638	AA041455 AI753075	Hs.209312 Hs.104627	ESTs Homo saplens cONA FLJ10158 fis, clone HE	1.00	1.72
	313638	AA740151	Hs.104627 Hs.130425	* ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
70	313672	AW468891	Hs.122948	ESTs	3.46 0.51	5.80 0.97
70	313690	Al493591	Hs.78146 Hs.133471	platelet/endothelksi cell adhesion molec ESTs	0.18	1.01
	313711 313723	AA398070 AA070412	ns. 13347 1	gb:zm68c10.s1 Stratagene neuroepithetium	1.08	1.03
	313726	Al744687	Hs.257806	ESTs	2.13	2.99
	313774	AW136836	Hs.144583	ESTs	1.38	1.19
75	313784	AA910514	Hs.134905	ESTs	3.88 0.22	5.78 2.06
	313790 313832	AW078569 AW271022	Hs.177043 Hs.133294	ESTs ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
	313835	AI538438	Hs.159087	FSTs	5.74	8.88
80	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16 2.09	1.14 4.06
	313854 313865	AW470806 AA731470	Hs.275002 Hs.163839	ESTs ESTs	3.41	4.09
	313865	AW471088	Hs.145950	ECTe	5.28	6.83
	313883	AI949384		about 76d01.s1 NO. CGAP Alv1 Homo saciens	2.90	10.91
85	313915	AI969390	Hs.163443	Homo saplens cDNA FLJ11576 fis, clone HE	1.00	1.00

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	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	A1870175	Hs.13957	ESTs FSTs	0.46 4.10	0.75 6.40
5	313983 314035	A8829133 AA164199	Hs.226780 Hs.270152	ESTS	5.88	7.90
,	314037	AW300048	Hs.275272	ESTS	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KJAA1340 protein	1.86	1.21
10	314103	AI028477	Hs.132775	ESTs	2.90	5.29
10	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218986	Hs.118854	ESTs Homo sapiens mRNA; cDNA DKFZp547C244 (fr	0.91 2.53	4.17 3.32
	314124 314126	AW118745 AA226431	Hs.9460	abino 18b12.s1 NCI_CGAP_Pr1 Homo sapiens	3.13	5.08
	314128	AA935633	Hs.194628	FSTs	2.90	6.35
15	314151	AA236163	Hs.202430	ESTS	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98 0.38	7.16 1.94
20	314262 314320	AW086215 AA811598	Hs.246095 Hs.275809	ESTs ESTs	3.34	5.66
	314332	AL037551	Hs.95612	FSTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo saplens clone 24629 mRNA sequence	4.35	4.78
	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p 15	0.77	0.86
25	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11 13.67
	314443 314458	AA827125 Al217440	Hs.192043 Hs.143873	ESTs ESTs	6.20 0.58	2.49
	314456	AA767818	Hs.122707	ESTS	2.53	2.62
30	314478	AJ521173	Hs.125507	DEAD-box protein	3.94	5.65
	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3,43 1,38	6.87 1.00
33	314546 314562	AW007211 AI564127	Hs.16131 Hs.143493	hypothetical protein FLJ12876 ESTs	2.29	5.27
	314579	AW197442	Hs.116998	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
	314585	AA918474	Hs.216363	ESTs	1.08	1.40
40	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90 4.56	2.60 6.29
	314803 314604	AA418024 AA946582	Hs.270670 Hs.8700	ESTs deleted in liver cancer 1	3.42	3.92
	314604	AA418241	Hs.188767	FSTs	2.97	4.55
45	314648	AA878419	113.100101	gb:EST391378 MAGE resequences, MAGP Homo	1.42	1.36
	314699	AI038719	Hs.132801	ESTs	3.66	4.97
	314701	AJ754634	Hs.131987	ESTs	0.03	0.90
	314710	A1669131	Hs.290989	EST	3.40 2.80	7.52 6.54
50	314750 314767	Al095005 AW135412	Hs.135174 Hs.164002	ESTs ESTs	3.20	4.26
50	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	A1694139	Hs.192855	ESTs	0.91	0.99
	314835	AJ281370	Hs.76064	ribosomal protein L27a	5.75	7.44
	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo saplen	1.68	4.34
55	314853	AA729232	Hs.153279	ESTs .	0.60	1.85 16.20
	314940 314941	AW452768 AA515902	Hs.162045 Hs.130650	ESTs ESTs	10.10 0.31	1.02
	314943	AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
	314955	AA521382	Hs.192534	ESTs	2.59	3.90
60	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	Al538613	Hs.298241	Transmembrane protease, serine 3	0.52 2.46	1.78 1.00
	315033 315035	A1493046 A1569476	Hs.146133 Hs.177135	ESTs ESTs	0.34	1.33
65	315056	Al202703	Hs.152414	ESTS ESTS	2.10	2.64
05	315069	AI821517	Hs.105866	ESTs	1.00	1.30
	315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
40	315078	AA568548	Hs.190616	ESTs	3.00	3.79
70	315080	AA744550	Hs.136345	ESTs	1.00	1.00 1.44
	315120 315175	AA564991 A1025842	Hs.269477 Hs.152530	ESTs ESTs	0.64 0.61	1.91
	315193	A1241331	Hs.131765	FSTs	1.06	0.97
	315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
75	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	AI474433	Hs.179556	ESTs	5.37	9.36
	315353	AW452608	Hs.279610	hypothelical protein FLJ 10493	1.00	1.30 2.24
	315397	AA218940	Hs.137516	fidgelin-like 1 ESTs	3.38 2.04	5.23
80	315403 315431	AW362980 AA622104	Hs.163924 Hs.184838	ESIS ESTs	2.36	8.04
00	315454	AAB22104 Al239473	10.104030	gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
	315455	AW393391	Hs.156919	ESTs	3.78	5.76
	315473	AJ681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
0.5	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
85	315526	Al193048	Hs.128685	ESTs	1.67	1.78

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	315530	AJ200852	Hs.127780	ESTs	1.05	1.01
	315541	Al168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.256578	ESTs	1.00	2.22 2.48
5	315562 315577	AA737415 AW513545	Hs.152826 Hs.17283	ESTs hypothetical protein FLJ10890	2.20	2.25
,	315587	AI268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7,44	12.56
10	315634	AA837085	Hs.220585	ESTs	0.50	1.40
10	315668	AA912347	Hs.136585	ESTs	0.43	1.22
	315677 315706	AI932662 AW440742	Hs.164073 Hs.155556	ESTs hypothetical protein FLJ20202	2.18	3.77
	315707	AJ418055	Hs.161160	ESTs	2.88	2.63
	315730	H25899	Hs.201591	ESTs	0.11	0.60
15	315745	Al821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gb:zl15a05.s1 Soares_fetal_liver_spleen_	1.78	2,63
	315801	AA827752	Hs.266134 Hs.258785	ESTs ESTs	4.31 2.35	6.23 3.01
	315820 315878	Al652022 AA683336	Hs.189046	ESTs	2.12	2.64
20	315905	Al821911	Hs.209452	ESTs	1.03	1.97
	315923	AI052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09 2.20	3.41 6.82
25	316001	A1248584	Hs.190745 Hs.201372	Homo sapiena cDNA: FLJ21326 fis, clone C ESTs	0.35	1.63
23	316011 316012	AW516953 AA764950	Hs.201372 Hs.119898	ESTs	6.56	8.13
	316040	AI983409	Hs.189226	ESTs	5.69	10.69
	316048	Al720759	Hs.224971	ESTs	2.84	10.45
	316076	AW297895	Hs.116424	ESTs	0.30	1.05
30	316124	Al308862	Hs.187028	ESTs	1.00	1.43 9.03
	316151 316187	Al806016 AW518299	Hs.156520 Hs.192253	ESTs ESTs	5.80 1.20	3.96
	316204	AA731509	Hs.192253 Hs.120257	ESIS ESTs	4.92	6.94
	316232	AW297853	Hs.251203	ESTs	1.48	1.60
35	316275	Al671041	Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26 8.34
	316344 316346	AA744518 Al028478	Hs.120610 Hs.157447	ESTs ESTs	3.66 3.51	6.69
40	316365	Al627845	Hs.210776	ESTS	2.50	4.33
-10	316380	A1393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46 4.70	2.89
45	316514	AA768037 Al929097	Hs.291671	ESTs . ab:ad10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.70 4.41	6.04 9.70
43	316519 316609	AW292520	Hs.122082	ESTs	1.00	2.89
	316633	Al125586	Hs.127955	ESTs	2.61	3.72
	316700	AW172316	Hs.252961	FSTs. Wealdy similar to ALU1 HUMAN ALU S	3.46	4.64
	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95 2.40
50	316713	A1090671 A1440266	Hs.134807 Hs.170673	hypothetical protein FLJ12057 ESTs, Wealdy similar to AF126780 1 retin	0.30	1.45
	316715 316787	AW369770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
	316811	AA922060	Hs.132471	ESTs	1.00	1.32
55	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124318	ESTs	0.67 3.53	1.81 6.00
	316824 316827	AA837418 Al380429	Hs.124299 Hs.172445	ESTs ESTs	0.72	1.56
	316891	AW298119	Hs.202536	ESTs	1.64	2.97
60	316951	AA134365	Hs.57548	ESTs ·	1.45	1.08
	316970	AA860172	Hs.132406	ESTs '	1.00	1.53
	316971	AA850212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs hypothetical protein FLJ11350	5.44 3.56	10.04 4.37
65	317001 317008	Al627917 AW051597	Hs.233694 Hs.143707	ESTs	0.69	1.37
05	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs. 125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
	317137	AW341567	Hs.125710	ESTs	2.82	5.12
70	317196	Al348258	Hs.153412	ESTs	1.98 1.86	2.51 2.83
	317212	A/866468 AW297920	Hs.148294 Hs.130054	ESTs ESTs	0.83	1.57
	317223 317224	D56760	Hs.93029	sparciosteonectin, owov and kazal-like d	2.74	0.86
	317266	AA906289	Hs.203614	ESTs	1.00	1.00
75	317282	AI807444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32 2.28
	317304	AW449899	Hs.130184	ESTs ESTs	1.38 3.58	8.13
80	317320 317413	AA927151 AW341701	Hs.130452 Hs.126622	ESTS	2.08	4.92
00	317417	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972965	Hs.135568	ESTs	4.22	9.21
	317519	AI859695	Hs.126860	ESTs	1.88	4.15 4.55
85	317521 317529	AI824338 AI916517	Hs.126891 Hs.126865	ESTs ESTs	3.12 2.73	4.55 3.34
05	317029	WALCOIL.	ris.120005	Lore	210	V.34

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	317570	Al733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.56
5	317627	Al346110	Hs.132553	ESTs ESTs	1.50 0.48	1.39 1.46
,	317650 317659	Al733310 AA961216	Hs.127346 Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
	317692	Al307659	Hs.174794	ESTs	5.33	9.59
10	317701	A)674774	Hs.128014	ESTs	1.00	1.00
	317711	AI733015	Hs.272189	ESTs	5.13 2.50	7.81 6.03
	317722 317756	A1733373 AA973667	Hs.128119 Hs.128320	ESTs ESTs	1.59	1.30
	317777	Al143525	Hs.47313	KIAA0258 gene product	1.00	2.48
15	317799	Al498273	Hs.128808	ESTs	1.78	2.11
	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	Al368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AJ820575	Hs.129086	Homo saplens cDNA FLJ12007 fis, clone HE	5.30 1.30	8.16 2.28
20	317850 317861	N29974	Hs.152982 Hs.129119	hypothetical protein FLJ13117 ESTs	2.18	5.93
20	317865	AW341064 Al298794	Hs.129119	ESTS	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease il beta	0.44	0.99
	317881	AJ827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
	317890	AI915599	Hs.129225	ESTs	4.68	7.48
25	317899	Al952430	Hs.150614	ESTs, Weakly similar to ALUA_HUMAN ALU S	3.14	3.37
	317988	Al005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28 5.12	1.66 9.97
	318001 318016	AW235697 AI016694	Hs.130980 Hs.256921	ESTs ESTs	1.86	4.50
	318023	AW243058	Hs.131155	ESTs	2.92	5.22
30	318054	AW449270	Hs.232140	ESTs	3.92	6.37
	318068	Al024540	Hs.131574	ESTs	1.21	1.27
	318117	Al208304	Hs.250114	ESTs	0.86	1.17
	318187	A1792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN IIII	5.90 1.05	6.98 0.90
35	318223 318240	A1077540 A1085377	Hs.134090 Hs.143610	ESTs ESTs	3.10	2.40
33	318255	AI085577 AI082692	Hs.134662	ESTs	0.02	1.05
	318266	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	AI093840	Hs.143758	ESTs	4.98	7.90
40	318369	AJ493501	Hs.170974	ESTs	2.48 0.77	5.62 0.45
40	318428	A1949409	Hs.194591	ESTs	3.54	4,92
	318458 318467	Al149783 Al151395	Hs.158438 Hs.144834	ESTs ESTs	4.56	5.62
	318467	A1151395 A1939339	Hs.146883	ESTs	2.08	4.05
	318476	Al693927	Hs.265165	ESTs	4.22	8.07
45	318487	Al167877	Hs.143716	ESTs	1.47	1.05
	318488	AJ217431	Hs.144709	ESTs	1.40	4.14
	318491	·T26477	Hs.22883	ESTs, Weakly similar to ALUS_HUMAN ALU S	1.84	1.90
	318499	T25451	11- 40054	gb:PTH1188 HTCDL1 Homo sapiens cDNA 5/3	2.58 3.26	5.20 4.18
50	318537 318538	AA377908 N28625	Hs.13254 Hs.74034	ESTs Homo seplens clone 24651 mRNA sequence	0.35	1.07
50	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22 2.46
55	318587	AA779704	Hs.168830	Homo saptens cDNA FLJ12136 fis, clone MA FST	0.85 4.88	4.93
	318596 318622	Al470235 T46325	Hs.172698 Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
	318637	AA243539	Hs.9196	hypothefical protein	1.72	3,57
60	318648	T77141	Hs.184411	albumin	6.27	9.91
	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96 1.53	8.84 0.81
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L ESTs	1.00	2.19
	318679 318711	T58115 AJ936475	Hs.10336 Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
65	318725	AJ962487	Hs.242990	ESTs	1.08	2.46
05	318728	Z30201	Hs.291289	ESTs. Wealthy similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	axidised low density lipoprotein (tectin	0.25	1.49
	318776	R24963	Hs.23766	FSTs	1.00	3.01
70	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70 3.90	3.86 7.13
70	318816	F07873	Hs.21273	ESTs gb:ym04f10.r1 Soares infant brain 1NIB H	2.25	3.58
	318865 318879	H10818 R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
75	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
	318925	Z43577	Hs.21470	ESTs	2.23	3.80 7.16
	318936	AI219221	Hs.308298	ESTs ESTs	1.86 5.84	7.16 9.79
	318982 318986	Z44140 Z44186	Hs.269622 Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
80	318986	Z44186 Z44720	Hs.169161 Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
-00	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13678	Hs.285306	gutative selenocystelne lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
85	319199	F07361	Hs.13306	ESTs	3.53 5.87	5.66 7.26
ده	319242	F11472	Hs.12839	ESTs	5.67	7.20

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	319263	T65331	Hs.81360	Homo saplens cDNA: FLJ21927 fis, clone H	1.81	1.57		
	319267	F11802	Hs.6818	ESTs	1.10	4.72		
	319270 319279	R13474 T65094	Hs.290263 Hs.12677	ESTs CGI-147 protein	4.80 1.50	10.40 2.11		
5	319282	AA461358	Hs.12876	ESTs	1.00	1.00		
•	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68		
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62		
	319293 319312	F12119 Z45481	Hs.12583	ESTs ab:HSC2QE041 normalized infant brain cDN	3.13 1.10	4.50 1.00		
10	319370	240481 H54254	Hs.325823	ESTs, Moderately similar to ALUS_HUMAN A	0.16	0.73		
	319391	R06304	Hs.13911	ESTs	1.26	2.43		
	319396	H67130	Hs.301743	ESTs	0.70 2.45	0.76		
	319398 319407	AA359754 R05329	Hs.191196	ESTs gb:ye91b04.r1 Soares fetal liver spleen	2.45	3.59 3.54		
15	319407	T82930		gb:yd39l07.r1 Soares fetal liver spicen	4.28	8.81		
	319433	R06050	Hs.191198	ESTs	6.15	14.13		
	319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68		
	319466 319471	AI809937 R06546	Hs.116417 Hs.19717	ESTs ESTs	1.76 4.29	5.65 4.84		
20	319480	R06933	Hs.184221	ESTs	1.00	1.00		
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88		
	319486	A1382429	Hs.250799	ESTs	2.08 2.80	2.82 4.39		
	319508 319523	T99898 T69499	Hs.270104 Hs.191184	ESTs, Moderately similar to ALU8_HUMAN A ESTs	1.55	3.25		
25	319545	R83716	Hs.14355	Homo saplens cDNA FLJ13207 fis, clone NT	1.65	1.19		
	319546	R09692		gb:yf23b12.r1 Soares fetal liver spieen	5.11	8.54		
	319552	AA096106	Hs.20403	ESTs	1.89	3.36		
	319582 319586	782998 D78808	Hs.250154 Hs.283683	hypothetical protein FLJ12973 chromosome 8 open reading frame 4	3.48 0.26	4.82 0.82		
30	319604	R11679	Hs.297753	vimentin	1.68	3.41		
	319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24		
	319611	H14957		gb:ym19c10.r1 Soares Infant brain 1NIB H	2.76 2.51	4.24 3.55		
	319653 319657	AA770183 R19897	Hs.173515 Hs.106604	uncharacterized hypothalamus protein HT0 FSTs	5.32	7.68		
35	319858	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00		
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55		
	319662 319708	H06382	Hs.21400 Hs.22664	ESTs	1.58 1.00	1.56 1.22		
	319742	R15372 T77668	Hs.22004 Hs.21162	ESTS ESTS	2.48	3.13		
40	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85		
	319772	R76633	Hs.22646	ESTs	4.36	11.61		
	319788 319805	AA321932 R92857	Hs.117414 Hs.271350	KIAA1320 protein likely ortholog of mouse polydom	2.56 4.63	3.68 6.56		
	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32		
45	319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94		
	319878	T78517	Hs.13941 Hs.291392	ESTs	3.99 5.09	6.44 7.36		
	319882 319912	AA258981 177559	Hs.291392 Hs.94109	ESTs Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21		
	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42		
50	319944	T79248	Hs.133510	ESTs	3.31	5.39		
	319947 319962	AA160967 H06350	Hs.14479 Hs.135056	Homo sapiens cDNA FLJ14199 fis, clone NT Human DNA sequence from clone RP5-850E9	2.90 1.81	4.95 1,57		
	320007	AA336314	F15. 100000	cb:EST40943 Endometrial tumor Homo saple	3.42	6.29		
	320018	T83263		abord40h09.r1 Soares fetal liver spicen	2.77	5.14		
55	320030	H63789	Hs.296268 Hs.292664	ESTs, Weakly similar to KIAA0638 protein ESTs, Weakly similar to A46010 X-linked	4.10 3.27	6.69 3.27		
	320032 320040	AI699772 AA233671	Hs.292664 Hs.87164	hypothetical protein FLJ14001	1.81	1.64		
	320047	T86564	Hs.302256	EST	3.38	7.36		
ć0	320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73		
60	320096 320099	H58138 AW411307	Hs.117915 Hs.114311	ESTs CDC45 (cell division cycle 45, S.cerevis	2.08 1.00	4.47 1.00		
	320112	T92107	Hs.188489	FSTs	2.27	2.06		
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00		
65	320188	AW419200	Hs.172318	ESTs	1.26 2.58	1.00		
03	320193 320195	AA831259 R62203	Hs.17132 Hs.24321	ESTs Homo saplens cDNA FLJ12028 fis, clone HE	2.85	6.23 4.53		
	320199	R78659	Hs.29792	ESTs	0.40	0.94		
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18		
70	. 320219	AA327564	Hs.127011	tubulcintarstitlal nephritis antigen	1.00	1.17		
70	320220 320225	AF054910 AF058989	Hs.127111 Hs.128231	bektin 2 (testicular) G antigen, family B, 1 (prostate associa	0.18 5.26	1.09 13.75		
	320231	H03139	Hs.24683	ESTs	1.59	1.93		
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56		
75	320267 320268	AL049337 H06019	Hs.132571 Hs.151293	Homo sapiens mRNA; cDNA DKFZp564P016 (fr Homo sapiens cDNA FLJ10664 fis, clone NT	1.00 5.58	1.92 5.70		
13	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01		
	320325	AJ167978	Hs.139851	caveolin 2	0.05	0.67		
	320330	AF026004	Hs.141660	chloride channel 2	2.17	1.26		
80	320339 320388	H10807 H16065	Hs.281434 · Hs.31286	Homo sapiens cDNA FLJ14028 fis, clone HE ESTs	1.81	2.32 3.22		
00	320402	R22291	Hs.23368	Homo saplens clone FLC0578 PRO2852 mRNA,	1.41	1.36		
	320413	AA203711	Hs.173269	ESTs	2.31	3.61		
	320432	R62786	Hs.124136	ESTs	11.25 2.22	20.78 3.49		
85	320438 320438	AA253352 W24548	Hs.293663 Hs.5669	ESTs ESTs	3.53	8.14		
00	020400							

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	320448	AJ240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo saplens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	folistatin-like 1	0.65 3.44	1.18 7.15
5	320499 320514	R32555 AB007978	Hs.24321 Hs.158278	Homo sapiens cDNA FLJ12028 fis, clone HE KIAA0509 protein	5.44 6.44	13.62
,	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
	320536	AA331732	Hs.137224	ESTs	2.83	5.83
10	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22 1.84	0.81
	320587 320635	Z44524 R54159	Hs.167456 Hs.80506	Homo saplens mRNA full length insert cDN small nuclear ribonucleoprotein polypept	1.00	2.44 6.25
	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo saciens mRNA for KIAA1708 protein,	1.00	1.53
•••	320651	AA489268	Hs.111334	ferritin, light polypepiide	0.14	0.79
	320664	A1904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
20	320683	R59291	Hs.26638 Hs.171929	ESTs, Weakly similar to unnamed protein ESTs, Weakly similar to A54849 collagen	0.37 1.27	1.31 1.02
20	320689 320696	AA334609 AW135016	Hs.171929 Hs.172780	ESTs, Weakly stream to AS4649 Collegen	3.53	4.60
	320714	AW135010 Al445591	FIS. 172700	gb:yq04a10.r1 Soares fotal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
	320771	Al793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
25	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 Inducible signaling pathway protein	0.10	0.79
	320824 320830	AF120274	Hs.194689 Hs.266416	artemin claudin 14	1.16 1.06	1.11 1.75
	320830	AJ132445 AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
30	320849	D60031	Hs.34771	ESTs	5.30	7.49
50	320853	Al473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uroplakin 1B	5.90	2.55
	320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17 1.46
25	320927 320957	Al205786	Hs.213923	ESTs	0.18 1.67	1.46 2.18
35.	320957 320997	AI878933 H22544	Hs.92023	core histone macroH2A2.2 gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321046	H27794	Hs.269055	ESTs	2.69	4.25
	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
40	321059	AI092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76 4.79	5.20 7.41
	321067 321102	AF131782 AA018306	Hs.241438	Homo sapiens clone 24941 mRNA sequence ab:ze40d08.rl Soares retina N2b4HR Homo	1.79	4.27
	321130	H43750	Hs.125494	ESTs	1.00	3.14
45	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21 5.69	4.46 8.01
50	321199	AW385512 H54178	Hs.226469	gb:yy56d10.s1 Soares_multiple_scierosis_ Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
30	321206 321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs. 18192	Ser/Arg-related nuclear matrix protein (1.00	1.00
	321244	AF068654		ob:Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
	321270	R83560		gb:yv76c06.s1 Soares fetal liver spleen	3.80	5.26
55	321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65 1.00
	321318	AB033041	Hs.137507	KIAA1215 protein KIAA protein (similar to mouse paladin)	0.44	0.93
	321325 321342	AB033100 AA127984	Hs.300646 Hs.222024	transcription factor BMAL2	4.94	4.93
	321356	R93443	Hs.271770	ESTs	3.10	4.66
60	321418	AJ739161	Hs.161075	ESTs	2.28	2.54
	321420	AI368667	Hs.132743	ESTs	1.13	0.97
	321430	U05890		gb:H.saplens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo saplens cDNA: FLJ21930 fls, clone H gb:Human 2a12 mRNA for kappa-immunoglobu	1.60 0.42	3.11 0.72
65	321467 321468	X13075 AA514198	Hs.38540	ESTs	2.46	6,50
05	321491	H70665	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
	321510	AA703650	Hs.255748	ESTs	2.14	3.94
70	321513	H84972	Hs.108551	ESTs .	2.78	5.37
	321516	AI382803	Hs.159235	ESTs	3.06 4.89	7.19 7.82
	321565 321577	AL525773 H84260	Hs.266514	hypothetical protein FLJ11342 gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
	321581	AA019964	Hs.28803	ESTs	4.88	6.73
75	321582	AA143755	Hs.21858	trinucleotide reneat containing 3	1.00	2.08
	321587	H95531		abys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
80	321642	AW085917	Hs.247084	ESTs ESTs	1.52 2.17	1.38 2.45
80	321669 321687	H95404 AA625149	Hs.294110	gb:af70c12.r1 Soares_NhHMPu_S1 Homo sapl	4.31	6.95
	321687	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
	321700	N55160	Hs.167260	ESTs	4.57	7.46
85	321701	AW390923	Hs.42568	ESTs	1.00	1.00

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	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	Al694875	Hs.202312	Homo saplens clone N11 NTera2D1 teratoca	1.00	1.00
5	321777	Al637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.68	0.45
2	321779	N42729	Hs.163835	ESTs	0.90 2.69	0.90 3.89
	321829 321846	D81993 AA281594	Hs.8966 Hs.87902	turnor endothelial marker 8 ESTs	5.11	7.64
	321846	AL109670	Hs.302809	ESTS	6.49	9.58
	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
10	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	Al651866	Hs.195689	ESTs	2.89	5.47
15	321956	AL110177	Hs.132882	ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1,00 4,00	1.83 6.47
	321991	AL133627 AA328801	Hs.158923 Hs.84522	Homo sapiens mRNA; cDNA DKFZp434K0722 (f ESTs	2.10	3.48
	322002 322035	AA328801 AL137517	Hs.84522 Hs.306201	hypothetical protein DKFZp564O1278	1.00	1.90
	322035	AW340926	AS.300201	gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20	9.67
20	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	AI341937	1201101010	gb:gt10e03.x1 NCI_CGAP_GC4 Homo saplens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein.	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
~~	322091	AI819863	Hs.106243	ESTs	1.59	1.75
25	322125	R93901		gbayq16c12.r1 Soares fetal liver spicen	2.06	5.27
	322130	R98978	Hs.117767	ESTs ESTs	10.12 0.94	16.49 0.64
	322147	AF085919 AF085958	Hs.114176	gb:yr68b03.r1 Soares fetal liver spleen	4.09	6.67
	322166	AF085958 H52567		gb:yt85d04.rl Soares_pineal_gland_N3HPG	3.46	4.85
30	322173 322178	H56535		gb:yt88g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
50	322179	H92891		gb:yt94c02.s1 Soares_plneal_gland_N3HPG	4.52	7,50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20	5.04
	322212	AF087995	Hs.134877	ESTs	3.42	4.84
35	322221	AI890619	Hs. 179662	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	AI640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
	322284	Al792140	Hs.49265	ESTs	0.66 0.71	2.76 0.70
40	322288	AL037273 AF086419	Hs.7886	pellino (Drosophila) homolog 1 gb:zd78d03,r1 Soares_fetal_heart_NbHH19W	2.02	2.76
40	322320 322336	AF-086419 AA308526	Hs.76152	decode	2.92	4.44
	322339	W17348	rts./0132	gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
	322372	W25624	Hs.153943	ESTs	7.37	12.07
45	322374	Al394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
	322378	AF054819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related prolein complex 3, mu 1	3.20	5.80 1.57
50	322419	AA248987	Hs.14084	ring finger protein 7	1.64 0.83	1.00
30	322425 322431	W37943 AA069222	Hs.34892 Hs.141892	KIAA1323 protein ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTS .	5.18	12.67
	322465	AA137152	Hs.286049	nhosohoserine aminotransferase	3.41	2.23
	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
55	322473	AA744286	Hs. 266935	tRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo saplens full length insert cDNA	1.25 4.57	1.27
40	322560	AJ916847	Hs.270947 Hs.269587	ESTs ESTs	1.00	8.81 1.42
60	322566 322585	W87285 AA837622	MS.209307	gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
	322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
65	322664	AA011522		ob-z(03a07 rt Soares fetal liver sciena	1.92	2.18
00	322687	AI110759		gb:AF074668 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	notassium voltage-gated channel, shaker-	3.50	5.00
	322694	AI110872	Hs.279812	PR00327 protein	1.80	1.72
=0	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
70	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28 1.63	3.86 1.53
	322765	AW068805	Hs.288467	Homo saptens cDNA FLJ12280 fis, clone MA	1.53	1.06
	322770	AA045796	Hs.122682 Hs.38991	ESTs S100 calcium-binding protein A2	12.06	1.94
	322794 322810	AI608591 AI962276	Hs.127444	ESTs	4.09	6.90
75	322818	AW043782	Hs 293616	ESTs	1.20	1.63
, 5	322820	Al377755	Hs.120696	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	FSTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo saplens cDNA FLJ14035 fis, clone HE	5.26	1.22
	322887	Al986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
80	322913	AI733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	Al365585	Hs.146246	ESTs	0.30 2.06	1.14 1.13
	322968	A1905228	Hs.83484	SRY (sex determining region Y)-box 4	1.18	2.00
85	322971	C15953 AA493252	Hs.212760 Hs.159577	hypothetical protein FLJ13649 ESTs	2.28	2.61
03	322981	AM133232	115.139377	E310	2.20	2.01

		O 02/080				
	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AI733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
_	323025	AL157565	Hs.315369	Hamo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
5	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	A1700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
10	323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
	323232	AA148722	Hs.224680	ESTs	0.45	1.35
15	323266	AW003362	Hs.243865	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	A1697556	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12,68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
	323316	AL134620	Hs.280175	ESTs	2.98	5.93
20	323334	AI336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTS	1.43	1.68
	323359	AA234172	Hs.137418	ESTs	0.34	1.18
25	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	AI672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD (H.sapien	0.43	0.80
30	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ 10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	AI652287		gb:EST382593 MAGE resequences, MAGK Homo	2.21	3.08
	323515	AA282274	Hs.256083	ESTs	2.69	3.40
35	323541	AI185116	Hs.104613	RP42 homolog	1.20	1.09
	323545	AI814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
	323675	AA984759	Hs.272168	turnor differentially expressed 1	3.70	5.80
	323678	AL042121	Hs.20880	ESTs	3.33	5.10
40	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
	323856	AA355264	Hs.267604	hypothetical protein FLJ 10450	3.42	8.13
45	323857	T18988	Hs.293668	ESTS	5.97	12.51
	323870	AA341774	Hs. 129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo saplens BAC clone RP11-335J18 from	2.31	3.33
	323911	AL043212	Hs.92550	ESTs	4.38	5.41
50	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	AI869964	Hs.182906	ESTs	3.10	6.14
	324005	AA610011	Hs.208021	ESTs	5.34 1.00	10.07
	324036	AI472078	Hs.303662	ESTs		5.03
	324055	AA528794	Hs.128644	ESTs	0.86	1.00 0.91
55	324063	AW292740	Hs.272813	dual oxidase 1	0.45 2.82	
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.40	5.12 2.52
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H		4.30
	324095	AW377983	Hs.298140	Home saplens cDNA: FLJ22502 fis, clone H	1.32 1.40	1.77
60	324129	Al381918	Hs.285833	Home saplens cDNA: FLJ22135 fis, clone H	4.24	6.21
60	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	6.96	10,69
	324214	AA412395	Hs.225740	ESTs	0.81	0.53
	324227	AA295552	Hs.28631	Home saplens cDNA: FLJ22141 fis, clone H	2.42	4.05
	324266	AL047634	Hs.231913	ESTs	3.62	5.38
65	324275	AA429088	Hs.98523	ESTs ESTs, Wealdy similar to T14742 hypotheti	0.14	0.70
03	324281	AL048026	Hs.124675		3.71	4.34
	324290	AA432032	Hs.304420	ESTs	0.95	0.91
	324303	AL118754	11. 400470	gb:DKFZp761P1910_r1 761 (synonym: harry2)	4.06	5.91
	324312	Al198841	Hs.128173	ESTs	5.88	8.25
70	324325	AL138153	Hs.300410	ESTs	0.87	1.25
70	324338	AL138357	Hs.145078	regulator of differentiation (in S. pomb .	1.28	1,00
	324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	2.54	3.46
	324343	AW452016	Hs.293232	ESTs ESTs	5.85	8.36
	324371	AA452305	Hs.270319		0.76	1.64
75	324382	AW502749	Hs.24724	MFH-amplified sequences with feucine-ric	2.86	5.69
75	324384	AA453396	Hs.127656	KIAA1349 protein	1.81	1.99
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.00
	324388	A1924963	Hs.306206	hypothetical protein FLJ11215	2.73	2.17
	324432	AA464510	Hs.152812	ESTs	0.71	1.90
80	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein Homo saplens cDNA FLJ11569 fis, clone HE	1.00	1.00
ου	324510 324580	AI148353 AA492588	Hs.287425	gb:ng99c08.s1 NCI_CGAP_Thy1 Homo saptens	2.18	3.50
		AA492588 AA506935	U- 400000	ESTS, Weakly similar to ALU1_HUMAN ALU S	5.96	11.36
	324582		Hs.132036	ES14, THEBRIY SIRINGE SO ALLO I_HUMAN ALU S	2.92	4.22
	324633	AA572994 AW295832	Hs.325489	ESTs ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324640		Hs.134798		0.39	0.73
63	324675	AW014734	Hs.157969	ESTs	0.00	4.73

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	**	0 02/00				
	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
_	324801	AJ819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
5	324804	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AJ541214	Hs.46320	Small proline-rich protein SPRK (human,	1.07	0.95
	324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	1.68	1.21
10	324886	AA806794	Hs.131511	ESTs	2.56	5.61
10	324889	D31010	110.101011	gb:HUML12147 Human fetal lung Homo saple	2.20	4.65
			Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324948	AW383618	MS.200409		3.37	5.51
	324953	A1264628	Hs.125428	ESTs	5.37	9.81
1.5	324958	AA625076	Hs.132892	protocadherin 20	5.12	
15	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
	325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
	325114	D83901	Hs.315562	ESTs	2.73	3.17
20	325148	Al064690	Hs.171176	ESTs	1.86	3.41
	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	Al653682	Hs.197812	ESTs	6.50	11.31 .
	325228	7100000	10101012	2010	6.18	15.76
	325235				2.64	4.12
25	325328				2.87	4.42
23	325340				0.29	0.33
					16.56	24.29
	325367					1.22
	325373				0.63	
20	325389				0.88	1.05
30	325436				5.75	14.14
	325471				8.46	17.82
	325498				3.32	6.42
	325557				5.51	8.28
	325559				7.48	21.40
35	325560				4.08	6.25
-	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
	325597				2.98	13.40
40	325639				0.78	0.78
40	325685				0.46	0.66
	323000					
	325686				0.95	1.55
	325735				4.48	9.20
40	325739				0.59	0.88
45	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
	325895				7.78	15.98
50	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
	325971				4.88	7.42
55	326025				0.55	1.07
-	326046				7.21	14.72
	326099				3.60	5.98
					1.27	1.06
	326108 326163				3.27	5.70
60	320163				0.45	1.11
UU	326165					
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
	326274				1.00	8.09
65	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
	326515				1.24	5.84
	326589				9.20	13.49
70	326592				2.77	4.01
, ,	326605				201	2.53
	326692				1.00	1.00
	326693				1.00	1.31
					0.19	0.65
75	326720				2.13	7.20
13	326742				2.34 0.25	0.83
	326770				2.00	
	326818				3.09	4.56
	326936				2.08	3.45
	326964				0.41	1.70
80	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
	327053				3.55	6.31
85	327075				1.59	1.40
-	JE. 0/0					

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	wo	02/086443			
	327085			2.50	12.57
	327130 327156			5.38	8.04
	327156			3.74	6.58
5	327220			1.28	1.54
,	327224 327288	•		6.56 2.61	12.91 5.40
	327321			2.42	3.11
	327332			6.62	10.58
	327361			2.69	4.41
10	327377			2.04	6.72
	327396			2.61	4.50
	327414			1.00	8.01
	327442			5.91	9.65
15	327467 327473			6.58	18.01
13	327483			3.79 4.08	7.48 8.87
	327562			0.68	2.86
	327568			1.00	2 00
	327606			2.06	3.61 14.26
20	327611			5.90	14.26
	327642			4.06	8.74
	327654			1.05	2.08
	327734			1.00	1.00
25	327775			1.46	11.79
23	327796 327840			3.47 3.26	5.65
	327940			6.84	6.64 15.58
	327984			0.36	1.50
	328004			1.87	1.50 1.42
30	328021			0.42	0.59
	328068			2.83	4.68
	328100			3.04	5.39
	328101			3.54	5.20
35	328113 328157			0.72	0.91
55	328196			5.58 -5.76	5.16 11.13
	328197			5.98	10.58
	328264			3.11	4.88
	328299			2.20	3.06
40	328342			1.49	1.94
	328365			1.00	1.00
	328369			4.40	7.36
	328381 328451			1.86	4.93
45	328481			5.51	7.56 0.72
73	328500			0.13 2.71	3.97
	328530			5.41	7.62
	328600			3.14	10.68
	326606			4.56	8.17
50	328616			2.24	11.91
	328623			3.04	5.46
	328632			0.70	1.19
	328664 328666			3.48	6.80
55	328698			10.42 9.68	26.47
33	328700			2.74	14.56
	328708			0.15	0.57
	328735			6.23	8.91
	328743			3.62 0.22	6.54
60	328806			0.22	0.78
	328861			3.68	10.54
	328908			5.42	16.36
	328933 328934			2.02	5.29 4.45
65	328949			1.73	
05	329005			3.34 2.88	5.41 7.26
	329011			2.52	3.72
	329033			1.00	1.03
	329037			5.07	8.16
70	329067			1.98	2.41
	329134			2.24	3.25
	329157			2.30	11.04
	329178			2.64	5.02
75	329192			6.41	15.27
/3	329194			0.31	0.79
	329204 329224			1.60	3.75
	329224			2.99 0.83	6.11 0.83
	329268			0.63	1.01
80	329337			1.00	1.00
	329541			0.76	1.68
	329560			1.34	2.02
	329588			1.68	2.22
0.5	329643			4.18	11.77
85	329703			1.00	1.00

WO 02/086443 15.50 329764 5.78 329816 3.13 10.77 7.83 14 24 5 13.12 330030 3.32 330036 4.31 1.34 4.70 330052 7.97 330085 1 76 12.46 337086 10 330093 0.44 330100 4 83 2.14 330106 3 61 3.17 6.87 330107 330120 15 4.50 12.74 330123 33020 1 55 7.62 330263 13.10 23.38 220200 4.41 330313 3.00 20 0.67 330366 0.76 4.76 11.82 220372 karyopherin alpha 5 (Imporlin alpha 6) KIAA0103 gene product protease Inhibitor 3, skin-derived (SKAL ataxia-telangiectaska group D-associated microfibrillar-associated protein 4 330385 AA449749 Hs.182971 214 330397 D14659 L10343 Hs.154387 0.40 1.15 330468 He 112341 1.11 0.94 25 330472 330478 330493 L24203 L38486 Hs 82237 Hs.296049 0.46 1.07 microstritiller-associated protein 4 endogencus retoviral protease guarnire nucleotide binding protein (6 pr phospholosidistich 3-dinase, reginatary su \$100 cactum-binding protein A4 (catchum-zinc inger protein 9 (a cellular retrov tryptophen 2.5 dioxygenase hepatocyle nuclear factor 3, alpha (VONE) M27826 Hs.267319 0.95 330495 330506 0.96 M3132E Hs.71642 0.97 0.17 Hs.6241 M61906 30 330512 MROS63 He 81256 330537 Hs.2110 2.81 2.07 U19765 330547 U32989 U39840 U56244 Hs.183671 1 49 330551 330568 330599 330601 330605 330609 1.03 1.15 Hs.299867 (NÖKE) ghi-Human RP1 hornzlog mRNA, 3*UTR region brors sapiens cDNA F-LU3930 fis, clone H plasminogen activator, uroknass ubiquific carboxyl-terminal setterase L1 integrin, bat 4 reflectionable 2, EF-hand celcium bindin S100 activam-binding probleh AZ junction platoglobh EST, Wastly shirmlar ba LUT-HUMAN ALU S EST, Wastly shirmlar ba LUT-HUMAN ALU S 35 2.08 U90437 1.54 U90916 X02419 Hs.82845 0.89 1.35 Hs.77274 X04741 1.83 Hs.76118 Hs.85266 330817 X53587 1.54 1.15 40 330617 330630 330644 330660 330660 330692 330707 1.39 X78669 Hs.79088 1.19 1.13 Y07755 Z68228 Hs 38991 Hs.2340 1.25 AA347868 Hs.139293 15.50 29.07 AA017045 AA133891 1.00 Hs.6702 ESTs 1 00 45 0.20 ESTs He 293890 Homo sapiens cDNA FLJ11570 fis, clone HE Integrin, beta 8 ESTs 330715 AA233707 Hs.11571 1.40 5.42 330717 AA233926 Hs.52620 Hs.34382 6.62 1.40 330722 AA243560 Homo sapiens voltage-gated sodium channe receptor (calcitonin) activity modifying dTDP-D-ghucose 4,6-dehydratase Homo sapiens cDNA FLJ13103 fis, chore NT Hs.22654 0.27 2.04 330740 AA297746 50 330742 AA400979 AA406142 Hs.25691 0.44 0.90 330744 Hs.12393 0.71 3 23 AA428286 AA448663 Hs.29643 Hs.30469 1.66 0.52 0.37 330751 ESTs 330760 330763 AA450200 Hs.274337 hypothetical protein FLJ20666 ESTs, Moderately similar to ALU7_HUMAN A 0.97 55 0.84 330786 D60374 Hs.49136 Hs.105807 Hs.265398 0.78 0.23 330790 T48536 ESTs . Weakly similar to transformation-r AA015730 0.37 2 07 AA040332 330827 Hs.12744 ESTS 1.60 1.00 0.93 330844 330901 1 16 AA063037 Hs.66803 **ESTs** 60 Hs.267319 1.02 AA157818 endogenous retroviral protease hypothetical protein FLJ14033 similar to 0.88 330931 330952 F01443 Hs.284256 Hs.29567 0.24 0.24 0.08 1.29 0.48 0.29 H02855 a disintegrin and metalloproteinase doma 1.26 330961 330968 H10998 Hs.7164 ESTS H16568 Hs.23748 Hs.30340 65 331014 H98597 stical projein KIAA1165 0.74 hypoth ESTs 331046 N66563 N75081 Hs.191358 Homo saplens cDNA FLJ11883 fis, clone HE hypothetical protein ESTs 0.99 8.56 Hs.167148 1.24 1 00 331060 0.75 1.03 R36671 Hc 83937 331099 1.00 R41408 Hs.21983 2.75 331108 gb:yg87b07.s1 Soares infant brain 1NIB H ESTs 70 331131 10 68 R61398 0.80 0.96 331135 Hs.4197 Hs.159293 Hs.6640 2.63 ESTs 331170 T23461 T32448 Human DNA sequence from PAC 75N13 on chr 1.78 271 331180 1.00 1.70 1.20 331183 T40769 Hs.8469 3.01 75 (NONE) 3.80 331203 T82310 glycoprotein (transmembrane) nmb dachshund (Drosophila) homolog 331271 44059347 Hs 82228 331306 AA252079 Hs.63931 0.31 AA252079 AA281076 AA303125 AA416979 AA421562 AA448881 AA456001 331327 Hs.109221 ESTS Homo septens cDNA FLJ13496 fs, clone PL KIAA1462 protein anterior gradient 2 (Xenepus laevis) hom hypothetical protein FLJ11088 NADPH oxidase 4 **ESTs** 2.09 241 331341 Hs.23240 Hs.46901 0.72 2.43 80 0.09 0.91 331359 Hs.91011 1.02 0.87 331363 1.03 1.40 1.80 1.65 331378 Hs.49282 1.23 1.00 331384 Hs.93847 AA505135 He 44037 **ESTs** 331402 85 Hs.163628 ESTs. Moderately similar to ALU7_HUMAN

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	w	O 02/08	6443			
	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531	N51343	PS.20013	gb:yz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68
	331547	N54811		gb:q213g04.s1 NCI_CGAP_Ov2 Homo saplens	3.80	5.75
	331578	N67960	Hs.249989	FSTs	0.11	0.67
5	331589	N71027	Hs.152618	FSTs	1.09	1.38
-	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614	N92293	Hs.240272	EST	0.17	1.34
	331668	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
10	331676	W79834	Hs.58559	ESTs, Wealdy similar to motekin (M.musc	0.08	1.07 4.27
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dani	8.72	0.54
	331692 331717	W93592 AA190888	Hs.152213 Hs.153881	wingless-type MMTV integration site fami Homo sapiens NY-REN-62 antigen mRNA, par	0.94 1.57	1.34
	331718	AA191404	Hs.104072	ESTs	6.80	11.77
15	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo saplens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
20	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00 3.04	1.00 3.87
	331990 332002	AA478102 AA482009	Hs.139631 Hs.105104	ESTs ESTs	1.19	0.78
	332002	AA489671	Hs.65841	hypothetical protein FLJ20073	1.27	1.03
	332027	AA489697	Hs. 145053	FSTs	0.30	1.62
25	332033	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA496019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
	332074	AA599012		gb:ae41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
20	332083	AA600200	Hs. 155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
30	332085	AA600353	Hs.173933	nuclear factor I/A	0.30 0.22	1.50 0.62
	332125 332177	AA609861 F10812	Hs.312447 Hs.101433	ESTs ESTs	8.21	18.03
	332180	H03348	Hs.7327	claudin 1	2.27	1.57
	332185	H10356	Hs.101689	ESTs	0.09	1.18
35	332203	H49388	Hs.317769	EST	8.05	5.02
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 [0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275 332280	R08838 R38100	Hs.26530	serum deprivation response (phosphatidy)	0.27 0.39	0.75 1.88
40	332299	R69250	Hs.146381 Hs.21201	RNA binding motif protein, X chromosome nectin 3; DKFZP568B0846 protein	5.24	12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
45	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.11112	ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54 0.51	1.00
	332458 332504	M33493 AA053917	Hs.250700 Hs.15106	tryptase beta 1 chromosome 14 open reading frame 1	0.79	1.24
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-	332530	M31682	Hs.1735	inhibin, bete B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Wealdy similar to AF164793 1 prote	0.93	1.49
55	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13 1.00
23	332563	N92924	Hs.274407 Hs.25272	professe, serine, 16 (thyrnus)	1.00 0.36	1.05
	332565 332594	AA234896 AA279313	Hs.3239	E1A binding protein p300 methyl CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	538953	Hs.283750	tenascin XA	0.38	1.16
	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
60	332640	AA417152	Hs.5101	protein regulator of cytokinests 1	6.15	1.16
	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA496035 L00058	Hs.247926 Hs.79070	gap junction protein, alpha 5, 40kD (con	0.17 1.00	1.12 1.44
65	332716 332736	L13773	Hs.114765	v-myc avian myelocytomatosis viral oncog myeloid/ymphold or mbed-lineage leukem	1.00	1.81
05	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792	74 4004.00		nyponiatan promise a co	1.70	1.19
	332816				1.85	2.47
70	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00 4.40
	332912 332922				1.00	1.00
75	332922				0.42	0.88
,,,	332959				1.96	6.34
	332982				0.56	0.99
	332984				0.30	0.78
00	332998				1.47	2.01
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	333097 333121				2.14 2.76	3.19 3.70
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	339047		5.26	10.81	
	339100		5.10	6.88	
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	339170 339229		10.36	19.67	
	339229		4.08	13.48	
	339264		2.64	3.83	
~-	339293		1.73	1.94	
35					
		the second secon			

TABLE SI allow the accretion combers for floor Page 11 table 10 bits builting unique of 10°. For each probabet in him facility can be considered and experimental the second control and a second control and a sequence when detailed have done in sequence and a second control and a sequence of the second control and a sequence and a sequence when detailed have done in sequence artifictly using Cataleria; and Aligement Tools (Doublet well. Caldand California). The Genthank accession numbers for sequences comprising each duster are listed in the Accession or column.

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	Accession:	Genbank acc	ession numbers
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	321587	1615333_1	H95531 H95521 H84529
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	307760	Al342387	
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05			

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TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Unique number conseponding to an Eco probeset Sequence operation. The I digit numbers in this column are Genbank Identitier (CI) numbers. "Outham Let al." refers to the publication entitled "The DNA indicates DNA stand from which eachs were precisited. 5 Pkey: Ref:

	Nt_position:	Indicates nucleotide po	sitions of pred	icled exons.
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	Pkey	Ref Strand	Nt_position	
	332792	Dunham, I. et.al.	Plus	73381-73768
	332816	Dunham, I. et.al.	Plus	359844-360030
15	332906	Dunham, 1. et.al.	Plus	1923101-1923205
	332911	Dunham, f. et.at.	Plus	1961767-1961858
	332912	Dunham, I. et.al.	Plus	1962120-1962246
	332922 332956	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	2009620-2009738 2510528-2510658
20	332959	Dunham, I. et.al.	Plus	2518145-2518213
	333138	Dunham, I. et.al.	Plus	3369205-3369323
	333139		Plus	3369495-3369571
	333221 333380	Dunham, 1. et.al.	Plus Plus	3978070-3978187 4904775-4904846 4910935-4910997
25	333380	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	4904775-4904846
23	333512	Dunham, I. et.al.	Plus	5560510-5560564
	333524	Dunham, I. et.al.	Plus	5612620-5612780
	333585	Dunham, I. el.al.	-Plus	6234778-6234894
30	333618	Dunham, I. et.al.	Plus	6562391-6562566
30	333627 333628	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	6620584-6620903 6629004-6629233
	333650	Dunham, I. el.al.	Plus	6796852-6797128
	333678	Dunham, I. el.al.	Plus	7068223-7068288
	333750	Durham, I. el.al.	Plus	7608165-7608234
35	333763	Dunham, I. et.al.	Plus	7692491-7692630
	333767 333768	Dunham, I. et.al.	Plus Plus	7694407-7694623 7695440-7695697
	333769	Dunham, I. et.al. Dunham, I. et.al.	Pius	7696440-1693691 7696636-7696707
	333772	Dunham, I. et.al.	Plus	7696625-7696707 7706773-7706902 7746805-7746916
40 .	333777	Dunham, I. et.al.	Plus	7746805-7746916
	333846	Dunham, t. et.al.	Plus	8008623-8008757
	333884	Dunham, I. et.al.	Plus Plus	8153960-8154161 8154882-8155025
	333887 333891	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	8154882-8155025 8156437-8156709
45	333892	Durham, I. et.al.	Plus	8156825-8157001
	333948	Dunham, I. et.et.	Plus	8583497-8583627
	333954	Dunham, I. et.al.	Plus	6563186-6563335
	333966 333968	Dunham, I. et.al.	Plus Plus	8655643-8655826
50	334061	Dunham, I. et.al. Dunham, I. et.al.		8581004-8681241 9686941-9687077
-	334094	Dunham, I. et.al.	Plus Plus	9889953-9890105
	334113	Dunham, I. et.al.	Plus	10282459-10282597
	334161	Dunham, I. et.al.	Plus	10599033-10599180
55	334219 334239	Dunham, t. et.al.	Plus Plus	12716160-12716384
"	334333	Dunham, I. et.al. Dunham, I. et.al.	Plus	13603544-13603657
	334378	Dunham, I. et.al.	Plus	13907239-13907370
	334382	Dunham, I. et.al.	Plus	13915866-13916036
60	334562	Dunham, I. et.al.	Plus	14987847-14987940
00	334588 334616	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	15032740-15032817 15176123-15176470
	334633	Dunham, I. et.al.	Plus	15333206-153333305
	334866	Dunham, L et.al.	Phis	18872214-18872317
	334891	Dunham, I. et.al.	Plus	19299770-19299944 20103970-20104058
65	334934	Dunham, I. et.al.	Plus	20103970-20104058
	335015 335120	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	20682792-20682945 21436286-21436384
	335125	Dunham, I. et.al.	Plus	21441390-21441471
	335179	Dunham, I. et.al.	Plus	21634405-21634526
70	335188	Dunham, I. et.al.	Plus	21669118-21669328
	335211	Dunham, I. et.al.	Plus	21774611-21774680
	335361 335379	Dunham, I. et.al. Dunham, I. et.el.	Plus Plus	22807292-22807445 22899306-22899420
	335414	Dunham, I. et.el.	Plus	23235546-23235684
75	335416	Dunham, I. et.al.	Plus	23237354-23237465
	335496	Dunham, I. et.al.	Plus	24164386-24164545
	335497	Dunham, I. et.al.	Plus	24167666-24167869
	335558 335586	Dunham, I. et.al.	Plus Plus	24740167-24740347
80	335686	Dunham, I. et.al. Dunham, I. et.al.	Plus	24990333-24990497 25439839-25439920
	335784	Dunham, I. et.al.	Plus	25942710-25942792
	335823	Dunham, I. et.al.	Plus	26365925-26366004
	335983	Dunham, I. et.al.	Plus	27938968-27939070
85	335995 336021	Dunkam, I. et.al. Dunkam, I. et.al.	Ptus Ptus	28009044-28009184 28686482-28686559
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	336034	Dunham, I. et.al.	Plus	29014404-29014590
	336038	Dunham, I. et.al.	Plus Plus	29022963-29023165 29987731-29987869
	336107 336632	Dunham, I. et.al. Dunham, I. et.al.	Plus	983890-985529
5	336633	Dunham, I. et.al.	Plus	985591-986221
	336634	Dunham, I. et.al.	Plus	986296-986670
	336635	Dunham, I. et.al.	Plus	987908-988364
	336636 · 336637	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	988418-989185 989276-990813
10	336638	Dunham, I. et.al.	Plus	991906-993240
	336659	Dunham, I. et.al.	Plus	1896402-1896478
	336694 336721	Dunham, I. et.al.	Plus Plus	2420546-2420616 3371522-3371586
	336900	Dunham, I. et.al. Dunham, I. et.al.	Plus	10236423-10236523
15	336948	Dunham, I. et.al.	Plus	12692290-12692381
	337028	Dunham, I. et.al.	Plus	16644817-16644942
	337054 337162	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	17821742-17821922 23478943-23479145
	337183	Dunham, I. et.al.	Plus	23943606-23943696
20	337184	Dunham, I. et.al.	Phis	23973949-23974016
	337268	Dunham, I. et.al.	Plus Plus	28011979-28012034 29022656-29022775
	337299 337389	Dunham, I. et.al. Dunham, I. et.al.	Plus	31401509-31401579
	337493	Dunham, I. et.al.	Plus	31401509-31401579 33330760-33330981
25	337549	Dunham, i. et.al.	Plus	34474472-34474531
	337755 337809	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	3971764-3971900 4449069-4449193
	337871	Dunham, I. et.al.	Plus	5443027-5443101
••	337958	Dunham, I. et.al.	Plus	6969162-6969270
30	338008 338033	Dunham, LeLal.	Plus Plus	7697068-7697236 8092128-8092271
	338110	Dunham, I. et.al. Dunham, I. et.al.	Plus	10384481-10384621
	338112	Dunham, I. et.al.	Plus	10391398-10391600
35	338145	Dunham, I. et.al.	Plus Plus	11386629-11386692 11448985-11449085
33	338148 338179	Dunham, I. et.al. Dunham, I. et.al.	Plus	12808775-12808833
	338197	Dunham, I. et.al.	Plus	13638107-13638181
	338279 338316	Dunham, I. et.al.	Plus Plus	16168944-16169091 17089711-17089988
40	338322	Dunham, I. et.al. Dunham, I. et.al.	Plus	17132477-17132547
	338357	Dunham, I. et.al.	Plus	18062184-18062402
	338359 338366	Dunham, I. et.al.	Plus Plus	18074402-18074501 18252026-18252189
	338374	Dunham, I. et.al. Dunham, I. et.al.	Plus	18371200-18371282
45	338414	Dunham, I. et.al.	Plus	19345573-19345660
	338418 338501	Dunham, I. et.al.	Plus Plus	19435506-19435596 21244713-21244828
	338501	Dunham, I. et.al. Dunham, I. et.al.	Plus	21221871-21221953
	338523	Dunham, I. et.al.	Plus	21509763-21509864
50	338662 338804	Dunham, I. et.al.	Plus Plus .	24404720-24404899
	338836	Dunham, I. et.al. Dunham, I. et.al.	Plus . Plus	27236005-27236108 27792166-27792272
	338879	Dunham, I. et.al.	Plus	
	338937	Dunham, I. et.al.	Plus	29160655-29160725 30077787-30078184
55	338993 339047	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	30760793,30760968
	339100	Dunham, I. et.al.	Plus	31141580-31141765 31466454-31456519 31583467-31583536
	339114	Dunham, I. et.al.	Plus Plus	31456454-31456519
60	339121 339170	Dunham, I. et.al. Dunham, I. et.al.	Plus	32216399-32216527
00	339293	Dunham, I. et al.	Plus	33223571-33223819
	332858	Dunham, I. et.al.	Minus	1339607-1339397
	332982 332984	Dunham, I. et.al. Dunham, I. et.al.	Minus Minus	2628296-2628109 2632606-2632457
65	332998	Dunham, I. et.al.	Minus	2711704-2711565 3028925-3028811
	333058	Dunham, I. et.al.	Minus	3028925-3028811
	333097 333121	Dunham, I. et.al. Dunham, I. et.al.	Minus Minus	3204124-3204036 3308446-3308358 3309596-3309531
	333122	Dunham, I. et.al.	Minus	3309598-3309531
70	333123	Dunham, I. et.al.	Minus	3310817-3310749
	333140 333260	Dunham, I. et.al. Dunham, I. et.al.	Minus	3377220-3376309 4308400-4308304
	333603	Dunham, I. et.al.	Minus	3377220-3376309 4308400-4308304 6466335-6465727
	333604	Dunham, L et.al.	Minus	RAR7090_RARR7RR
75	333904 333906	Dunham, I. et.al. Dunham, I. et.al.	Minus Minus	8217374-8217261 8218238-8218063
	334183	Dunham, I. et.al.	Minus	11832582-11832508
	334187	Dunham, I. et.al.	Minus	11921456-11921205
80	334222 334223	Dunham, L et.al. Dunham, I. et.al.	Minus Minus	12732417-12732289 12734365-12734269
80	334255	Durham, I. et.al.	Minus	13200776-13200692
	334492	Dunham, I. et.ai.	Minus	14478333-14478172
	334648 334787	Dunham, I. et.al.	Minus Minus	15363301-15363222 16299093-16298937
85	334787	Dunham, I. et.al. Dunham, I. et.al.	Minus	20078117-20077991
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334967 Durham, I. et al. 334967 Durham, I. et al. 334969 Durham, I. et al. 334969 Durham, I. et al. 334969 Durham, I. et al. 33598 Durham, I. et al. 33598 Durham, I. et al. 33598 Durham, I. et al. 33599 Durham, I.		334945	O 02/086	443		20400005 0040000
334990 Dunham, I. et al. Minus 20041159.20x1469. 335030 Dunham, I. et al. Minus 2123787.2129714 335030 Dunham, I. et al. Minus 2123787.2129714 33503 Dunham, I. et al. Minus 2426782.212377 33503 Dunham, I. et al. Minus 2426782.222377 33503 Dunham, I. et al. Minus 2426782.22237.32233 33503 Dunham, I. et al. Minus 24267828.2428851 33503 Dunham, I. et al. Minus 2500267.25237.3223 33503 Dunham, I. et al. Minus 2500267.25237.32237 33503 Dunham, I. et al. Minus 2507767.3520267 35000 Dunham, I. et al. Minus 270767.352027 35000 Dunham, I. et al. Minus 3007767.352027 35000 Dunham, I. et al. Minus 300767.35202668 37000 Dunham, I. et al. Minus 300767		334967	Dunham,	l. et.al.	Minus	20138885-20138637
332898 Dunham, I. et al. 33289 Dunham, I. et al. 33281 Dunham, I. et al. 33282 Dunham, I. et al. 33282 Dunham, I. et al. 33282 Dunham, I. et al. 33283 Dunham, I. et		334990	Dunham,	l. et.al.	Minus	20341159-20341087
3352849 Durham, I. et al. Minus 2405973-25052878 10 335619 Durham, I. et al. Minus 2405973-25052878 110 335610 Durham, I. et al. Minus 25052877-2505248 120 335610 Durham, I. et al. Minus 25052877-2505248 1335612 Durham, I. et al. Minus 25052877-2505248 1335612 Durham, I. et al. Minus 25052877-2505248 15 335612 Durham, I. et al. Minus 25052877-2505248 15 335613 Durham, I. et al. Minus 25052878-25058787 20 335630 Durham, I. et al. Minus 25052878-25058787 20 335630 Durham, I. et al. Minus 25052878-25058787 20 335630 Durham, I. et al. Minus 25052818-25052874 20 335630 Durham, I. et al. Minus 25052847-2505788 20 335775 Durham, I. et al. Minus 2755084-77505788 20 335775 Durham, I. et al. Minus 3606483-3506874 20 335780 Durham, I. et al. Minus 3606885-3808773 30 30716 Durham, I. et al. Minus 3606897-35084773 30 30716 Durham, I. et al. Minus 3606897-35084773 30 30716 Durham, I. et al. Minus 3606897-35084773 30 30716 Durham, I. et al. Minus 360697-35084773 30 30716 Durham, I. et al. Minus 37606487-35084773 30 30716 Durham, I. et al. Minus 37606487-35084773 30 30716 Durham, I. et al. Minus 3760687-3508678 30 30717 Durham, I. et al. Minus 3760687-3508678 30 30718 Durham, I. et al. Minus 3760687-3508678 30 30718 Durham, I. et al. Minus 3760687-3508678	5	335093				21297367-21297214
335549 Dunham, I. dal. Minus 24662773-2466278 335521 Dunham, I. dal. Minus 24662773-2466278 335521 Dunham, I. dal. Minus 2566273-2466278 335521 Dunham, I. dal. Minus 2566278-2662678 335521 Dunham, I. dal. Minus 25662678-2662678 335525 Dunham, I. dal. Minus 25662678-2662678 335526 Dunham, I. dal. Minus 2766678-2766678 335627 Dunham, I. dal. Minus 2766678-2766678 335628 Dunham, I. dal. Minus 2766678-2766678 335627 Dunham, I. dal. Minus 2766678-2766678 336678 Dunham, I. dal. Minus 2766678-2766678 336779 Dunham, I. dal. Minus 2766678-2766678 337769 Dunham, I. dal. Minus 2766678-276678 337769 Dunham, I. dal. Minus 2766678-276678 337769 Dunham, I. dal. Minus 276678-276678 337769 Dunham, I. dal. Minus 276678	,	335288	Dunnam,	Letal.		22304275-22303770
10 335519 Dunham, I. et al. Minus 2002677-2502488 335725 Dunham, I. et al. Minus 2002677-2502488 335725 Dunham, I. et al. Minus 2002677-25026787 335725 Dunham, I. et al. Minus 2002677-25026787 335161 Dunham, I. et al. Minus 2776388-2502678 335816 Dunham, I. et al. Minus 2776388-2502678 335826 Dunham, I. et al. Minus 27763788-2502785 335826 Dunham, I. et al. Minus 27763788-2763788 33583 Dunham, I. et al. Minus 27763788-2763788 33583 Dunham, I. et al. Minus 27763788-2763788 33583 Dunham, I. et al. Minus 2776378-2763788 33584 Dunham, I. et al. Minus 2776378-2763788 33584 Dunham, I. et al. Minus 2776378-2763788 33584 Dunham, I. et al. Minus 3006878-3026853 337043 Dunham, I. et al. Minus 3006878-3026853 337043 Dunham, I. et al. Minus 3006878-3026853 337044 Dunham, I. et al. Minus 3006878-3026853 337045 Dunham, I. et al. Minus 3006878-3026853 337045 Dunham, I. et al. Minus 3006878-302683 337040 Dunham, I. et al. Minus 3006878-302683 337040 Dunham, I. et al. Minus 3006878-302683 337040 Dunham, I. et al. Minus 300688-302683-302683 337040 Dunham, I. et al. Minus 3006878-302683-30		335548	Dunham,	. et.al.	Minus	24662773-24662673
338229 Durbam, I. et al. 33821 Durbam, I. et al. 33822 Durbam, I. et al. 33822 Durbam, I. et al. 33823 Durbam, I. et al. 33822 Durbam, I. et al. 34822 Durbam, I. et		335551	Dunham,	l. et.al.		24679828-24678961
335862 Durham, 1 et al. 335875 Durham, 1 et al. 335885 Durham, 1 et al. 335886 Durham, 1 et al. 335887 Durham, 1 et al. 335888	10	335620	Dunham, I	. et al.	Minus	25082677-25082498
335625 Durham, I. et al. Misus 2751316-2571093 335615 Durham, I. et al. Misus 2753308-2575308-		335621				25098878-25098767
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1.5 338916 Dunham, I. et al. Minus 2305916-2359421		335755	Dunham,	l. et.al.		25763808-25763747
335835	15	335815	Dunham,	. et.al.		
335868 Durham, I. et al		335835	Dunham, I	Let.al.	Minus	26393311-26393245
20 335868 Dunham, I. et al. Minus 2897763-2867753-2867753 33505 Dunham, I. et al. Minus 2736074-2736900 335058 Dunham, I. et al. Minus 3736074-2736900 335058 Dunham, I. et al. Minus 30268675-2086538 335058 Dunham, I. et al. Minus 30268675-2086538 336275 Dunham, I. et al. Minus 30268675-2086538 336419 Dunham, I. et al. Minus 30268675-2086538 336419 Dunham, I. et al. Minus 30268675-2086538 337640 Dunham, I. et al. Minus 30268675-2086538 337043 Dunham, I. et al. Minus 30268675-2086538 337040 Dunham, I. et al. Minus 30268678-2086538 337040 Dunham, I. et al. Minus 3026583-4062445 337040 Dunham, I. et al. Minus 1140730-17407281 337129 Dunham, I. et al. Minus 2215255-22216074 337220 Dunham, I. et al. Minus 30268679-2086538 337220 Dunham, I. et al. Minus 307668679-26776681 337230 Dunham, I. et al. Minus 3076768-3076776181 337240 Dunham, I. et al. Minus 3076768-3076776181 337250 Dunham, I. et al. Minus 3076768-3076776181 337260 Dunham, I. et al. Minus 3076768-30767768181 337261 Dunham, I. et al. Minus 3076768-30767768181 3372760 Dunham, I. et al. Minus 3076768-30767768181 337261 Dunham, I. et al. Minus 3076768-30767768181 3372768 Dunham, I. et al. Minus 3076768-30767768181 3372768 Dunham, I. et al. Minus 307676818181818181818181818181818181818181		335851	Dunham, I	etal.		26604863-26604742
250 250		335896				26977639-26977558
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325557 6956502 Plus 59521-51950 325559 5245959 Miras 185939-119172 325559 6245959 Miras 135784-133981 325569 6245959 Miras 79527-520159 325559 5866932 Plus 159520-015939 325559 5866932 Plus 159520-015939		325471	6017034	Minus	289268-289	342
305 325590 6249595 Minus 133794-133991 325597 6862462 Plus 79927-80217 325597 6862462 Plus 73927-4128967 325597 5866992 Plus 737476-73574 325597 5866992 Plus 1059020-1065099		325557	6056302	Plus	50921-5105	0
325569 6249599 Plus 79927-00217 325587 6682462 Plus 126724-126967 325585 6682462 Plus 126724-126967 325597 5866992 Plus 10660020-1065099	30	325559 325560	6249595 6249596		118590-119	172
325587 6682462 Plus 126724-126967 325585 6682462 Plus 73476-73574 325587 5866992 Plus 1065020-1065089	- 3	325569	6249599		79927-8021	7
325597 5866992 Plus 73476-73574 325597 5866992 Plus 1065020-1065089 325639 5867002 Plus 253525-253608		325587	6682462	Plus	126724-126	967
35 325639 5867002 Plus 253525-253608		325585 325587			73476-7357	4 66080
	35			Plus	253525-253	608

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	325739 325740	5867038 5867038	Minus	205138-205269 207533-207690
	325792	6469828	Minus	1018-1176
_	325735	6552447	Minus	269122-269190
5	325685	6682468	Plus	117397-117483
	325686 325819	6682468 6682490	Plus Minus	118337-118439 130314-130370
	329764	6048195	Minus	109733-109968
10	329703	6065793	Minus	139994-140138
10	329643 329816	6448539	Plus Minus	53403-53537 70296-70423
	329860	6624888 6687260	Minus	183474-163605
	325883	5867087	Plus	22498-22663
15	325895 325925	5867097 5867124	Plus Plus	358317-358476 115749-115962
13	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969 325971	5867153 5867153	Plus Plus	101911-102081 105841-106035
20	329993	4567166	Minus	101307-101434
	330020	6671887	Plus	172397-172491
	326163 326274	5867168 6867171	Minus Minus	7831-8035 410289-410404
	326025	5867176	Plus	70854-70915
25	326046	5867182	Minus	62668-62825
	326099	5867186	Minus	661381-661510 23784-23903
	326108 326165	5867187 5867208	Minus	62787-62929
	326189	6867212	Plus Minus	69288-69413
30	326204	5867218	Minus	148088-148200
	326230 330052	5867230 4567182	Minus	301868-301972 352560-352963
	330036	6042048	Plus	117120-117216
35	326360	5867293	Plus	13627-13844
33	326589 326393	5867320 5867341	Plus Plus	22760-22919 41702-41841
	326505	5867435	Minus	8818-8949
	326515	5867439	Plus	36683-36809 23689-23828
40	326592 330107	6138928	Plus Minus	23689-23828 100091-100282
-10	330106	6015249 6015249	Minus	99443-99778
	330100	6015253	Plus	21166-21301
	330093 330088	6015278 6015293	Plus Plus	1043-1199 37517-37638
45	330085	6015302	Minus	59613-59770
	330120	6571864	Minus	127553-127656
	330123 326742	6671869 5867611	Minus Minus	35311-35406 95187-95248
	326605	5867637	Plus	24656-24749
50	326818	6117831	Minus	15199-15309 84525-84677
	326720 326770	6552456 6598307	Plus Minus	513603-513668
	326692	6682602	Plus	117697-117899
55	326693	6682502	Minus	335002-335095 16023-16581
23	326983 326991	5867657 5867660	Minus	18147-18339
	326936	6004446	Minus	10217-10357
	326964	6469836	Plus Plus	75340-75456 783670-783817
60	327040 327053	6531965 6531965	Plus	2247267-224743
••	327075	6531965 6531965	Plus	4041318,404143
	327085	6531965	Plus	4734947-473506
	327036 327130	6531965 6531976	Plus Plus	319951-320040 20247-22343
65	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
	327332 327220	5867516 5867525	Minus	56361-56532 65701-65781
	327224	5867534	Plus	188468-188544
70	327321	6249562	Minus	99745-99836
	327361 327396	6552412 5867743	Minus Plus	81013-62130 8702-8820
	327414	5867750	Plus	102461-102586
ac	327442	5867759	Plus	111483-111618
75	327467 327473	5867772 5867775	Plus	88030-88151 75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
80	327562 327568	5867804 5867811	Minus	343989-344474 46152-46287
30	327568 327606	5867811 6004463	Plus	46152-46287 200262-200495
	327611	5867868	Minus	175063-175392
	327642 327654	5867891	Minus	2513-2743 97564-97710
85	327654 327734	5867910 5867940	Minus Minus	31003-31583

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	327775	6867964	Minus	130791-130871		
	327796	5867982	Plus	85267-85405		
	327840	6249578	Minus	73065-73206		
5	330208	6013599	Plus	66517-66931 101503-101634		
,	330263 328004	6671884 5867993	Minus	157407-157887		
	328101	5868020	Plus	289920-290014		
	328100	5868020	Minus	263545-263635		
	328113	5868024	Minus	80378-80491		
10	328157	5868064	Plus	73326-73615		
	328196	5868080	Minus	16551-16729		
	328197	5868081	Minus	42133-42438		
	327940	5868197	Minus	95240-95428		
10	327984	5868216	Plus	6661 1-66677		
15	328021	5902482	Plus	713478-714590		
	328068	6117819	Plus Plus	253903-254022		
	328264 330300	6381912 2905862	Minus	55086-55404 3246-3302		
	328608	5868222	Minus	87770-87953		
20	328600	5868229	Minus	38889-40010		
20	328616	5868239	Plus	293920-294224		
	328623	5868246	Minus	120020-120126		
	328632	5868247	Plus	76734-76853		
	328666	5868254	Minus	778-901		
25	328698	5868264	Minus	625555-625633		
	328700	5868264	Plus	764089-764203		
	328708	5868271	Minus	68114-68854		
	328735	5868289	Plus	89389-89455		
30	328743 328806	5868289 5868324	Plus	274638-274726 29408-29684		
30	328299	5868366	Minus	149708-149889		
	328342	5868383	Plus	59955-60094		
	328365	5868387	Minus	270724-270798		
	328369	5868368	Plus	75371-75583		
35	328381	5868392	Plus	662758-662848		
	328451	5868425	Minus	217275-217336		
	328481	5868449	Minus	8987-9180		
	328500	5868464	Plus	59098-59481		
40	328530	5868482	Plus Plus	334973-335406		
40	328664 328861	6004473 6381928	Minus	1193739-119386 108317-108403		
	328908	5868493	Plus	117002-117059		
	328933	5868500	Plus	771755-771889		
	328934	5868500	Plus	846342-846448		
45	328949	6456765	Minus	43552-43519		
	330313	6042030	Minus	33642-33775		
	329005	5868542	Plus	85470-85673		
	330366	2944106	Plus	151837-151914		
50	330372	6580495	Minus	317461-317688		
30	329033	5868561	Minus	5390-5479		
	329037 329067	5868562 5868591	Minus Minus	32466-32562 146417-147652		
	329134	5868679	Plus	29959-30018		
	329157	5868687	Minus	145940-146155		
55	329178	5868704	Plus	179177-179463		
	329192	5868716	Plus	166936-167020		
	329194	5868716	Minus	304450-304559		
	329204	5868720	Minus	3050-3190		
	329224	5868728	Plus	27422-27664		
60	329228	5868728	Minus	50118-50287		
	329288	5868771	Plus	25554-26299		
	329337 329011	5868806 6682532	Minus Plus	467155-467222 48658-48741		
	323011	0002532	rius	19109-02091		

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TABLE 9A: Potential Theranguilic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung lumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous end carcinoid lumors) relative to normal body discues. These genes were selected from about 59680 probesets on the Ecul/Mirmetrix Hu03 Genochip array.

Table SB show the accession numbers for those Pkey's tacking UnigeneID's for table 9A. For each probeset we have listed the gene cluster number from which the objective objective with the properties of the prop

10 Table 9C show the genomic positioning for those Pikey's tacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15 Pkey: ExAccn: UnigenelD: Unigene Title: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number

Unigene number

Unique gene title

Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the R1: average of normal lung sample

R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples Pkey 400195 ExAcco UnigenelD Unigene Title NM_007057*:Homo sapiens ZW10 interactor NM_006265*:Homo sapiens RAD21 (S. pombe) 1.00 1.00 25 400205 15.80 396.00 400220 Eas Control 2.28 2 84 9.72 400277 Fos Control 1.00 Eas Control 400285 Eos Control integrin, alpha 5 (fibronectin receptor, matrix metalloproteinase 10 (stromelysh six transmembrane epithellal antigen of estrogen receptor 1 X06256 Hs.149609 1.04 2.24 4002RE 30 Hs.2258 400289 X07820 132 45 4 00 43.86 74.00 400200 AA032279 400298 X03835 Hs.1657 1.00 AA242758 Hs.79136 LIV-1 protein, estrogen regulated transporter 2, ATP-binding cassette, sub 1.75 1.65 400303 400328 X87344 Hs.180062 0.87 1.80 35 156.55 AF084545 253 00 400419 Target NM_030878*:Homo sepiens cytochrome P450, 400512 2.00 400517 AF242388 3.67 87.00 lengsin NM_030878*Homo sapiens cytochrome P450, NM_030878*Homo sapiens matrix metallopro NM_032425:Homo sapiens matrix metallopro NM_032425:Homo sapiens matrix metallopro NM_03245:Homo sapiens sortiin-related Anneer 1 00 1.00 20.26 45.00 400664 40 400665 1.36 1.07 3.22 1.00 91.00 400749 7.63 1.00 24.00 400763 Target Exon Target Exon 401027 1.00 C12000586*:glj6330167jdbjjBAA86477.1] (A 45 155.00 401093 1 00 Target Exon
C12000457*:gi[7512178]pi[T30337 polypr
ENSP0000247172*:HYPOTHETICAL 126.2 kDa
C14000397*:gi[7498988]piri[T33295 hypoth
histone deacetylase 5 1.00 401203 1.00 400.00 401212 1 00 72 00 64.00 401435 1.00 50 AF039241 401464 ENSP00000241802*:CDNA FLJ11007 FIS. CLON 40.00 401714 2.02 Homo sapiens keratin 17 (KRT17) 128.43 68 00 401747 35.00 401760 Tornel Exec 1.74 401780 NM_005557*:Homo sapiens keralin 16 (foca 10,50 55 401781 Target Exon NM_002275":Homo sapiens keratin 15 (KRT1 10.33 4.61 401785 4.13 2.70 Target Exon NM_021626:Homo saplens serine carboxypep 401797 1.44 1.41 401061 401985 AF053004 class I cytokine receptor 1.00 177.00 60 Target Exon
ENSP00000251056*:Plasma membrane calcium
NM_001436*:Homo eaplens fibrillarin (FBL 61.84 47.00 1.00 402075 1.00 402260 1.58 Target Exon

NM_030920*:Homo sapiens hypothetical pro
C1000823*:pj[10432400]emb|CAC10290.1| (A 402265 2.09 35.00 92.00 402297 1.00 28.87 65 13.00 402408 1.00 1.44 402674 7.44 1.00 70.00 402802 1.37 1.43 402994 70 403137 1.00 19.00 NM_006825 1.00 43.00 403306 transmembrane prossii (1997), Maria Integra ENSP00000231844*Ecotropio virus Integra NM_022342:Homo sapiens kinesin protein 9 C3001813*:gl[12737279]refPXP_012163.1] k 61.00 A03320 1.00 119.00 402391 403478 28.13 136.00 75 76.00 20.23 6.30 29.33 403627 Target Exon 1.30 35.00 403715 Target Exon
ENSP00000237855*D.1398C3.2 (NOVEL PROTEI
NM_016020*Homo sapiens CGI-75 protein (
C8000950;gl423560jbrjl;A47318 RNA-kindl
NM_005610Homo sapiens ret finger protei
ENSP00000244562:NRH dehydrogan ase [quino 1.00 54.00 91.00 404076 14 29 80 1.00 404140 404165 54.00 Target Exon
NM_005936:Homo saplens myeloid/lymphoid
NM_021058*:Homo saplens H2B histone fami 1 00 117 00 5 93 13.77 85 404253

	111/	O 02/086	443			
	404287	0 02/000	***	C6001909:gij704441 dbj]BAA18909.1 (D298	29.71	42.00
	404298			C6001238*:gij121715 sp P26697 GTA3_CHICK	1.30	1.00
	404347			Target Exon	1.00	1.00
-	404440			NM_021048:Homo sapiens melanoma antigen,	1.00	15.00
5	404721 404794	NM_000078		NM_005596*:Homo sapiens nuclear factor I	1.00 1.07	60.00 1.38
	404794	NIN_00001R		cholesteryl ester transfer protein, plas Target Exon	1.61	2.01
	404877			NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
	404927			Target Exon	1.00	1.00
10	404996			Target Exon	1.00	1.00
	405449			CY000047*:gi[11427234 reffXP_009399.1] z	1.00	1.00
	405568			NM_031413*:Homo sapiens cat eye syndrome	1. 0 0 0.76	78.00
	405572 405646			Target Exon C12000200:gij4557225[ref[NP_000005.1] al	1.01	1.14 1.28
15	405676	BE336714		cytochrome c-1	1.13	2.89
	405770	DC000114		NM_002362:Homo saplens melanoma antigen,	45.52	37.00
	405932			C15000305:gij3806122fgbjAAC69198.1) (AF0	1.99	1.99
	405137			NM_000179 :Homo sapiens mutS (E. coli) h	2.77	2.38
20	406360 406399			Target Exon NM 003122*:Homo sapiens serine protease	1.00 1.00	35.00 39.00
20	406399			Target Exon	1.00	1.00
	406621	X57809	Hs.181125	Immunodobulin lambda locus	1.41	1.74
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
0.5	406663	U24683	Hs.293441	immunoglobulin heavy constant mu	2.07	2.93
25	406671 406673	AA129547 M34996	Hs.285754 Hs.198253	met proto-oncogene (hepatocyte growth fa	15.00 0.98	51.00 3.09
	406676	M34996 X58399	Hs.81221	major histocompetibility complex, class Human L2-9 transcript of unrearranged im	1.30	1.53
	406678	U77534	110.01221	gb:Human clone 1A11 Immunoglobulin varia	1.33	1.45
	406685	M18728		gb:Human nonspecific crossreacting antig	1.48	2.85
30	406687	M31126	Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
	406690	M29540	Hs.220529	carcincembryonic antigen-related cell ad	226.37	350.00
	406696 406815	X03058 AA833930	Hs.73931 Hs.288036	major histocompatibility complex, class tRNA isopentenylpyrophosphate transferas	1.01 20.25	2.52 32.00
	406851	AA609784	NS.200030	major histocompatibility complex, class	0.75	1.91
35	406964	M21305		gb:Human elpha satellite and satellite 3	38.15	1114.00
	406967	M24349		ob:Human parathyroid hormona-like protei	1.00	1.00
	406974	M57293		gb:Human paralltyroid hormone-related pep	1.00	1.00
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.77	1.10
40	407128 407137	R83312 T97307	Hs.237260	EST	1.00 142.70	1.00 135.00
40	407157	R45175	Hs.117183	gb:ye53h05.s1 Soares fetal liver spicen ESTs	2.16	18.00
	407239	AA078350	Hs.67846	laukocyte immunoglobulin-like receptor,	1.10	1.57
	407242	M18728		gb:Human nonspecific crossreacting antig	1.12	2.85
45	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	3.24	15.38
45	407289	AA135159	Hs.203349	Homo saplens cDNA FLJ12149 fis, clone MA	3.53 19.74	3.68 73.00
	407300 407366	AA102616 AF026942	Hs.120769 Hs.271530	gb:zn43e07.s1 Stratagene HeLa cell s3 93 gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	1.00	26.00
	407430	AF169351		gb:Homo sapiens protein tyrosine phospha	1.00	25.00
50	407453	AJ132087		gb:Homo saplens mRNA for axonemal dynein	1.00	75.00
	407577 407634	AW131324 AW016569	Hs.246759 Hs.136414	hypothetical protein MGC12538 UDP-GlcNAcrbetaGal beta-1,3-N-acetylgluc	1.00 111.20	1.00 228.00
	407710	AW022727	Hs.23616	ESTS	1.00	28.00
	407720	AB037776	Hs.38002	KIAA1355 protein	1.89	1.31
55	407746	AK001962		hypothetical protein FLJ11100	1.00	1.00
	407756	AA116021	Hs.38260	ubiquifin specific protease 18	4.51	5.00
	407758	D50915 AA608956	Hs.38365 Hs.112619	KIAA0125 gene product ESTs, Moderately similar to PURKINJE CEL	1.00 0.97	28.00 1.14
	407782 407788	BE514982	Hs.112019 Hs.38991	S100 calcium-binding protein A2	7.88	3.83
60	407790	AI027274	Ha.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	89.96	109.00
	407839	AAQ45144	Hs.161566	ESTs	173.91	108.00
	407944	R34008	Hs.239727	desmocollin 2	111.30	70.00 8.00
65	408000 408031	L11690 AA081395	Hs.620 Hs.42173	bullous pemphigold antigen 1 (230/240kO) Homo saplens cDNA FLJ10366 fis, clone NT	151.17 9.91	93.00
05	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	195,78	231.00
	408070	AW148852	1.0.10010	ab:xf05d05.x1 NCI_CGAP_Bm35 Homo saplen	1.00	1.00
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	37.84	61.00
70	408122	AJ432652	Hs.42824	hypothetical protein FLJ10718	0.85	1.71
70	408212 408243	AA297567 Y00787	Hs.43728 Hs.624	hypothetical protein interleukin 8	5.88 4.27	7.91 9.98
	408349	BE546947	Hs.44276	homeo box C10	3.79	3.46
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein \$17	1.88	1.65
	408354	AI382803	Hs.159235	ESTs	1.00	73.00
75	408369	R38438	Hs.182575	solute carrier family 15 (H???? transport	1.41	16.50
	408380	AF123050	Hs.44532	diubiquitin	15.19	37.22
	408482 408522	NM_000676 Al541214	Hs.45743 Hs.46320	adenosine AZb receptor Small proline-rich protein SPRK (human,	1.65 1.98	1.19 1.24
	408522	AW381532	Hs.46320 Hs.135188	ESTs	1.55	1.50
80	408545	AW235405	Hs.253690	ESTs	1.00	1.00
	408572	AA055611	Hs.226558	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
	408633	AW963372	Hs.46677	PRO2000 protein	107.16	56.00
	408660	AA525775 AA057264	Hs.238936	ESTs, Moderately similar to PC4259 femi ESTs, Weakly similar to (define not ava	1.00 52,24	1.00 141.00
85	408761	AW732573	Hs.238936 Hs.47584	potassium voltage-gated channel, delayed	3.05	109.00
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	w	O 02/086	443			
	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00 45.00
	408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00 58.00
5	408841 408873	AW438865 AL046017	Hs.256862 Hs.182278	ESTs	1.00 1.00	89.00
,	408908	BE296227	Hs.250822	calmodulin 2 (phosphorylase kinase, delt serine/hreonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guarine nucleotide binding protein (G pr	1.00	1.00
	408996	Al979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1,44	1.24
10	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02 80.44	1.93 40.00
15	409103 409142	AF251237 AL136877	Hs.112208 Hs.50758	XAGE-1 protein SMC4 (structural maintenance of chromoso	14.87	6.00
13	409142	AF154830	Hs.50966	carbanoyl-phosphate synthetase 1, miloch	1.00	1.00
	409228	A1654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	AI879419	Hs.27206	ESTs	1.00	1.00
	409268	AA625304	Hs.187579	ESTs	11.90	23.00
20	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
25	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10 4.00
25	409446	Al561173	Hs.67688	ESTs	1.00	
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97 15.98	28.00 141.00
	409522 409582	AA075382 AA401369	Hs.190721	gb:zm87b03.s1 Stratagene ovarian cancer ESTs	1.00	17.00
	409682	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	292.12	79.00
30	409705	M37782	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
50	409719	Al769160	Hs.108681	Homo sapiens brain turnor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thyrnosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo saplans mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
35	409866	AW502152		gb:UI-HF-BR0p-air-f-11-0-UL:1 NIH_MGC_5	1.00	1.00
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
	409902	AJ337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.63 2.17	2.11 4.01
40	409956 409958	AW103364 NM_001523	Hs.727 Hs.57697	inhibin, beta A (activin A, activin AB a hyaturonan synthase 1	0.91	2.07
40	410001	AB041036	Hs.57771	kalikoh 11	1.04	2.28
	410032	BE065985	ns.arrri	gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
45	410048	W76467	Hs.58218	profine coddase homolog	1.03	1.44
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo saplens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
50	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00 42.01	1.00 51.00
30	410193	AJ132592	Hs.59757	zinc finger protein 281	1.72	1.32
	410274 410309	AA381807 BE043077	Hs.81762 Hs.278153	hypoxia-inducible protein 2 ESTs	1.00	2.00
	410309	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
	410348	AW182663	Hs.95469	ESTs	1.00	1.00
55	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
-	410418	031382	Hs.63325	transmembrane protease, serino 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
60	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92 57.00
	410781	Al375672	Hs.165028 Hs.67846	ESTs leukocyte immunogłobulin-like receptor,	1.00 1.62	3.78
	41 1027 41 1074	AF072099 X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
65	411089	AA456454	ns.00137	cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58
05	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	- 84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
	411263	BE297802	Hs.69360	kinesin-like 6 (milotic centromere-assoc	3.44 1.35	2.55
70	411365	M76477	Hs.289082	GM2 ganglioside activator protein NRAS-related gene	1.35	2.02
	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
	411579	AC005258	Hs.70830	U8 anRNA-associated Sm-like protein LSm7	1.08	1.90
75	411617	AA247994	Hs.90063	neurocalcin delta	1.74 1.02	2.57 1.00
15	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.34	2.19
	411773 411789	NM_006799 AF245505	Hs.72026 Hs.72157	protease, serine, 21 (testisin) Adilcan	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	23.34	34.00
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
80	412115	AK001763	Hs.73239	hypothetical protein FLJ 10901	2.07	1.64
00	412140	AA219691	Hs.73625	RARS interacting, kinesin-like (rabkines	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.49
	412464	T78141	Hs.22826	ESTs, Wealthy similar to 155214 salivary	1.16	1.34
~-	412530	AA766268	Hs.266273	hypothetical protein FLJ 13346	41.52	84.00
85	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

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		O 02/086				
	412659	AW753865	Hs.74376	difactomedin related ER localized protei	14.65	47.00
	412719	AW016610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
-	412811	H06382		ESTs	1.00	11.00
5	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
	412863	AA121673	Hs.59757	zinc tinger protein 281	17.63	58.00 22.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19 1.22	2.05 1.88
10	413011	AW/068115	Hs.821	bighycan		
10	413048	M93221	Hs.75182	mannose receptor, C type 1	0.30 3.43	6.23 8.71
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote		
	413129	AF292100	Hs.104613	RP42 homolog	4.67 1.92	4.77 2.59
	413142	M81740	Hs.75212	ornithine decarboxylase 1	5.73	27.00
16	413223	AI732182 ·	Hs.191866	ESTs	0.99	1.06
15	413248	T64858	Hs.21433	hypothetical protein OKFZp547J036	1.00	18.00
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.10	1.09
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	95.94	69.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	1.00	1.00
20	413364	BE536218	Hs.137516	fidgetin-like 1	0.95	2.09
20	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	1.00	1.00
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	31.00
	413453	AA 129640	Hs. 126065	ESTs	1.08	1.46
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	79.15	114.00
25	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	1.00	1.00
25	413573	AI733859	Hs.149089	ESTs	8.80	10.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	1.00	1.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
	413690	BE157489	11- 25420	gb:RC1-HT0375-120200-011-e06 HT0375 Homo	3.16	2.32
30	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B small inducible cytokine subfamily A (Cy	2.88	9.52
30	413719	BE439580	Hs.75498	small inductible cytokine subtartily A (Cy	144.10	108.00
	413753	U17760 M62246	Hs.75517	laminin, beta 3 (niceln (125kD), kalinin	1,00	17.00
	413801		Hs.35406	ESTs, Highly similar to unnamed protein centromere protein E (312kD)	1.00	1.00
	413833 413882	Z15005	Hs.75573 Hs.184492	ESTs	64.24	148.00
35		AA132973	HS.184492	ESTS	1.00	67.00
22	413926	AA 133338 AW 294416	Hs.54310	Homo sapiens cDNA FLJ12981 fis, done NT	43.42	42.00
	413943		Hs.144587		1.23	1.11
	413995	8E048146	Hs.75671	syntaxin 1A (brain)	2.02	2.51
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
40	414142	AW368397	Hs.334485	Homo Saprens CUNA PLJ 14430 No. Clone No.	8.92	77.00
40	414180	A1863304	Hs.120905 Hs.75850	Homo saplens cDNA FLJ11448 fis, done HE	1.00	1.00
	414245	BE148072		WAS protein family, member 1	1.60	59.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein phosphogluconate dehydrogenase	1.52	1.73
	414317	BE263280	Hs.75888	hypothetical protein FLJ10036	1.78	1.72
45	414334	AA824298 D80004	Hs.21331	KIAA0182 protein	33.90	151.00
73	414341	W70171	Hs.75909 Hs.75939	undine monophosphate kinase	171.60	97.00
	414368 414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AV4408965 AI346201	Hs.76118	ubiquitin carboxyl-terminal estorase 1.1	226.15	66.00
	414570	V00285	Hs.76473	Insulin-like growth factor 2 receptor	1.64	1.98
50	414618	Al204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
50	414675	R79015	Hs.296281	Interteuten enhancer binding factor 1	1.51	1.39
	414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Plok disease, type C1	28.63	71.00
	414711	Al310440	Hs 288735	Homo saplens cDNA FLJ13522 fis, clone PL	14.86	42.00
55	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410976	Hs.77152	minichromosomo maintenance deficient (S	1.64	1.44
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	65.01	74.00
	414781	AU077228	Hs.77256	enhancer of zeste (Orosophila) homolog 2	130.35	121.00
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
60	414806	D14694	Hs.77329	phosphalidylserine synthase 1	1.63	1.53
	414809	AM34699	Hs.77358	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	103.22	143.00
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.80	1.69
65	414883	AA926960		CDC28 protein kinase 1	14.29	10.06
	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telanglectasia and Rad3 related	3.00	2.90
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
70	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
	415227	AW821113	Hs.72402	ESTs	1.87	49.00
70	415238	R37780	Hs.21422	ESTs	1.00	1.00
75	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00 166.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
00	415674	BE394784	Hs.78596	proleasome (prosome, macropain) subunit,	1.48	1.39
80	415709	AA649850	Ha.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Wealdy similar to 138022 hypotheti	1.00 6.23	72.00 31.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	24.30	1.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	32.51	35.00
85	415857	AA866115	Hs.127797	Homo saplens cDNA FLJ11381 fis, clone HE		1.00
85	415989	Al267700		ESTs	78.89	1.00

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	416018	AW138239	Hs.78977	proprotein convertase subtillsin/kexin t	1.00	1.00
	416065	BE267931 AA033813	Hs.78996 Hs.79018	proliferating cell nuclear antigen	3.35 39.03	2.32 3.00
	416111 416177	AA033813 AA174069	Hs.79018 Hs.187607	chromatin assembly factor 1, suburit A (1.00	9.00
5	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
•	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
10	416250 416322	AA581386 BE019494	Hs.73452 Hs.79217	hypothetical protein MGC10791 pyrroline-5-carboxylate reductase 1	1.96 2.08	2.12 1.73
10	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
10	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96 3.68	5.00 33.00
	416722 416819	AA354604 U77735	Hs.122546 Hs.80205	hypothetical protein FLJ23017 pim-2 oncogene	1,59	1.84
	416936	N21352	Hs.42987	ESTs, Weakly similar to S21348 probable	1.00	1.00
	417034	NM .006183	Hs.80962	neurolensin	1.00	1.00
20	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	32.95	156.00
	417079	1)65590	Hs.81134	Interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00 2.05
	417233	W25005	Hs.24395 Hs.81892	small inducible cytokine subfamily B (Cy KIAA0101 gene product	3.38 82.94	25.36
25	417308 417315	H60720 Al080042	Hs.8180450	ribosomal protein S24	106.61	121.00
23	417324	AW265494	15.100-100	ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	8.97	3.27
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.59	1.82
20	417428	N87579	Hs.278871	gb:LL2030F Human felal heart, Lambda ZAP	1.00	52.00
30	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75 1,24	173.00 1.34
	417466 417512	A1681547 A1979168	Hs.59457 Hs.344096	hypothetical protein FLJ22127 glycoprotein (transmembrane) mmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
35	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.86366	ESTs	8.35	2.75
	417720	AA205625	Hs.208067	ESTs ESTs	113.31 39.98	56.00 16.00
	417791 417830	AW965339 AW504786	Hs.111471 Hs.122579	hypothetical protein FLJ10461	2.61	31.00
40	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.81	5.21
45	417975 417991	AA641836 AA731452	Hs.30085 Hs.190008	hypothetical protein FLJ23186 ESTs	12.49 1.00	38.00 26.00
45	417991	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalioproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
60	418057	NM_012151	Hs.83363	coegulation factor VIII-associated (intr	1.54	1.69
50	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82 1.26	5.22 1.46
	418140 418203	BE613836 . X54942	Hs.83551 Hs.83758	microfibrillar-associated protein 2 CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
55	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00 3.00
	418281 418283	U09550 S79895	Hs.1154 Hs.83942	oviductal glycoprotein 1, 120kD (mucin 9 cathepsin K (pycnodysostosts)	1.00 3.98	5.18
	418300	AI433074	Hs.86682	Homo saplens cDNA: FLJ21578 fis, clone C	3.18	2.91
60	418322	AA284166	Hs.84113	cyclin-dependent kinase Inhibitor 3 (COK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription ta	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379	AA218940	Hs.137516 Hs.84746	fidgetin-like 1	21.68 1.00	44.00 8.00
65	418397 418403	NM_001269 D86978	Hs.84790	chromosome condensation 1 KIAA0225 protein	16.91	18.98
05	418462	BE001596	Hs.85266	Integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase Inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 18 (monocarboxylic	2.04	2.21
70	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33 1.04	37.00 1.23
	418543 418574	NM_005329 N28754	Hs.85962	hyaturonan synthese 3 M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
75	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418586 418689	Z36830 Al360883	Hs.87268 Hs.274448	annexin A8 hypothetical protein FLJ11029	1,54 1,19	1.98 1.04
80	418589 418712	Z42183	ris.219448	gb:HSC08F041 normalized infant brain cDN	1.00	12.00
00	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
85	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97 57.09	23.00 35.00
ره	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	51.09	33.00

WO 02/086443 AA360392 Hs.87113 ESTs 418971 Hs. 191518 ESTs 4.89 28.00 418973 AA233056 insulinoma-associated 1 Hs.89584 100 419078 1.98 Hs.18844 Hs.18878 1.00 419079 AW014836 ESTs hypothetical protein FLJ21620 inlegrin, beta 8 mucin 1, transmembrane 5 Atonon AW/15/1026 51.00 A1538323 Hs.52620 419088 419092 J05581 Hs.89603 4 11 193 mucin 1, transmerribrane parathyroid hormone-like hormone protein lyrosine phosphatase, receptor t cytochrome P450, subfamily XXIV (vitamin small inducible cytokine subfamily B (Cy 1.00 419121 AA374372 Nº 80838 1.00 419171 NM_002846 U60669 He 89655 1.10 10 Hs.89663 1.00 1.00 419183 419216 AU076718 Hs.164021 3 18 2 43 small inductible cytostime severance. EST1 hypothetical protein FLJ12888 apolitoprotein H (festa 2-glytocyrolein I) chromosome segregation 1 (yeast homolog) KAAA0007 protein gb-HLMS165(10B Contech human aorta polyA PTK7 protein tyrosino Mnase 7 1.00 34 00 AA256106 Hs.87507 Hs.284137 419335 AWSSD146 22.63 54.00 M62830 He 1252 A1035A 15 Hs.90073 2.50 1 08 419359 AL043202 D26488 Hs.90315 100 7.00 1.00 12.00 419443 D62703 1.64 1.84 Hs.90572 U33635 AW968619 419474 Hs.155849 13.63 20 419485 419488 Hs.99807 Hs.90691 2.26 AA489023 4.27 3.66 AA316241 115.00 A10500 A11076704 AF070590 Hs.90869 74.60 117.00 419539 Hs.91093 1.47 4.98 419556 25 1.00 419569 AI971851 Hs.91143 94.00 AA013051 Hs.91417 419703 Al793257 15 26 50.00 He 128151 ESTs aquapatin 4 ghrucSI303.1 NICI_CGAP_SS1 Homo sapians utbuttelli carrier proble E2-C slog (chicken homolog), dric larger prot ESTs, Modernally winitar to ZASI _HUMAM Z phospholgase A2, group VII (plablet-ac phospholgase) A3, group VIII (plablet-ac p NM_001650 AA586442 419721 Hs.288650 1.00 101 00 59.00 1 00 419729 Hs.21411 30 1.08 NM 007019 A107A1 He grons AF042001 AA249573 1.00 1.00 Hs.93005 419745 Hs.152618 29.87 77.00 419752 50.99 214.00 U24577 Hs.93304 419936 A1792788 1.00 35 419937 419983 AB040959 Hs.93836 2.47 W55956 Hs.94030 15.72 94.00 Horno Saparra Incurvo. ESTs brefeldh A-inhibited guarine aucteotide Horno sapiens cDNA FLJ10651 fis, clone NT cyclif-dependent kinsse 4 Human DNA sequences from done RPS-1103G7 catchum channel, voltage-dependent, P/Q AW271106 1 43 Hs.133294 315 12.45 39.00 Hs.94631 Hs.94694 420047 A1478658 117.00 420058 AK001423 1.43 2.35 0.77 40 Hs.95577 1 21 420162 BE378432 3.23 420251 AW374968 Hs.348112 Hs.96253 1.15 420259 AF004884 Al623693 54.00 31.00 Hs.323494 ESTs 45.04 420291 ESTs, Weakly similar to ALU5_HUMAN ALU S scrine (or cystelne) proteinase inhibito AW043837 NM_001756 AA640891 49.22 420309 Hs.21766 0.05 45 420332 Hs.1305 chondremodulin I precursor similar to rab11-binding protein hypothetical protein ESTs Hs.102406 Hs.97932 274 420380 AF050147 1.00 49.74 94.65 100 420462 AK001978 Hs.98510 133.00 420552 AKMMA92 He gagne 50 420560 420610 A\W207748 He 59115 17.00 AI683183 Hs.99348 1.00 13.00 50.09 95.00 ESTS ZAP3 protein 31.00 A20721 AA927802 He 159471 Homo sapiens cDNA FLJ11381 fis, clone HE lectin, galactoside-binding, soluble, 7 1.00 48.00 420759 T11832 Hs.127797 Hs.99923 55 1 25 420783 2.24 7.00 420900 AL045633 He 44269 ESTS ESTs small inducible cytokine B subfamily (Cy transcription factor 17 8.00 AF044197 420931 Hs.100431 AF116030 1.00 27.00 421002 Hs 100932 421027 AA761198 2.87 38.00 60 AI684808 N36914 1.00 421037 Hs.197653 ESTs, Moderately similar to 138022 hypot metastasis associated 1 cathepsin E ESTS 98.00 421041 He 14691 1 46 421073 NM 004689 Hs.101448 421110 AJ250717 Hs.1355 119.47 427.00 AA401369 Hs.190721 ESTs 1.10 17.00 421133 lysyl oxidase Homo saplens mRNA; cDNA DKFZp434B0425 (f SMA5 65 Hs.189902 Hs.102267 1.45 421150 AI913562 15.00 421155 421307 H87879 Hs.103305 1.37 1.10 RF539976 21 00 421316 AA287203 Hs.324728 1 00 small inducible cytokine subfamily B (Cy 1.92 3.94 421379 Y15221 No 103092 70 ESTs 5.89 Hs.50831 421451 AA291377 ESTs southe carrier family 1 (glutamate trans thymriden kinese 1, softble absent in melanes 1, softble absent in melanes 1, softble adjula 2, 6-sishyltransferase 1, 1 GDHF samly receptor sights 1 DKFZP5640023 problen secretated frizzled-related protoin 4 detensity, beta 2 throtol factor 1 (breast cancer, estroge souther period). U76362 Hs.104637 1 46 1.76 421474 1.08 BE302798 Hs.105097 1.56 421506 5.11 5.23 421508 NM_004833 Y11339 Hs.105115 3.00 421515 Hs.105352 Hs.105445 75 421524 AA312082 2.63 10.58 421526 AL080121 Hs.105460 1 46 1.88 421552 AF026692 He 105700 AJ000152 Hs.105924 1.74 421574 AI910275 1 23 1.00 421582 80 1.00 116.00 421633 AF121860 Hs.106260 sorting nextn 10 protocadherin 17 6.33 NM_014459 421659 Hs.106511 Hs.38282 ESTs 1.31 1.42 A21677 H64092

BE314828

W69233

Hs.107911

Hs.112457

He 109196

421753

A21777 RE562088

85

1.20

1.14

1.41

1.12

ATP-binding cassette, sub-family B (MDR/

HSPC037 protein

		O 02/086				
	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660 Hs.45107	ATP-binding cassette, sub-family C (CFTR ESTs	1.8B 11.84	1.59 22.80
	421896 421928	N62293 AF013758	Hs.45107 Hs.109643	polyadenylate binding protein-interactin	45.89	90.00
5	421931	NM 000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
-	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00 62.00
10	422094 422095	AF129535 AI868872	Hs.282804	F-box only protein 5	67.61 4.37	2.34
10	422109	S73265	Hs.1473	hypothetical protein FLJ22704	4.18	95.50
	422128	AW881145	113.1470	gastrin-releasing peptide ab:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
	422134	AW179019	Hs.112110	mitochandrial ribosomal protein L42	41.59	96.00
15	422158	L10343	Hs.112341	protease Inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psortas	3.29 4.93	1.68 5.73
	422278 422282	AF072873 AF019225	Hs.114218 Hs.114309	frizzied (Drosophila) homolog 6 apolipoprotein L	1.49	1.71
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerovis	25.99	10.91
20	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	enimoulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
25	422406	AF025441	Hs.116206	Opa-Interacting protein 5	18.33 1.71	53.00 3.21
25	422424 422440	AI186431	Hs.296638 Hs.116724	prostate differentiation factor aldo-keto reductase family 1, member B10	47.53	32.00
	422487	NM_004812 AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
30	422656	AI870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dani	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05 3.88	1.46 1.53
	422765 422809	AW409701 AK001379	Hs.1578 Hs.121028	baculoviral IAP repeat-containing 6 (sur hypothetical protein FLJ10549	99.56	53.00
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
22	422938	NM 001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transform)	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
40	422963	AA401369	Hs.190721	ESTs	171.41 2.12	17.00 1.62
40	422976 422981	AU076657 AF026445	Hs.1600 Hs.122752	chaperonin containing TCP1, subunit 5 (e TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AF-026445 AA319777	Hs.122152 Hs.221974	FSTs	12.40	32.47
	423034	AL119930	113.22.1074	gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
45	423081	AF262992	Hs,123159	sperm associated antigen 4	1.82	2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640 Hs.125845	collagen, type VII, alpha 1 (epidermolys	2.14 7.18	1.69 14.00
	423248 423309	AA380177 BE006775	Hs.125845 Hs.126782	ribulose-5-phosphate-3-epimerase sushi-repeat protein	21.90	64.00
50	423361	AW170055	Hs.47628	ESTs	1.00	1.00
-	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
	423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
	423551	AA327598	Hs.233785	ESTs	3.54	4.33
55	423554	M90616	Hs.1674	glutamine-fructose-6-phosphate transamin Homo sapiens cDNA FLJ11576 fis, clone HE	1.00 38.88	50.00 70.00
	423575 423624	C18863 AI807408	Hs.163443 Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
60	423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix matalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00 4.20	59.00 1.00
	423725 423761	AJ403108 NM_006194	Hs.132127 Hs.132576	hypothetical protein LOC57822 paired box gene 9	1.00	1.00
65	423761	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
05	423816	AF151064	110.200201	hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	 Homo saplens mRNA; cDNA DKFZp761J1324 (f 	1.00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
70	423934 423954	U89995 AW753164	Hs.159234 Hs.288604	forkhead box E1 (thyroid transcription f	51.33 5.81	31.00 10.87
	423954	D13666	Hs.136348	KIAA1632 protein osteoblast specific factor 2 (fasciciln	3.55	3.30
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
	424012	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
75	424028	AF055084	Hs.153692	Homo senions cDNA FLJ14354 fis. clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424086	AI351010	Hs.102267	lysyl oxidasa	21.91 137.82	70.00 54.00
	424098	AF077374	Hs.139322	small proline-rich protein 3 ESTs	1.00	1,00
80	424120 424165	T80579 AW582904	Hs.290270 Hs.142255	islet amyloid polypeptide	1.00	34.00
00	424200	AA337221	110.1442200	gb:EST41944 Endometrial tumor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	Irvetochen hydroxylase (tryotophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164,58	87.00
0.5	424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
85	424340	AA339036	Hs.7033	ESTs	0.88	1.15

WO 02/086443 14-3 hs. 145567 hypothetical protein Hs. 201189 ESTs, Weakly similar to G01763 atrophin-Hs. 146539 protein Marse Chie Hs. 146549 crystallin, beta A2 Hs. 146680 prostaljandin E synthase Hs. 147097 HZA histone family, member X 424351 1 03 DE622117 424364 AW383226 3.24 424381 AA285249 424411 424420 3.25 NM_005209 1 63 5 1.63 BE614743 424441 1.82 1.29 Y14850 HZA hátana family, member X ingaila lingaila lin 424502 AF242388 Hs.149585 424503 X06256 Hs.149609 1.02 2 24 424513 BE385864 Hs.149894 1.00 17.00 10 He 150402 108.00 102911 424568 Hs.150595 AE005418 424602 AK002055 Hs.151046 31.87 25.00 2 37 424629 M90656 Hs.151393 3.58 42AC4C 100 1 00 NM_014682 Hs.151449 424645 424687 2.23 15 2.12 105070 He 151738 1.00 1.00 424717 AW992292 Hs.152213 424717 424834 424840 424867 424905 424979 424999 425048 AK001432 Hs.153408 Hs.153479 56 19 12 00 2.66 1 30 D79987 AI024860 1.23 Hs.153591 20 NM_002497 Hs.153704 21.35 1.00 D87989 AW953120 H05468 Hs.154073 1.36 1 15 gb:EST365190 MAGE resequences, MAGB Homo ESTs 1.41 Hs.164502 1.00 ESTs achaete-scute complex (Drosophila) homol minichromosome maintenance deficient (S. methylone tetrahydrotiate dehydrogenase carbamoyi-phosphate synthetase 2, spart ESTs, Weakly similar to 138022 hypotheti ESTs, Weakly similar to 138022 hypotheti ESTs, Weakly similar to 138022 hypotheti stanniocatcin 2 Hs.164502 Hs.1619 Hs.154443 Hs.154672 Hs.154868 425057 AA826434 7.46 87.00 25 X74794 425081 2.52 AU076611 425118 NM 004341 3.62 2.73 425150 Hs.152049 Hs.165909 425202 AW962282 1.00 53.00 100.77 44 00 425234 AW152225 30 Hs.155223 Hs.155314 stenicoción 2 (AAA005 pen probot matrix mistilicroteinase 11 (abomelysin adapha-feloprolion enischromasorra matriamano distriant (mi prolin hisnas, DNA-advahrad, calabilic chose 5-phosphate isomerase A (rifose 5 mosobhari bopokomerase (DNA) il albina (170KO) hypothodical probon (NLPSR ELKL.morti kinase ELKL.morti kinase ELKL.morti kinase ELKL.morti kinase ELKL.morti kinase A25236 AWARTRAD 1.91 2.32 425245 A1751768 425247 NM 005940 Hs.155324 1 41 1 49 68.00 425266 Innazz Hs.155421 Hs.155462 1.00 1.97 425274 BE281191 35 425322 1163630 Hs.155637 141.49 123 00 425349 AA425234 Hs.79886 Hs.155981 1.00 84.00 D49441 J04088 1.59 425371 425397 He 158348 14.90 BF538911 Hs.234545 1.00 40 425424 NM_004954 Hs.157199 10.58 9 74 EÜd. moff kinase FAT humor supressor (Drosophila) hamolo UL 16 binding protein 2 galanin desmoglein 3 (peruphiyus vulçaris antigen N-acepturansferase 1 (arylamine N-acety protein yrvaline phosphilase, non-recept peptidylejohen eiph-amidding omorouvy peruthyrvold hormone receptor 2 ESTs ESTs 1.40 425483 425566 425580 AF231022 Hs.158159 1.74 Hs.250618 AW162943 53.29 33.45 L11144 Hs.1907 233.00 425650 425692 425695 NM_001944 Hs.1925 1 00 45 1.00 D90041 Hs.155956 Hs.159238 Hs.159396 NM 005401 10.00 425734 AF056209 1.00 41.00 48.00 425776 1125128 Hs.159499 1.00 27.39 425R10 A1923627 Hs.31903 50 425811 AL039104 Hs.159557 karyopherin alpha 2 (RAG cohort 1, Impor serum/glucocorticoid regulated kinase death receptor 6, TNF superfamily member 1 58 425849 AI077288 Hs.296323 71.16 3.42 425852 426067 AK001504 AA401369 1,34 Hs.159651 1.35 ESTs 17.00 Hs 190721 ESTs ATPasa, Class I, typo 88, member 1 stamboodin 2 stam 426088 AF038007 26.26 47.00 Hs.166196 55 426215 AW067800 Hs.155223 2.90 25.00 Hs.154299 Hs.168950 428227 22.40 1167058 H15302 1.00 1.00 426269 NM_003937 AL389951 MB6699 426283 Ha.169139 01 20 229.00 4.34 4.08 426329 426427 Hs.271623 60 1.00 Hs.169840 426432 AF001601 Hs.169857 1.16 1.68 426440 426459 426471 BE382756 2 59 1 71 1.66 AF151812 Hs.169992 1.56 M22440 Hs. 170009 65 426496 426501 426514 D31765 Hs.170114 9.81 22.00 AA401369 Hs.190721 ESTs 19.23 17.00 bone morphogenetic protein 7 (osteogenic ESTs BE616533 AI949749 103 74 41.00 Hs 170195 Hs.44441 A26536 ESTs hypothetical protein FLJ11183 UDP glycosyltransferase 1 family, polype PCTAIRE protein kinase 1 urtiline monophosphate synthetase (orotat 426572 426682 AB037783 Hs. 170623 1.00 43.00 70 AV660038 NM_006201 J03626 X69490 U03749 160.06 8.00 1.35 426691 426746 Hs.171834 1.51 2.13 Hs 2057 Hs.172004 5.14 426752 1.72 1.71 426784 Hs.172216 chromogranin A (parathyrold secretory pr 426807 426812 426814 426831 SETS sclute carrier family 12 (potassium/chlo myelin transcription factor 1-like S-adenosythomocysteine hydrolase 75 AA385315 Hs.156682 1 30 AF105365 1.53 He 172613 AF036943 Hs.172619 1.00 1.00 BE296216 Hs.172673 1.51 1.25 AA401369 NM_001196 NM_000088 AA393739 Al493134 426697 Hs.190721 141.56 17.00 426597 426925 426935 426964 426966 Homo sapiens cDNA: FLJ22373 fis, clone H collagen, type I, alpha 1 Homo sapiens cDNA FLJ11439 fis, clone HE 80 Hs.315689 Hs.172928 32.61 38.00 2.65 3.16 3.49 Hs.287416 1.97 1.00 Homo sapiens cDNA FLJ10674 fis, clone NT odd Oz/ten-m homolog 2 (Drosophila, mous 426991 AK001536

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Hs.173560

A 24

17.00

	W	O 02/086	443		1.58	1,05
	427239	BE270447	Hs.174070	ubiquitin carrier protein gb:ae70b06.s1 Stratagene schizo brain S1	1.34	1.60
,	427260 427281	AA663848 AA906147	Hs.102869	FSTs	1.00	66.00
	427335	AA448542	Hs.251677	Gantigen 7B	51.83	4.00
5	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427356	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00 1.32
	427383 427427	NM_005411 AF077345	Hs.177582 Hs.177936	surfactant, pulmonary-associated protein lectin, superfamily member 1 (cartilage-	1.00	20.00
10	427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
10	427445	X80818	Hs.178078	glutamate receptor, metabotropic 4	0.97	1.03
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
16	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45 1.50	92.00 3.24
15	427546	AA188763	Hs.36793 Hs.26534	hypothetical protein FLJ23188 FSTs	6.81	40.00
	427562 427585	R56424 D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427660	Al741320	Hs.114121	Homo sapiens cONA: FLJ23228 fis, clone C	2.70	49.00
	427666	Al791495	Hs. 180142	calmodulin-like sidn protein	1.37	1.88
20	427688	AA298760	Hs.180191	hypothetical protein FLJ14904	29.55	67.00
	427677	NM_007045	Hs.180296	FGFR1 oncogene partner	3.52	2.63
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41 15.84	34.00 70.00
	427711	M31659 Al393122	Hs.180408 Hs.134726	solute carrier family 25 (mitochondrial ESTs	7.03	4.52
25	427719 427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
23	427747	AW411425	Hs.180655	serine/threanine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfami	9.63	69.00
	427961	AW293165	Hs.143134	ESTs	41.97	118.00
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	23.82 1.40	1.00 1.33
30	428023	AL038843	11. 007504	Homo sapiens cDNA: FLJ23602 fis, clone L	96.28	167.00
	428046 428093	AW812795 AW594506	Hs.337534 Hs.104830	ESTs, Moderately similar to I38022 hypot ESTs	1.25	1.29
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60
	428129	AJ244311	Hs.26912	ESTs	1.00	42.00
35	428169	Al928984	Hs.182793	coloi phosphoprotein 2	2.76	2.11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1,00 85,59	1.00 181.00
	428227 428242	AA321649	Hs.2248 Hs.2250	small inducible cytokine subfamily B (Cy leukemia inhibitory factor (cholinergic	8.57	21.64
	428242	H55709 1.22524	Hs.2256	matrix metalloproleinase 7 (matriysin,	7.77	15.90
40	428434	A1909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53	204.00
	428471	X57348	Hs.184510	stratifin	6.00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	56.54 3.53	16.00 2.15
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino chromogranin B (secretogranin 1)	1.00	1.00
43	428505 428532	AL035461 AF157326	Hs.2281 Hs.184786	TBP-Interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AX001666	Hs. 189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
	428598	AA852773	Hs.334838	KIAA1866 protein	187.37	255,00
50	428728	NM_016625	Hs.191381	hypothetical protein	47.24 1.00	80.00 87.00
	428748	AW593206	Hs.98785 Hs.98502	Ksp37 protein hypothetical protein FLJ14303	1.06	1.13
	428768 428771	AA433988 AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
	428801	AW277121	Hs.254881	FSTs	1.67	6.15
55	428810	AF068236	Hs.193788	nitric colde synthase 2A (inducible, hep	1.03	1.27
	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845	AL157579	Hs.153610	KIAA0751 gene product	1.00 15.16	1.00 27.00
	428959	AF100779	Hs.194680 Hs.194689	WNT1 inducible signaling pathway protein arternin	1.36	1.24
60	428969 429038	AF120274 AL023513	Hs.194089	seizure related gene 6 (mouse)-like	0.97	3.31
00	429065	A1753247	Hs.29643	Homo sapiens cONA FLJ13103 fis, clone NT	6.82	16.47
	429164	A1688663	Hs.116586	ESTs	19.08	67.00
	429170	NM_001394	Hs.2359	dual specificity phosphalase 4	16.18 79.72	105.00 104.00
60	429183	AB014604	Hs.197955	KIAA0704 protein	1.00	1.00
65	429201 429211	X03178 AF052693	Hs.198246 Hs.198249	group-specific component (vitamin D bind gap junction protein, beta 5 (connexin 3	1.33	1.09
	429220	AW207206	115.150245	ESTs	1.00	7.00
	429228	A1553633	Hs.326447	ESTs	39.47	29.25
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
70	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00 142.00
	429276	AF056085 W00482	Hs.198612	G protein-coupled receptor 51 matrix metalloproteinase 14 (membrane-in	3.70 1.30	1.94
	429359 429412	NM_006235	Hs.2399 Hs.2407	POU domain, class 2, associating factor	94.09	86.00
	429413	NM 014058	Hs.201877	DESC1 protein	41.91	10.00
75	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
	429504	X99133	Hs.204238	Epocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs. 190721	ESTs	1.06 2.89	17.00 65.00
80	429551 429563	AW450624 BE619413	Hs.220931 Hs.2437	ESTs eukaryolic translation initiation factor	1.49	1.37
30	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
0.5	429616	Al982722	Hs.120845	ESTs COLOR	1.00 1.00	1.00 4.00
85	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

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	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic, turnor necrosis factor receptor superfami	69.95 1.25	104.00 1.21
	429736 429782	AF125304 NM_005754	Hs.212680 Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
5	429918	AW873986	Hs.119383	ESTs	1.00	78.00
	429978	AA249027		ribosomal protein S6	1.98 1.00	3.09 48.00
	429986 430044	AF092047 AA464510	Hs.227277 Hs.152812	sine oculis homeobox (Drosophila) homolo ESTs	69.27	59.00
	430114	AA847744	Hs. 152612 Hs. 99640	FSTs	1.00	1.00
10	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.00	51.00
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759 Hs.32976	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00 3.80	127.00 1.47
	430294 430300	A1538226 U60805	Hs.238648	guanine nucleotide binding protein 4 oncostatin M receptor	1.00	35.00
15	430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
	430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	5.28 16.76	66.00 38.00
	430388 430393	AA356923 BE185030	Hs.240770 Hs.241305	nuclear cap binding protein subunit 2, 2 estrogen-responsive B box protein	1.63	1.50
20	430439	AL133561	ns.241303	DKFZP434B061 protein	1.00	1.00
~~	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466 430481	AF052573 AA479678	Hs.241517 Hs.203269	polymerase (DNA directed), theta ESTs, Moderately similar to ALU8_HUMAN A	2.47 1.00	1.91 31.00
25	430486	BE052109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
23	430508	AI015435	Hs.104637	ESTS	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Wealdy similar to T17268 hypotheti	1.00	1.00
	430563	AF146074	Hs.108660	ATP-blinding cassette, sub-family C (CFTR	1.00 1.72	1.59 1.30
30	430677 430678	Z26317 AA401369	Hs.94560 Hs.190721	desmoglein 2 ESTs	0.90	17.00
30	430686	NM_001942	Hs.2633	desmoglain 1	1.00	1.00
	430788	Al742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
35	430935 430985	AW072916 AA490232	Hs.27323	zinc finger protein 131 (clone pHZ-10) ESTs, Wealdy similar to 178885 serine/th	90.28 0.94	132.00 1.28
33	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395	110.70000	ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	Al332764	Hs.125757	ESTs	13.46	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43 0.44	62.00 2.20
40	431164 431211	AA493650 M86849	Hs.94367 Hs.323733	Homo saplens cDNA: FLJ23494 fis, clone L gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs	1.00	86.00
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
45	431342 431384	AW971018 BE158000	Hs.21659 Hs.285026	ESTs gb:MR2-HT0377-150200-202-e03 HT0377 Homo	1.00 0.94	53.00 1.14
	431384 431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	26.00
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41 5.66	1.87 15.00
50	431548 431630	AI834273 NM 002204	Hs.9711 Hs.265829	novel protein integrin, alpha 3 (antigen CD49C, alpha	0.99	1,44
	431630	AW972448	Hs.163425	FSTs	0.99	3.51
	431770	BE221880	Hs.268555	5-3 exoribonuclease 2	67.12	91.00
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36 4.49	4.71 2.51
55	431846	BE019924 X17033	Hs.271580 Hs.271986	uroplakin 1B integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
	431890 431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	61.17	46.35
	432006	AL137382	Hs.272320	Homo saplens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
60	432023	R43020	Hs.236223 Hs.298241	EST	0.94 1.10	47.00 2.24
	432201 432210	AI538613 AI567421	Hs.273330	Transmembrane protease, serine 3 Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cytidylyttransferase 1, cholin	1.00	1.00
	432239	X81334	Hs.2936	matrix metallograteinase 13 (collagenase	18.67	1.00
65	432265	BE382679	Hs.285753	SCG10-like-protein	1.09 40.98	1.21 58.00
	432281 432365	AK001239 AK001106	Hs.274263 Hs.274419	hypothetical protein FLJ10377 hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo saplens cDNA FLJ11346 fis, clone PL	157.34	37.00
	432375	BE536069	Hs.2962	S100 catclum-binding protein P	1.65	1.06
70	432407	AA221036		gb:zr03f12.r1 Stratagene NT2 neuronal pr	73.71 56.35	75.00 72.00
	432441	AW292425 AI804855	Hs.163484 Hs.207530	ESTs ESTs	1.00	24.00
	432489 432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
75	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine prolesse, granzyme 3;	2.87 26.63	6.22 56.00
	432625 432653	A1243596 N62096	Hs.94830 Hs.293185	ESTs, Moderately similar to T03094 A-kin ESTs, Weakly similar to JC7328 amino aci	1.92	5.29
	432677	NM_004482		UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
80	432715	AA247152	Hs.200483	FSTs. Weakly similar to KIAA1074 protein	45.13	31.00
	432753	NM_014075	Hs.336938	Homo saplens PRO0593 mRNA, complete cds	1.00 2.69	68.00 3.67
	432788 432842		Hs.178499 Hs.334822	Homo saplens cDNA: FLJ23117 fls, clone L hypothetical protein MGC4485	1.22	1.34
	432842	AW016936	Hs.233364	ESTs	1.00	1.00
85	432917	NM_014125		PRO0327 protein	10.25	6.62

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	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	432920	AF217513	Hs.279906	done HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
-	433042	AW193534	Hs.281895	Homo saciens cDNA FLJ11660 fis, clone HE	1.00	10.00
5	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20 13.82	1.09 39.00
	433159 433183	AB035898 AF231338	Hs.150587 Hs.222024	kinesin-like protein 2 transcription factor BMAL2	1.00	69.00
	433163	AF231338 AA622788	Hs.222024 Hs.203613	ESTs, Weakly similar to ALUB_HUMAN IIII	1.00	1.25
	433409	AJ278802	Hs.25661	ESTs	44.81	117.00
10	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	Al493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	AI733692	Hs.112488	ESTs	8.66 25.16	55.00 83.00
	433547 433556	W04978	Hs.303023 Hs.111460	beta tubulin 1, class VI calcium/calmodulin-dependent protein kin	1.00	19.00
15	433556	W56321 AA603367	Hs 222294	ESTs	20.30	49.00
13	433658	1.03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097	Hs.112765	ESTs	3.71	8.00
•	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
20	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108,91 1,00	47.00 1.00
	434088 434094	AF116677 AA305599	Hs.249270 Hs.238205	hypothelical protein PRO1966 hypothelical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presentins associated rhombold-like pro	1.22	1.23
	434217	AW014795	Hs.23349	FSTs	14.11	57.00
25	434340	Al193043	Hs.128685	ESTs, Wealdy similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98	17.00
	434414	A1798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens Homo sapiens cDNA: FLJ23523 fis, clone L	1.48 1.00	1.56 64.00
	434424 434467	AI811202 BE552368	Hs.325335 Hs.231853	Horno sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
30	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
50	434627	AJ221894	Hs.39311	ESTe .	1.00	1.00
	434699	AA543687	Hs.149425	Homo sapiens cDNA FLJ1 1980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00 44.00
35	434792	AA649253	Hs.132458 Hs.256150	ESTs Homo sapiens, Similar to RIKEN cDNA 2810	8.52 11.33	1.00
33	434808	AF165108 D90070	Hs 96	phorbol-12-myristate-13-acetate-induced	. 1.00	1.00
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00	6.00
	434928	AW015595	Hs.4267	Homo saplens clones 24714 and 24715 mRNA	1.00	1.00
40	435013	H91923	Hs.110024	Target CAT	1.26	1.10 1.37
	435066 435087	BE261750 AW975241	Hs.4747 Hs.23567	dyskeralosis congenita 1, dyskerin ESTs	1.69 1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
	435159	AA668879	Hs.116649	ESTa	1.00	1.00
45	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70 139.00
	435304	H10709	Hs.269524	ESTs	27.58 1.00	14.00
	435313 435505	AI769400 AF200492	Hs.189729 Hs.211238	ESTs Interleukin-1 homolog 1	1.00	38.00
50	435509	AI458679	Hs.181915	ESTs	1.00	1.00
-	435525	AI831297	Hs.123310	FSTs	1.00	56.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.saplans polyA site DNA	3.42 3.95	3.92
55	435602 435766	AF217515 R11673	Hs.283532 Hs.186498	uncharacterized bone marrow protein BM03 ESTs	1.00	1.80 28.00
33	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	AI056879	Hs.263209	ESTs	1.00	58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
60	436213	AA325512	Hs.71472	hypothetical protein FLJ 10774; KIAA1709	1.42 57.97	1.27 31.00
	436217 436238	T53925 AK002163	Hs.107 Hs.301724	fibrinogen-like 1 hypothetical protein FLJ11301	2.51	1.71
	436251	BE515065	Hs.296585	sucleolar protein (KKE/D repeat)	2.33	1.64
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
65	436302	AL355841	Hs.99330	hypothetical grotein FLJ23588	0.75	2.81
	436398	AW992292	Hs.152213	wingless-type MMTV integration site famil	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50 0.95	2.19 1.33
	436419 436443	AI948626 AW138211	Hs.171356 Hs.128746	ESTs ESTs	1.12	9.26
70	436474	AJ270693	Hs.199887	FRTs	1.00	1.00
,,	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553	X57809 W15573	Hs.181125	immunoglobulin lambda locus ESTs, Weakly similar to A47582 B-cell gr	1.08 19.20	1.74 9.75
13	436557 436608	W15573 AA628980	Hs.5027	down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
	436839	AA401369	Hs.190721	FSTe	1.00	17.00
80	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15
	436944	AW268614	Hs.5840	ESTs	1.00	1.00 25.00
	436961	AW375974	Hs.156704	ESTs	25.13 1.59	1.46
	436972 437016	AA284679 AU076916	Hs.25640 Hs.5398	claudin 3 quantne monphosphate synthetase	2.35	1.78
85	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

		O 02/086	143			
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00 40.55	17.00 82.00
	437204 437205	AL110216 AL110232	Hs.22826 Hs.279243	ESTs, Weakly similar to I55214 salivary Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
	437259	Al377755	Hs.120695	ESTs	1.00	205.00
5	437270	R18087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
	437271	AL137445	Hs.28846	Homo saplens mRNA; cDNA DKFZp566O134 (fr	113.25 1.82	125.00 4.57
	437370 437390	AL359567 Al125859	Hs.161962 Hs.112607	Homo sapiens mRNA; cDNA DKFZp547D023 (fr FSTs	1.35	1.75
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3,20
10	437435	Al306152	Hs.27027	hypothetical protein OKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568	A1964795 D63880	Hs.156135 Hs.5719	ESTs chromosome condensation-related SMC-asso	1.00 1.95	19.00 1.57
	437623 437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
15	437814	Al088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852 437879	BE001836 BE262082	Hs.256897 Hs.5894	ESTs, Weakly similar to dJ365O12.1 [H.sa hypothetical protein FLJ10305	1.68 1.87	3.26 2.52
	437915	Al637993	Hs.202312	Homo sapiens done N11 NTera2D1 teratoca	74.05	35.00
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
	437937	AI917222	Hs.121655	ESTs	1.00	1.00
	437942 438091	Al888256 AW373062	Hs.307526	ESTs . nuclear recoptor subfamily 1, group I, m	12.28 1.53	31.00 10.85
	438113	AV4575062 AI467908	Hs.8882	ESTs	1.80	2.39
25	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36,90
	438274	Al918906	Hs.55080	ESTs	1.00	1.00
	438378 438403	AW970629 AAR06607	Hs.86434 Hs.292206	hypothetical protein FLJ21816 ESTs	38.92 1.00	38.00 1.00
	438494	AA908678	Hs.130183	ESTS	2.05	80.00
30	438546	AW297204	Hs.125811	ESTs	1.00	131.00
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AI879064	Hs.54618	ESTs	1.00 1.33	34.00 1.10
	438724 438746	AW612553 AI885815	Hs.114670 Hs.184727	Human DNA sequence from clone RP11-16L21 Human melanoma-associated anticen p97 (m	2.42	1.59
35	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	A1886558	Hs.184987	ESTs	6.42 22.41	88.00 17.00
	438898 438915	AA401369 AA280174	Hs.190721 Hs.285681	ESTs Williams-Beuren syndrome chromosome regi	1.00	1,00
40	438958	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
	439000	AW979121		ab:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTS	1.17 1.00	1.31 28.00
	439024 439128	R96696 Al949371	Hs.35598 Hs.153089	ESTs ESTs	1.00	67.00
45	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223	AW238299	Hs.250618	UL16 blading protein 2	1.93	1.64
	439285	AL133916	Hs.6527	hypothetical protein FLJ20093	46.23 2.00	139.00 2.20
	439318 439343	AW837046 AF086161	Hs.114611	G protein-coupled receptor 56 hypothetical protein FLJ11808	8.10	7.37
50	439394	AA401369	Hs.190721	ESTs	3.39	17.00
	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451 439452	AF086270 AA918317	Hs.278554 Hs.57987	heterochromatin-like protein 1 B-cell CLL/ymphoma 11B (zinc finger pro	23,28 18,76	52.00 122.00
	439452	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
55	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
	439492	AF086310	Hs. 103159	ESTs	7.46	39.00
	439523 439592	W72348 AF086413	Hs.185029 Hs.58399	ESTs ESTs	1.00 1.00	1.19
	439696	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
60	439670	AF088076	Hs.59507	ESTs, Wealty similar to AC004858 3 U1 sm	1.00	1.00
	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527 BE246502	Hs.59761 Hs.9598	ESTs, Weakly similar to DAP1_HUMAN DEATH sema domain, immunoglobulin domain (lg),	86.55 2.36	11.00 1.88
	439738 439750	AL359053	Hs.57664	Homo saciens mRNA full length Insert cDN	2.02	6.08
65	439759	AL359055	Hs.67709	Homo saplens mRNA full length insert cDN	1.00	21.00
	439780	AL109688		gb:Homo saplens mRNA full length insert	7.27	25.00
	439840 439926	AW449211 AW014875	Hs.105445 Hs.137007	GDNF family receptor alpha 1 ESTs	1.00 32.58	1.00 71.00
	439963	AW247529	Hs.6793	platelet-activating factor acetythydrola	21.28	9.55
70	439979	AW600291	Hs.6823	hypothetical protein FLJ 10430	68.83	61.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02 2.54
	440028 440106	AW473675 AA864968	Hs.125843 Hs.127699	ESTs, Weakly similar to T17227 hypotheti KIAA1603 protein	1.42 1.00	54.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ 10201	24.18	52,00
75	440273	AI805392	Hs.325335	Horno sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
	440289	AW450991	Hs.192071	ESTs	38.63	113.00
	440325 440492	NM_003812 R39127	Hs.7164 Hs.21433	a disintegrin and metalloproteinase doma hypothetical protein DKFZp547J036	62.88 2.35	147.00 3.62
	440492	AV657117	Hs.21433 Hs.184164	ESTs, Moderately similar to \$65657 elpha	10.84	57.00
80	440659	AF134160	Hs.7327	claudin 1	3.18	2,37
	440704	M69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440943 440994	AW082298 Al160011	Hs.146161 Hs.272068	hypothetical protein MGC2408 ESTs	2.02 1.29	1,41
	441020	AA401369	Hs.190721	FSTs	142.99	17.00
85	441031	Al110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

	W	O 02/086	443		4.13	3.50
	441128 441290	AA570256 W27501	Hs.89605	ESTs, Weakly similar to T23273 hypotheti cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	8E614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	130.23	43.00
_	441377	BE218239	Hs.202656	ESTs	22.03	1.00
5	441390	Al692560	Hs.131175	ESTs	3.65	7.70
	441497 441525	R51064 AW241867	Hs.23172 Hs.127728	ESTs ESTs	1.00 1.53	1.00 1.42
	441553	AA281219	Hs.121296	ESTs	1.89	1.57
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	1.47	2.11
10	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	218.22	363.00 2.05
	441636	AA081846	Hs.7921	Homo saplens mRNA; cDNA DKFZp566E183 (Ir	2.31 1.30	1.49
	441737 441790	X79449 AA401369	Hs.7957 Hs.190721	adenosine deaminase, RNA-specific ESTs	44.15	17.00
	441801	AW242799	Hs.86366	ESTs	1.00	1.00
15	441919	AJ553802	Hs.128121	ESTs	1.00	122.00
	441937	R41782	Hs.22279	ESTs	0.86 1.48	1.37 1.39
	441954 442025	A1744935 AW887434	Hs.8047 Hs.11810	Fanconi anemia, complementation group G CDA11 protein	1.00	46.00
	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	9.92	45.00
20	442072	AJ740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	25.05	77.00
	442108	AW452649	Hs.166314	ESTs	3.61	3.14
	442117	AW664964	Hs.128899	ESTS	3.00 1.00	5.49 1.00
	442137 442159	AA977235 AW163390	Hs.128830 Hs.278554	ESTs, Weakly similar to Z192_HUMAN ZINC heterochromatin-like protein 1	1.92	1.66
25	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	181.59 10.59	76.00 144.00
	442530 442547	A1580830 AA306997	Hs.176508 Hs.217484	Homo saplens cDNA FLJ14712 fis, clone NT ESTs, Wealdy similar to ALU1_HUMAN ALU S	109.23	98,00
30	442556	AL137761	Hs.8379	Homo saplens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
20	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	A)015831	Hs.23210	ESTS	1.00	19.00 5.00
	442717 442875	R68362 BE623003	Hs.180591 Hs.23625	ESTs, Wealty similar to T23976 hypotheti Homo sapiens clone TCCCTA00142 mRNA sequ	1.00 22.85	50.00
35	442875 442914	AW188551	Hs.99519	hypothetical protein FLJ14007	25.33	82.00
55	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	3.18	4.41
	442942	AW167087	Hs.131562	ESTs	8.45 1.00	64.00 27.00
	443068 443204	AI188710	Hs.29643	ESTs Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
40	443211	AW205878 Al128388	Hs.143655	ESTs	12.42	2.00
-10	443247	BE614387	Hs.333893	c-Myc target JPO1	128.84	96.00
	443324	R44013	Hs.164225	ESTs	0.02	4.59 47.00
	443383 443400	AJ792453 R28424	Hs.166507 Hs.250648	ESTs ESTs	1.00 18.52	61.00
45	443400 443426	AF098158	Hs.250548 Hs.9329	chromosome 20 open reading frame 1	4.02	1.75
73	443572	AA025610	Hs.9605	cleavage and polyadroviation specific fa	2.98	2.57
	443575	AI078022	Hs.269636	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00 18.00
	443614	AV655386	Hs.7645 Hs.9654	fibrinogen, B beta polypeptide similar to pregnancy-associated plasma p	1.00 1.00	39.00
50	443633 443648	AL031290 Al085377	Hs.143610	ESTs	39.81	70.00
50	443715	AI583187	Hs.9700	cyclin E1	48.74	7.00
	443723	Al144442	Hs.157144	syntaxin 6	1.29	1.30 1.61
	443802	AW504924	Hs.9805 Hs.9914	KİAA1291 protein follistatin	1.75 1.35	1.13
55	443859 443892	NM_013409 AA401369	Hs.190721	ESTs	1.00	17.00
33	443947	W24187	110.100721	ab:zb47f09.r1 Soares fetal lung_NbHL19W	1.33	1.64
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87 1.92
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14 ESTs	1.47 1.00	77.00
60	444009 444017	Al380792 U04840	Hs.135104 Hs.214	neuro-oncological ventral antigen 1	1.00	1.00
00	444127	N63620	Hs.13281	ESTs	1.00	29.00
	444129	AW294292	Hs.256212	ESTs	1.00 0.60	1.00 7.80
	444279 444371	U62432 BE540274	Hs.89605 Hs.239	cholinergic receptor, nicofinic, alpha p forkhead box M1	2.91	1.14
65	444378		Hs.12569	ESTs	1.00	1.00
05	444381	BE387335	Hs.283713	ESTs, Weakly similar to \$64054 hypotheti	469.00	656.00
	444461	R53734	Hs.25978	ESTs, Wealdy similar to 2109260A B cell	12.88 24.91	105.00 90.00
	444471 444489	AB020684 Al151010	Hs.11217 Hs.157774	KIAA0877 protein ESTs	1.00	111.00
70	4444819		Hs.8172	ESTs, Moderately similar to A46010 X-lin	1.00	70.00
,,	444665		Hs.47783	B aggressive lymphoma gene	30.56	139.00
	444707		Hs.41690	desmocollin 3	1.00 77.02	1.00 90.00
	444735		Hs.243122 Hs.11950	hypothetical protein FLJ13057 similar to GPI-anchored metastasis-associated prote	1.57	1.31
75	444781 444783	NM_014400 AK001468	Hs. 11950 Hs. 62180	anilin (Drosophila Scraps homolog), act	77.55	2.00
,,	445236	AK001676	Hs.12457	hypothetical protein FLJ 10814	1.00	27.00
	445258	Al635931	Hs.147613	ESTS	1,00	73.00 50.00
	445413	AA151342	Hs.12677	CGI-147 protein	28.14 1.81	2.62
80	445417 445443		Hs.12680 Hs.322971	Homo saplens cDNA FLJ10196 fis, clone HE ESTs	1,00	1.00
00	445462		Hs.288649	hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	Hs.12830	hypothetical protein	1.87	70.08
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.71 1.52	2.72 1.34
85	445580 445654	AF167572 X91247	Hs.12912 Hs.13046	skb1 (S. pombe) homolog thioredoxin reductase 1	1.51	1.52
65	44000	. A91247	ns. 13090	and output tourneyou		

		O 02/086	443			
	445669	A1570830	Hs.174870	ESTs FSTs	10.95 1.00	11.45 1.00
	445818 445873	BE045321 AA250970	Hs.136017 Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	49.42	54.00
_	445885	AI734009	Hs.127699	KIAA1603 protein	1.00	132.00
5	445898	AF070623	Hs. 13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00 36.00
	445903 445932	AI347487 BE046441	Hs.132781 Hs.333555	class I cytokine receptor Homo sapiens clone 24859 mRNA sequence	1.00 2.41	2.88
	445982	8E410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
•••	446078	Al339982	Hs.156061	ESTs	1.00	42.00
10	446102 446157	AW168067 BE270828	Hs.317694 Hs.131740	ESTs Homo sapiens cDNA: FLJ22562 fis, clone H	1.00 1.70	1.00 1.53
	446269	AW263155	Hs.14559	hypothelical protein FLJ10540	73.01	48.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
15	448293	Al420213	Hs.149722	ESTs	1.00	2.00
15	446423 446428	AW139655 AW082270	Hs.150120 Hs.12496	ESTs ESTs, Weakly similar to ALU4_HUMAN ALU S	1.10 0.53	4.19 3.26
	446432	Al377320	Hs.150058	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
20	448574	AJ310135	Hs.335933 Hs.313	ESTs secreted phosphoprotein 1 (asteopontin,	3.89 32.03	72.00 20.23
20	446619 446636	AU076643 AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4,19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	8E091926	Hs.16244	mitotic spinule coiled-coil related prot	110.28	28.00
25	446849 446856	AU076617 AI814373	Hs.16251 Hs.164175	cleavage and polyadenylation specific fa ESTs	3.26 6.38	2.94 11.30
23	446872	X97058	Hs. 16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	Al811807	Hs.108646	Homo saplens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921 446989	AB012113	Hs.16530 Hs.16740	small inducible cytokine subfamily A (Cy hypothetical protein FL/11036	1.67 2.82	3.90 3.12
30	447022	AK001898 ,AW291223	Hs.157573	ESTs Profess PLAT 1030	1.00	170.00
50	447033	Al357412	Hs,157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs	47.24	24.00 17.88
	447081	Y13896 NM 004585	Hs.17287 Hs.17466	potassium inwardly-rectifying channel, s retinoic acid receptor responder (tazaro	0.12 0.97	1.48
35	447131 447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
-	447153	AA805202	Hs.315562	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo saplens cig5 mRNA, partial sequence	1.00	67.00 50.00
	447178 447250	AW594641 AM78909	Hs.192417 Hs.17883	ESTs protein phosphatase 1G (formerly 2C), ma	3.42 1.60	1.52
40	447289	AW247017	Hs.36978	melanoma antigen, family A. 3	1.00	1.00
	447342	Al199268	Hs.19322	Homo saplens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343 447350	AA258641 AI375572	Hs.236894 Hs.172634	ESTs, Highly similar to S02392 alpha-2-m ESTs	146.62 1.00	51.00 12.00
	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
45	447415	AW937335	Hs.28149	ESTs, Wealdy similar to KF38_HUMAN KINES	0.91	1.13
	447425	AI963747 1146258	Hs.18573 Hs.339665	acylphosphatase 1, erythrocyte (common) ESTs	1.00 59.89	35.00 49.00
	447519 447532	AK000614	Hs.18791	hypothe6cal protein FLJ20607	1.23	1.63
	447534	AA401369	Hs. 190721	ESTs	1.00	17.00
50	447636	Y10043		high-mobility group (nonhistone chromoso Target CAT	1.41 1.00	1.11 39.00
	447688 447733	N87079 AF157482	Hs.19236 Hs.19400	MAD2 (mitolic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
	447802	AW593432	Hs.161455	ESTs	0.73	2.34 116.00
55	447850 447924	AB018298 Al817226	Hs.19822 Hs.313413	SEC24 (S. cerevisiae) related gene famil ESTs, Weakly similar to T23110 hypotheti	86.45 1.00	1.00
	447973	AB011169	Hs.20141	similar to S. cerevistae SSM4	3.50	4.27
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.00
60	448105	Al538613	Hs.298241	Transmembrane protesse, serine 3	1.15 15.84	2.24 1.00
60	448243 448278	AW369771 WQ7369	Hs.52620 Hs.11782	integrin, beta 8 ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo saplens cDNA FLJ14162 fis, clone NT	2.42 1.44	2.17 1.08
65	448357 448390	BE274396 AL035414	Hs.108923 Hs.21068	RAB38, member RAS oncogene family hypothetical protein	1.00	43.00
05	448469	AU504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797 ESTs	3.29 1.00	46.00 21.00
70	448672 448733	AI955511 NM 005629	Hs.225106 Hs.187958	solute carrier family 6 (neurotransmitte	1,82	1.08
70	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
	448757	. Al366784	Hs.48820	TATA box binding protein (TBP)-associate	23,53	20.00
	448775 448826	AB025237 Al580252	Hs.388 Hs.293246	nudix (nucleoside diphosphate linked mol ESTs, Wealdy similar to putative p150 [H	2.34 74.07	1.97 62.67
75	448830	AL031658	Hs.22181	hypothetical protein dJ310013.3	1.37	1.31
	448844	AJ581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993 449003	Al471630 X76342	Hs.389	KIAA0144 gene product alcohol dehydrogenase 7 (class IV), mu o	1.63 1.00	1.49 1.00
80	449003	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc FSTs	27.13 8.33	90.00 44.00
	449053 449054	A/625777 AF 148848	Hs.344766 Hs.22934	ESTS myoneurin	8.33 73.85	104.00
85	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

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	449167	T05095	Hs.19597	KIAA1694 protein	1.61 2.36	2.36 1.56	
	449207 449228	AL044222 AJ403107	Hs.23255 Hs.148590	nucleoportin 155kD protein related with psoriasis	1.15	1.15	
_	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00	
5	449305	A1638293		qb:tt09b07.x1 NCI_CGAP_GC6 Homo sapiens	17.28	45.00	
	449318 449448	AW236021 060730	Hs.78531 Hs.57471	Homo saplens, Similar to RIKEN cDNA 5730 ESTs	26.39 1.00	35.00 1.00	
	449467	AW205006	Hs.197042	ESTs	1.00	1.00	
10	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	56.80	216.86	
10	449722	BE280074 H06350	Hs.23960 Hs.135056	cyclin B1 Human DNA sequence from clone RP5-850E9	150.03 2,16	1.00 2.85	
	449976 450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	1.17	1.45	
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38	
15	450101 450149	AV649989 AW969781	Hs.24385 Hs.132863	Human hbc647 mRNA sequence	1.00	69.00 1.00	
13	450193	AW969781 AI916071	Hs.15607	Zic family member 2 (odd-paired Drosophi Homo sapiens Fanconi anemia complementat	29.85	34.00	
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00	
	450372	BE218107	Hs.202436	ESTs	1.00	1.00	
20	450375 450447	AA009647 AF212223	Hs.8850 Hs.25010	a disintegrin and metalloproteinase doma hypothetical protein P15-2	51.26 123.20	93.00 181.00	
20	450568	AL050078	Hs.25159	Homo saplens cDNA FLJ10784 fis, clone NT	1.00	19.00	
	450589	AJ701505	Hs.202526	ESTs	1.00	23.00	
	450684 450701	AA872605 H39960	Hs.25333 Hs.288467	Interteukin 1 receptor, type il Homo saniens cDNA FLJ12280 fis, ctone MA	1.00 1.89	100.00 1.55	
25	450705	U90304	Hs.25351	troquois homeobox protein 2A (IRX-2A) (1.00	45.00	
	450832	AA401369	Hs.190721	ESTs	25.17	17.00	
	450937	R49131	Hs.26267 Hs.25740	ATP-dependant interferon response protei	90.92	90.00 1.70	
	450983 451105	AA305384 AI761324	HS.25/40	ERO1 (S. cerevisiae)-like gb:wl60b11.x1 NCI_CGAP_Co16 Home sapiens	15.02	124.00	
30	451110	A1955040	Hs.285398	ESTs, Weakly similar to transformation-r	1.00	143.00	
	451253	H48299	Hs.26126	claudin 10	3.02 1.00	2.29 1.00	
	451291 451320	R39288 AW498974	Hs.6702	ESTs diacytglycerol kinase, zeta (104kD)	2.92	18.00	
	451380	H09280	Hs.13234	ESTs	6.90	6.67	
35	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	35.75	72.00	
	451437 451462	H24143 AK000367	Hs.31945 Hs.26434	hypothetical protein FLJ11071 hypothetical protein FLJ20360	1.00 1.83	69.00 2.10	
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07	
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33	
40	451592 451635	AI805416 AA018899	Hs.213897 Hs.127179	ESTs	1.00 1.52	1.00 1.92	
	451743	AA401369	Hs.190721	cryptic gene ESTs	4.95	17.00	
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00	
45	451807	W52854	11- 440500	hypothetical protein FLJ23293 slmilar to	1.55 1.81	35.00 2.53	
43	451871 451952	AJ821005 AL120173	Hs.118599 He 301663	ESTs ESTs	1.00	22.00	
	452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26	
	452046	AB018345	Hs.27657	KIAA0802 protein	56.59 1.67	19.00 4.09	
50	452194 452206	AI694413 AW340281	Hs.332649 Hs.33074	offactory receptor, family 2, subfamily Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00	
50	452240	AA401369	Hs.190721	ESTs	13.42	17.00	
	452256	AK000933	Hs.28661	Homo saplens cDNA FLJ10071 fis, clone HE	39.03 153.01	94.00 340.00	
	452281 452291	T93500 AF015592	Hs.28792 Hs.28853	Homo sapiens cDNA FLJ11041 fis, clone PL CDC7 (cell division cycle 7, 6, cerevisi	1.95	23.00	
55	452295	9E379936	Hs.28866	programmed cell death 10	42.33	61.00	
	452304	AA025386	Hs.61311	ESTs, Weakly similar to \$10590 cysteins	1.17	2.14 13.00	
	452340 452349	NM_002202 AB028944	Hs.505 Hs.29189	ISL1 transcription factor, LIM/homeodoma ATPase, Class VI, type 11A	1.00 1.09	1.42	
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00	
60	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	32.00	
	452410 452461	AL133619 N78223	Hs.108106	Homo saplens mRNA; cDNA DKFZp434E2321 (f transcription factor	1.26 24.47	1.99 36.00	
	452571	W31518	Hs.34665	ESTs	54.61	102.00	
	452613	AA461599	Hs.23459	ESTs	1.39	1.32	
65	452699 452705	AW295390 H49805	Hs.213062 Hs.246005	ESTs ESTs	1.00 1.00	26.00 1.00	
	452747	AF160477	Hs.61460	Ig superfamily receptor LNIR	112.87	1.29 .	
	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00	
70	452795 452823	AW392555 AR012124	Hs.18878 Hs.30696	hypothetical protein FLJ21620	1.00 7.91	1.00 75.00	
70	452823 452833	BE559681	Hs.30736	transcription factor-like 5 (basic helix KIAA0124 protein	3.16	1.92	
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	174.35	1.00	
	452862	AA401369	Hs.190721	ESTs	98.26	17.00	
75	452865 452934	AW173720 AA581322	Hs.345805 Hs.4213	ESTs, Weakly similar to A47582 B-ceil gr hypothetical protein MGC16207	1.55 1.73	1.00 1.19	
,,	452946	X95425	Hs.31092	EphA5	1.00	1.00	
	452976	R44214	Hs.101189	ESTs	1.58	1.98	
	453028 453095	AB006532	Hs.31442 Hs.252756	RecQ protein-like 4	1.80 0.77	1.60 1.50	
80	453095 453102	AW295660 NM_007197	Hs.252756 Hs.31664	ESTs frizzled (Drosophila) homolog 10	1.00	1.00	
-	453103	AI301052	Hs.153444	ESTs	1.00	1.00	
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20 83.00	
	453153 453160	N53893 AI263307	Hs.24360 Hs.239884	ESTs H2B histone family, member L	1.00 1.00	30.00	
85	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00	

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		AL133161	Hs.32360	hypothetical protein FLJ10667	1.69	1.93		
	453240	AI969564	Hs.166254	hypothetical protein DKFZp566I133	1.00	1.00		
	453317	NM_002277	Hs.41696	keratin, hair, acidic,1	1.19	1.27		
5	453323	AF034102 AI240665	Hs.32951 Hs.8850	solute carrier family 29 (nucleoside tra ESTs	4.90 199.42	4.11 340.00		
,	453331 453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00		
	453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00		
	453439	AI572438	Hs.32976	guarrine nucleotide binding protein 4	3.44	5.17		
10	453459	BE047032	Hs.257789	ESTs	2.84	5.58	4.58	90.00
10	453563 453633	AW608906.co AA357001	mp Hs.34045	Hs.181163 hypothelical protein FLJ20764	nypotneucai p 1.74	rotein MGC5629 1.60	4.30	90.00
	453775	NM_002918	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830	AA534296	Hs.20953	ESTs	24,92	25.00		
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00		
15	453867 453883	AI929383 AI638516	Hs.33032 Hs.347524	hypothetical protein DKFZp434N185 cofactor required for Sp1 transcriptions	1.00 1.97	39.00 1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00		
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALUS_HUMAN ALU S	20.41	16.00		
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
20	453941	U39617 Al961486	Hs.36820 Hs.12744	Bloom syndrome ESTs	29.75 1.00	19.00 1.00		
	453964 453968	AA847843	Hs.62711	Horno sapiens, clone IMAGE:3351295, mRNA	2.06	1.81		
	453976	BE463830	Hs.163714	ESTs	3.02	131.00		
~ ~	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
25	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23 30.63	1.02 171.00		
	454042 454059	T19228 NM_003154	Hs.172572 Hs.37048	hypothelical protein FLJ20093 statherin	1.00	1,00		
	454066	X00356	Hs.37058	exicitanin/exicitanin-related potypeptid	1.01	1.45		
	454098	W27953	Hs.292911	ESTs, Highly similar to \$60712 band-6-pr	1.26	1.11		
30	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
	454417	Al244459 AW819152	Hs.110826 Hs.154320	trinucleotide repeat containing 9 DKFZP566O1646 protein	4.30 1.00	7.82 1.00		
	454439 455175	AW993247	PIS. 15452U	gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
	455601	Al368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00		
35	456237	AA203682		gb:zx52e07.r1 Soares_fetal_fiver_spleen_	1.00	1.00		
	456321	NM_001327	Hs.87225	cancer/testis antigen	1.14	1.10 48.00		
	456475 456508	NM_000144 AA502764	Hs.95998 Hs.123469	Friedreich ataxia ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor oseudo	2.12	1.80		
40	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	1.15	1.94		
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00 16.42	1.00 84.00		
	456990 457200	NM_004504 U33749	Hs.171545 Hs.197764	HIV-1 Rev binding protein thyroid transcription factor 1	0.57	1.76		
	457234	AW968360	Hs.14355	Homo saplens cDNA FLJ13207 fis, clone NT	2.71	4.15		
45	457465	AW301344	Hs.122908	DNA replication factor	46.37	47.00		
	457489	A)693815	Hs.127179	cryptic gene	1.12 1.55	1.35 2.51		
	457646 457733	AA725650 AW974812	Hs.112948 Hs.291971	ESTs ESTs	1.00	55.00		
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	4.36	3.18		
50	458092	BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098	BE550224	II. WASS	metalioihionein 1E (functional) U2 small nuclear ribonucleoprotein auxil	1.00 2.06	22.00 1.88		
	458207 458242	T28472 BE299588	Hs.7655 Hs.28465	Homo saplens cDNA: FLJ21869 fis, clone H	1.00	1.00		
	458247	R14439	Hs.209194	ESTs	7.00	9.85		
55	458679	AW975460	Hs.142913	ESTs	1.00	3.00		
	458778	AW451034	Hs.326525	arylsuffatase D	1.31 1.98	2.01 1.71		
	458933 459352	Al638429 AW810383	Hs.24763 Hs.206828	RAN binding protein 1 ESTs	12.60	63.00		
	459670	F01020	Hs.172004	film	1.00	1.00		
60	459702	A1204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		
	TABLE 9	no.		•				
	INDLE	10						
65	Pkey:	Unique E	os probeset ide	entifier number				
	CAT nur Accessio	nber: Gene clus	iter number accession nun	-t				
	ACCBSSN	on: Genoank	accession nun	nours				
	Pkey	CAT Numb	er Acces	sion				
70	407746	10125_1	AK001	1962 R69415 BE464605 AA418699 AA053293 AA1490	75 AA058396 AW33	8226 AW272659 A	4454607 AI13953	5 AW469852 AI275461
			AW27	1982 AA730033 AA576507 AA981217 AA782067 AI98 51 T27343 AA306950 AA360989 R58778	5851 AA805864 AA	N05598 AW4698571	K69546 AA96827	9 AWUU1047 NG3320
	408070	1036688_1	D8250	8852 BE350895				
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75	409522	113735_1	AA075	5382 AA075431				
	409866	1156522_1	AW50	2152 H41202 H29772				
	410032 411089	1170435_1 123172_1	BE06	6985 BE065944 BE066008 BE066083 BE066093 6454 AA713730 AA091294 AA584921 NB6077 AW8367	R1 AA601031 AA57	9876 &&551106 &&	633188 AW9055	77 A1955808 A1679386
	411089	123112_1	A1070	DDE AAELAZEA AAAEAERO AIDROSSO AAEGEROO AAEGE	351 AA586369 AA66	na appropria a arpro	ARRESSON AASES 129	17 AA5651B8
80	411152	1234028_1	DEGRE	0400 AW036042 AW877466 AW819782 AW035706 AW	/R35546 AW/936042	RE069121 AW8356	625 AVV877536 AV	N935885 BED69202
			A14/82	20010 AM/035037 RE160180 AW/9350AS RE069101 RFI	369125 AW877527 F	RE160316 RE16039	ir aw935794 aw	835701 AW935784
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			1 234V AWOS	3918 AA927051 AA889823 BE003094 AW390155 AW	360805 AW360823 A	W360810 AA4254	72 A1694282 AL04	14114 AI684577 AI809865
			,,,,,,,					

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AA478773 A160445 A1674630 N69088 AW665529 IM9278 A1129239 AA57890 A1621264 AW297152 A268215 AA60787 A288170 A017982

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	412811	132943 1	AI963541 AI469807 AI969353 BE552356 NG6509 AA736741 AA382555 AW075811 AW292026 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148
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	413690 414883	1383256_1 15024_1	BE157489 BE157560 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245
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10			AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150
10			AA872039 W72395 T99530 A1422691 H98460 N31428 BE255916 H03265 A1857676 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 A1865147 A1423153 AW262230 AA584410 AA583187 AW024595 AW069734 A1828996 AA282997 A8876046
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15			AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI33680 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850
13			A1994230 A1278887 AA982596 A192600 W80435 AA001979 R97424 A1129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785
			Al494211 AW059601 AW886710 R92790 N59755 Al361128 AW589407 H47725 H97634 H48076 H48450 T99631 AW300758 H03431 R76769
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	417324	166714 1	AW265494 AA455904 AA195677 AW265432 AW991605 AA456370
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			100307 100401 133391 172301 17239 10037 1 100901 1712 172021 104730 174031 172031 100000 17205 17225 17225 10227 10224 1
30			T73203 T70498 T61409 T68925 NM_000508 M54982 T88301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719
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45			AA344583 T60362 H56121 T95711 T72603 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835
			T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068
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			BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 Al001051 AW050700 AW750216 AA614539
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	423034	224122_1	AL119930 AA320696 AW752565
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	424999	273896_1	AW95312U K96325 AA349662 AI493134 AI498691 AW771508 AI498457 AI768408 AI783624 AI383985 AI580267 D79813 AA393768
	426991	27415_1	AK001636 AA191092 AW510354 Al554256 AL353968 AA134266
60	427260	276598_1	AA663848 AA400100 AA401424
	428023	28589_2	Ald38843 Aa161338 BE268213 AA425597 N87306 AA092969 BE666038 AA247451 N47392 A1928802 AW182584 AW027872 A1819831 A1936994 W56258 A1653448 A1276611 A1283557 A1824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 A1038904 A1292064
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65			AA652043 Al203503 AA583959 W35283 Al129926 Z41844 AW020925 AW575848 Al684603 AA493297 Al140689 Al277175 AA425444
05	429220	301384_1	AI932767 W02632 BE396786 R37261 AW207206 AW341473 AA448195 AI951341
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			BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720
	434414	38585_1	AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 AJ798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
80	707117	·····	AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
			T61139 AA149776 AA699829 AW879188 AW813567 AW813538 Al267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705
			AA157730 AA157715 AA0S3524 AW849581 AW849580 C05254 AW882836 T92637 AW812621 AA208583 AA209204 BE156909 AA226824 A4829309 AW991957 N56951 AA527374 H66215 AA045564 A4694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662
			AIB29309 AW891957 R00951 AA527374 H00215 AA045564 AID94266 H00008 AA149726 AW195620 BEU01333 BEU73429 AW817662 AW817705 AW817703 AW817659 BE081531 H59570
85	436608	42361_3	AA628980 Al126603 BES04035

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5	438091	44964_1	AA AA AA AA	NETISSES TESSES ALDES 190 GET L'AZTO, ANDISCON INIUST I WOLDES RIGITORIA DE ACCESSES ANDISCON ACCESATA ANDISCON
	******	******	Al	985913 BE174196 AA029094 AW592159 T55581 N79072 AE11201 AA910812 ALZZI/13 AW149300 AL750412 MUHS/13 R73750 R75050
	439000 439285	467716_1 47065_1	A3	133916 N79113 AFD86101 N76721 AW950828 AA364013 AW955684 AJ346341 AJ867454 N54784 AJ655270 AJ421279 AW014882
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	441128	51021_2	Δ.	ASTRICES AWO 14761 AASTRICE ALIVARED ALIVARED ALIVARED AASTRICE AASTRICE AASTRICE AASTRICE AWO 14761 AASTRICE AASTRICE ALIVARED AASTRICE A
	443068	558874_1	Al	359627 AIO05068 AI356557 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923 188710 AIO32142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390
15	443947 447636	586160_1 7301_1	A. A.	74197 WARI 94 R.17739 WORD HAIL, DOSEN JACKS JOSEPH JACKS JOSEPH JACKS
20			A	A096002 NB3992
25	448993	79225_1	A A	THE SECTION AND STATE AND
25	449305 451105	804424_1 859083_1		17C1 224 AWREDOOM AWREDOOM
	451320`	86576_1	A	WT1807.2 NGS 1962 T15734 A4224195 A1701458 W20198 F25305 AA980570 N90552 AW071907 A1571352 A1376562 T03517 R88265 11/10/08 A4224385 A1884316 A4354686 T35652 A14071 9 A1720211 T03490 A1672637 T15415 AW205836 AA530384 T03515 T33230 A071731 A443207 373622 A1225255 T3351 T337365 A419966 D55612
30	451807	8865_1		V52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 W450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380331 AA886045 AA774409 BE003229 Z41756
	452410	9163_1	A	l 133619 Aa468118 Aa383064 Alfa47 T09430 Alf73768 Aa524895 Albut346 Alsuucza awabbat arcootoz austa 27 Ab60240 Ab02400 Aa905453 Al204595 Aw166541 Aa157456 Aa156269 Aa383652 Aa431072 Aw592707 Al43541 Ab730440 Al215594 Aa622747 Ab02400 Aa905453 Al204595 Aw166541 Aa157456 Aa156269 Aa383652 Aa431072 Aw592707 Al43541 Ab730440 Al15754 Al20081
35				(2019) NISSUST ARBUTE 2 NINST 327 NINST 327 NINST 327 NINSBESS ARBUTE 2 NINSBESS ARB
	454241	1067807_1	8	E144666 BE184942 AW238414 BE184946
	455175 456237	1257335_1 168730_1		W993247 AW851464 从203682 R11958
40	458098	47395_1	A	IEGESZEA AMAZZI 19 MAGAZ AMBRISKY TAZQAS 9 ERISKOÐ WOTFTT AWFORÐS AZZSFTAI AMAZZIT 19 EKSÚSSÁ HIRI 151 WTYZZA AFÐRÓSSÁ MAKÍSÍÐ WTÁSÍ 19 MAGAZ AMBRISKA MENDE SERTÍ ISSA FOZASÓ A MYLÁSÐZ AMAZDÓ ALÍSSÐÓS AWRÓSTA ÞÁZTSÁ 19 EKÐRÓS AZ UZTÍ 154 AZZZZBÁ AHZZSÍT AZÍTONÁ AMZITZT ALÍBSZEA AGASÐÍ 64 BELÁSÐÍ A AWISTÖRS AISÐANGOS BESÚSSÁH AMASÐYÍ 8 BELZIZHÓT EKRÍZNÍ BEZÍ 1821 ERISKTÍFÁ AMSÐÓS BEÐRÓSIA JÁTRÍ DÓ EZZTÖRÍ
45				
	TABLE 9	С		
50	Pkey: Ref: Strand:	Sequence	source. of huma	rresponding to an Eos probesed: The 7 digit numbers in this colcium are Genhank Identifier (GI) numbers. "Dunham I. et el." refers to the publication entitled "The DNA nethromosome 22" Dunham I. et al., Nature (1999) 402-489-495. And from Which accurs were producted.
	NL posit		nucleotid	e positions of predicted exons.
	Pkey	Ref	Strand	Nt position 1439-1615
55	400512 400517	9796593 9796686	Minus Minus	4999-50346
	400560 400664	9843598 8118496	Plus Plus	94182-94323,97056-97243,101095-101236,102824-103005 13558-13721,13942-14090,14554-14679
	400665	8118496	Plus	16879-17023
60	400566 400749	8118496 7331445	Plus Minus	17982-18115,20297-20456 9162-9293
	400763	8131616	Minus	35537-35784
	401027 401093	7230983 8516137	Minus Minus	70407-70554,71060-71160 22335-23166
65	401203	9743387	Minus	172961-173056,173868-173928
	401212 401411	9858408 7799787	Plus Minus	87839-88028 144144-144329
	401435	8217934	Minus	54508-55233
70	401464	6682291 6715702	Minus	170688-170834 96484-96681
70	401714 401747	9789672 9929699	Minus Plus	30040-90001 118596-118816, 119119-119244, 119609-119761, 120422-120990, 130161-130381, 130466-130593, 131097-131258, 131866- 131932, 132461-132575, 133590-134011 83126-83250, 85200-85404, 8719-965287
	401760 401780	7249190	Minus	28397-28617.28920-29045.29135-29298.29411-29567.29705-29787,30224-30573
75	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814 165776-165996,166189-166314,166408-166569,167112-167268,167387-167459,168634-168942
	401785 401797	7249190 6730720	Minus Plus	6973-7118
	401961	4581193	Minus	124054-124209
80	401985 401994	2580474 4153858	Ptus Minus	61542-61750 42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
60	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402260	3399665	Minus	113765-113910,115653-115765,116808-116940
	402265 402297	3287673 6598824	Plus Plus	21059-21168 35279-35405,35573-35659
85	402297 402408	9798239	Minus	35279-3540,35573-3555

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	w	O 02/08	6443	
	402420	9796339	Pius	129750-129919
	402674	8077108	Minus	39290-39502
	402802	3287156	Minus	53242-53432
	402994	2996643	Minus	4727-4969
5	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403306	8099945	Plus	127100-127251
	403329	8516120	Phis	96450-96598
	403381	9438267	Minus	26009-26178
	403478	9958258	Ptus	116458-116564
10	403485	9966528	Plus	2888-3001.3198-3532.3655-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Mirais	225757-225939
	404076	9931752	Minus	3848-3967
15	404101	8076925	Minus	125742-125997
	404140	9843520	Phus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
	404210	5006246	Plus	169926-170121
20	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
	404440	7528051	Plus	80430-81581
25	404721	9856648	Minus	173763-174294
	404784	4826439	Plus	101619-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
	404927	7342002	Plus	68690-69563
30	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40874,42351-42450
-	405449	7622497	Plus	42236-42570
	405568	6006906	Plus	35912-36065
	405572	3800891	Plus	85230-85938
	405646	4914350	Plus	741-969
35	405876	4557087	Plus	73195-73917
	405770	2735037	Plus	61057-82075
	405932	7767812	Minus	123525-123713
	405137	9166422	Minus	30487-31058
	406360	9256107	Minus	7513-7673
40	406399	9256288	Minus	63448-63554
	406467	9795551	Plus	182212-182958

TABLE 104: Potential Therapouts, Diagnostic and Prognestic largets for Thorapy of Lung Carner and Non-malignant Lung Disease
Table 2A shows about 370 genes up-regulated in non-malignant lung disease relative to being lumors and normal body disease and/or down-regulated in lung furnors relative to
normal lung and non-malignant lung disease. These genes were selected from about 2500 probased to the libe Daily/Smithet NHOS Genicolity array. 45

Table 168 show the accession numbers for floors Play's ladding Uniquenel/Or for lable 169. For each probased we have listed the gene duster number from which the olipproadecides were designed. Come dusters were compiled using sequences derived from Genbank ESTs and mRMAs. These sequences were clustered based on sequences serially every Castering and Alignment Tools (Doublet Vest, Calismic Cefformia). The Genbank excession numbers for sequences comprising each duster are issed in the "Accession Column." 50

Table 10C show the genomic positioning for those Prey's lacking Unigene IU's and accession numbers in table 10A. For each predicted exen, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

55

60	Pikey: ; ExAcon: UnigenelD: Unigene Title: R1:	Exemp Unigen Unigen Averag	lar Accession of the number to gene title to of lung tumo	identifier number number, Genbank accession number ire (Including squamous cell carcinomas, adenoca ng samples nami tung diseaso samples (Including bronchills,			
65	Pikey Ext	•	UnigenelD	Unigene Title	Rf	R2	
05	404394		Gingeriaio	ENSPRORMON THE PROTEIN.	0.79	3.10	
	404916			Target Exon	1.00	159.00	
	405257			Target Exon	1.00	422.00	
		5079	Hs.155376	hemoglobin, beta	0.47	2.33	
70		740984	Hs.62699	ESTs	1.00	123.00	
		36323	Hs.31141	Homo sagiens mRNA for KIAA1568 protein,	1,00	230.00	
		376836	Hs.76728	ESTs	1.00	128.00	
		51152	Hs.63668	tof-like receptor 2	39.65	149.00	
		102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00	•
75		326	Hs.167793	ESTs	1.14	13.14	
		35960	Hs.73828	T-ceil acute lymphocytic laukemia 1	0.37	2.27	
		998	Hs.285243	trypothetical protein FLJ22029	1.00	173.00	
		140178	Hs.142003	ESTs	0.10	11.90	
	414154 AW	205314	Hs.323060	ESTs	0.62	2.09	
80	414214 D49	958	Hs.75819	glycoprotein MSA	0.03	4.55	
	414998 NM	002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97	
	415122 D60	0708	Hs.22245	ESTs	0.07	8.97	
	415765 NM	005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65	
	415775 HO	7747	Hs.29792	ESTs, Weakly similar to (38022 hypotheti	0.29	2.64	
85	415910 U20	350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00	

	W	O 02/086 AB15601	443	and the second second	45.00	237.00
	416319 416402	AI815601 NM_000715	Hs.79197 Hs.1012	CO83 antigen (activated B lymphocytes, i complement component 4-binding protein,	15.32 0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type 8	0.01	3.90
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
5	417511	AL049176	Hs.82223	chardin-like	1.00	179,00 6.00
	418489 418726	U76421 BE241812	Hs.85302 Hs.87860	adenosine dearninase, RNA-specific, B1 (h protein tyrosine phosphatase, non-recept	0.02 1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
10	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74 6.90
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03 1.48	5.13
	419235 419407	AW470411 AW410377	Hs.288433 Hs.41502	neurotrimin hypothetical protein FLJ21276	37.55	336.00
	420556	AA278300	Hs.124292	Homo saplens cDNA: FLJ23123 fis, clone L	0.80	3.65
15	420656	AA279098	Hs.187636	ESTs	1.65	8.07
	420729	AW964897	Hs.290825	ESTs	2.99 0.46	25.82 1.95
	421177 422060	AW070211 R20893	Hs.102415 Hs.325823	Homo saplans mRNA; cDNA DKFZp586N0121 (f ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
	422426	W79117	Hs.58559	ESTs	0.03	7.44
20	422652	AW967969	Hs. 118958	syntaxin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor 1	0.01 0.75	3.16 141.75
	424433 424585	H04607 AA464840	Hs.9218 Hs.131987	ESTs ESTs	1.00	167.00
	424711	NM 005795	Hs.152175	calcitonin receptor-like	0.43	3.01
25	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
	425023	AW956889	Hs. 154210	endothelial differentiation, sphingolipi	0.14 1.00	3.35 94.00
	425654 425998	AJ006276 AU076629	Hs.159003 Hs.165950	transient receptor potential channel 6 fibroblast growth factor receptor 4	0.68	1.42
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
30	426753	T89832	Hs. 170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00 2.20
	427983 428467	M17706 AK002121	Hs.2233 Hs.184465	colony stimulating factor 3 (granufocyte hypothetical protein FLJ11259	0.75 0.76	2.25
	428927	AA441837	Hs.90250	ESTs	0.01	3.62
35	429498	AA453800	Hs.192793	ESTs	1.00	138.00
	430468	NM_004673	Hs.241519	anglopoietin-like 1	1.00	132.00
	431385 431728	BE178536 NM_007351	Hs.11090 Hs.268107	membrane-spanning 4-domains, subfamily A multiments	1.00	157.00 157.00
	431720	AJ378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
40	432128	AA127221	Hs.117037	ESTs	0.00	1.15
	432519	AJ221311	Hs.130704	ESTs, Wealdy similar to BCHUIA S-100 pro	0.01 1.00	2.06 267.00
	433043 433803	W57554 A1823593	Hs.125019 Hs.27688	lymphoid nuclear protein (LAF-4) mRNA ESTs	1.00	105.00
	434730	AA644669	Hs.193042	ESTs	1.05	3.15
45	435472	AW972330	Hs.283022	triggering receptor expressed on myoloid	0.83	1.94 218.00
	436532	AA721522	11- 477042	gb:nv54h12.r1 NCI_CGAP_Ew1 Homo saplens ESTs	1.00 1.00	133.00
	437119 437140	AI379921 AA312799	Hs.177043 Hs.283689	activator of CREM in testis	0.67	122.67
	437211	AA382207	Hs.5509	ecctropic viral integration site 2B	1.00	142.00
50	437960	AI669586	Hs.222194	ESTs	1.00	147.00
	438202 438873	AW169287 AJ302471	Hs.22588 Hs.124292	ESTs Homo sepiens cDNA: FLJ23123 fis, clone L	1.00 0.71	141.00 3.66
	438875	AA827640	Hs. 189059	ESTA CONTROL Y COLUMN TO A CONTROL OF CONTRO	23.32	370.00
	441048	AA913488	Hs.192102	ESTs	0.77	8.50
55	441188	AW292830	Hs.255609	ESTs ESTs	3.43 1.00	16.36 167.00
	441499 444513	AW298235 AL120214	Hs.101689 Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
60	445279	R41900	Hs.22245	ESTs	0.60 0.18	141.00 2.39
	446017 446984	N98238 AB020722	Hs.55185 Hs.16714	ESTs Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sepiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
	447357	Al375922	Hs.159367	ESTs	0.46	2.64
65	448106 448253	A1800470 H25899	Hs.171941 Hs.201591	ESTs ESTs	18.05 1.00	296.00 141.00
	448253	AW450848	Hs.205457	periado	0.56	1.38
	450400	AJ694722	Hs.279744	ESTs	0.88	4.33
	450698	AI654223	Hs. 16026	hypothetical protein FLJ23191	0.52	2.08 2.01
70	450726	AW204600 H83294	Hs.250505 Hs.284122	refinoic acid receptor, alpha Wnt inhibitory factor-1	0.79 0.35	2.03
	451497 451533	NM_004657	Hs.26530	serum deprivation response (phosphatidy)	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
76	458332	AI000341	Hs.220491	ESTs	1.00 0.20	192.00 2.98
75	459580 400269		Hs.176065	ESTs Eos Control	0.40	2.40
	403421			NM 016369° Homo saviens claudin 18 (CLDN	0.53	1.77
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
80	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56 0.64	1.74 1.50
60	414517 417204	M24461 N81037	Hs.76305 Hs.1074	surfactant, pulmonary-associated protein surfactant, pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	sclute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
85	421502 421798		Hs.105039 Hs.29877	solute carrier family 34 (sodium phospha N-acylsphingosine amidohydrolase (acid c	0.78 0.59	1.90 1.54
0.5	421790	147 4000	rs-290//	14-cm halamidanana mranan langana (ang a		1.01

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	423354	AB011130	44.3 Hs.127436	calcium channel, voltage-dependent, alph	0.59	1.55
	423334	AB002134	Hs.132195	airway trypsin-like prolease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
	425438	T62216	Hs.270840	FSTs	0.23	9.45
5	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
,	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26
	430280	AA361258	Hs.237868	Interleukin 7 receptor	0.48	2.43
	431433	X65018	Hs.253495	surfactant, pulmonary-associated prolein	0.57	1.59
10	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51 1.78
	442275	AW449467	Hs.54795	ESTs	0.55	1.78
	443709	A1082692	Hs.134662	ESTs	0.00	3.02
15	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	A)904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	0.00	3.30
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
20	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20 297.00
	400754			Target Exon	1.00	
	401045			C11001883*:gij6753278 ref[NP_033938.1] c	1.00	109.00 1.39
	401083			NM_016582*:Homo sapiens peptide transpor	0.89 1.45	4.47
25	402474			NM_004079:Homo sapiens cathepsin S (CTSS ENSP00000235229:SEMB.	1.00	1.87
23	402808			C21000030:gij9955960/refjNP_063957.1 AT	1.00	149.00
	403021 403438			NM_031419*:Homo sapiens molecule possess	1.06	2.96
	403436			NM_007037*:Homo sapiens a disintegrin-li	0.04	4.89
	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
30	404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
50	404288			NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
	404518	Al815601		CD83 antigen (activated B lymphocytes, I	0.02	1.83
	405106	A013001		C11001637*:gij5032241[ref[NP_005732.1] z	1.00	235.00
	405381			Target Exon	1.00	93.00
35	406387			Target Exon	1.37	6.02
-	406646	M33600		major histocompatibility complex, class	0.86	2.46
	406714	Al219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
40	407248	U82275	Hs.94498	teukocyte immunoglobulin-like receptor,	1.00	64.00
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000068	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
	408045	AW138959	Hs.245123	ESTs	1.00	70.00
45	408074	R20723		ESTs	1.00	112.00
	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs .	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00 4.55
50	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	
50	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01 1.00	3.72 79.00
	409238	AL049990	Hs.51515	Homo sapiens mRNA; aDNA DKFZp584G112 (fr	0.14	27.35
	409389	AB007979	Hs.301281	Homo saplens mRNA, chromosome 1 specific	1.00	113.00
	409718 410798	D86640 BE178622	Hs.56045 Hs.16291	src homology three (SH3) and cysteine rl gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
55	411020		Hs.67726	macrophage receptor with collagenous str	0.55	2.40
"	411687	NM_006770 BE160198	115,07720	gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
60	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
-	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Ha.846	interleukin 8 receptor, beta	0.02	2.42
	413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
65	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	Al129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to \$65657 alpha-1 C-	1.00	213.00
~~	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
70	414376	BE393856	Hs.66915	ESTs. Weakly similar to 16.7Kd protein [1.00	115.00 1.94
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	
	414700	H63202	Hs.38163	ESTs	0.03	3.75 1.95
	415078	AA311223	Hs.283091	found in Inflammatory zone 3		1.95
75	415120	N64464	Hs.34950	ESTs	1.00 0.60	2.48
75	415323	BE269352	Hs.949	neutrophii cytosolic factor 2 (65kD, chr	1.00	95.00
	415335	AA847758	Hs.111030	ESTs	1.00	136.00
	415582	W92445 H15261	Hs.165195 Hs.21948	Homo saplens cDNA FLJ14237 fis, clone NT ESTs	0.02	8.07
	416030	H15261 BE244050		Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
80	416427 416464	NM_000132	Hs.79307 Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
00	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
85	417673	T87281	Hs.16355	ESTs	0.15	15.54

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		O 02/086				
	418067 418296	Al127958 C01566	Hs.83393 Hs.86671	cystatin E/M ESTs	0.81 1.00	1.74 99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
	418832	X04011	Hs.88974	cytochrome b-245 beta polypepiide (chro	2.40	14.74
5	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67 1.00	3.16 73.00
	419261 419564	X07676 U08989	Hs.89791 Hs.91139	wingless-type MMTV integration site fami solute carrier family 1 (neuronal/epithe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
• •	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
10	420256	U84722	Hs.76206 Hs.293878	cadherin 5, type 2, VE-cadherin (vascula ESTs, Moderately similar to ZN91_HUMAN Z	0.52 1.00	1.70 172.00
	420285 420577	AA258124 AA278436	Hs.186649	ESTs Moderately string to 2No 1_Now-N 2	1.00	97.00
	421262	AA286746	Hs.9343	Homo saniens cDNA FLJ14265 fis, clone PL	1.00	64.00
	421445	AA913059	Hs.104433	Homo sepiens, clone IMAGE:4054868, mRNA	0.88	1.61 11.26
15	421470 421478	R27496 AI683243	Hs.1378 Hs.97258	annexin A3 ESTs, Moderately similar to \$29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	grandysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31.57
20	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	1.00 1.00	129.00 101.00
20	421913 421952	Al934365 AA300900	Hs.109439 Hs.98849	osteoglycin (osteoinductive factor, mime ESTs, Moderately similar to AF161611 1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98 3.59
25	423168	R34385	Hs. 124940	GTP-binding protein	0.34 0.55	2.00
23	423196 423387	AK001866 AJ012074	Hs.125139	hypothetical protein FLJ11004 vasoactive intestinal peptide receptor 1	0.09	2.13
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
	423456	AL110151	Hs. 128797	DKFZP586D0824 protein	1.00	66.00
20	423696	Z92546		Sushi domain (SCR repeat) containing	0.73 0.54	1.27 2.58
30	424027 424212	AW337575 NM_005814	Hs.201591 Hs.143131	ESTs glycoprotein A33 (transmembrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
25	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18 1.00	2.56 78.00
35	426486 427507	BE178285 AF240467	Hs.170056 Hs.179152	Homo saplans mRNA; cDNA DKFZp586B0220 (1 toll-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM 002980	Hs.2199	secretin receptor	0.97	1.42
40	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00 1.00	105.00 80.00
40	428709 428769	BE268717 AW207175	Hs.104916 Hs.106771	hypothetical protein FLJ21940 ESTs	0.09	2.55
	428780	A1478578	Hs.50636	ESTs	1.00	98.00
	428833	AI928355	Hs. 185805	ESTs	1.00	113.00
45	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protel gb:nc67f04.s1 NCI_CGAP_Pr1 Homo saplens	1.00	52.00 132.00
45	430212 430226	AA469153 BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
	430414	AW365665	Hs.120388	ESTs	0.50	6.96
50	430656		Hs.162080 Hs.119514	ESTs ESTs	1.00	70.00 90.00
30	430843 430998	Al734149 AF126847	Hs.204038	Indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91 0.66	1.67 2.63
55	432178 432203	AW090386 AA305746	Hs.112278 Hs.49	arrestin, beta 1 macrophage scavenger receptor 1	1.00	76.00
55	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.48
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522		Hs.51	phosphatidylinositol glycan, class A (pa	1.93 0.04	4.83 5.79
60	432596 432850	AJ224741 X87723	Hs.278461 Hs.3110	matriin 3 engiotensin receptor 2	1.00	187.00
00	432330		Hs.59729	semaphorin sem2	0.04	9.16
	433563	AI732637	Hs.277901	ESTs	1.00	91.00
	433588 434445	AI056872 AI349306	Hs.133386 Hs.11782	ESTs FSTs	120.16 0.60	315.00 1.84
65	434445 435496	AW840171	Hs.265398	ESTs, Wealdy similar to transformation-r	1.00	128.00
00	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	436061	AJ248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860 T27503	Hs.120655 Hs.15929	ESTs hypothetical protein FLJ12910	1.00 1.00	87.00 105.00
70	437207 437311		Hs.15929 Hs.9456	SWVSNF related, matrix associated, acti	1.00	71.00
,,,	437439	H29796	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00 0.30	80.00 3.10
	439551 440515		Hs.11112 Hs.7239	ESTs SEC24 (S. cerevisiae) related gene famili	1.00	77.00
75	440887	AJ799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79 1.00	1.89 75.00
	441735		Hs.127346 Hs.235768	ESTs ESTs	0.78	5.83
80	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	147764	Hs.132917 Hs.23767	ESTS	1.00	197.00 253.00
	443547 443951	AW271273 F13272	Hs.111334	hypothetical protein FLJ12666 ferritin, light polypeptide	0.55	2.09
85	444330	AJ597655	Hs.49265	ESTs	1.00	90.00

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WO 02/086443
                                                                                                                                                                                                                                                                                                                                                                  PCT/US02/12476
                                                                                                                     ESTs
ESTs
                                                                                                                                                                                                                                                                                            84.00
                        444515 AW204908
                                                                                    Hs. 169979
                        445769
                                                                                      Hs.23666
                                                                                                                                                                                                                                                0.02
                                                                                                                                                                                                                                                                                             4.38
                                                AI741471
                                                                                                                                                                                                                                                                                             97.00
                        445908
                                                                                                                       Homo saplens clone 24425 mRNA sequence
                                                                                                                                                                                                                                                1.00
                                                                                      Hs.13436
                                                                                                                                                                                                                                                                                             1.69
                        446291
                                                BF397753
                                                                                      Hs.14623
                                                                                                                      Interferon, gamma-Inducible protein 30
                        446917
                                                                                      Hs.156672
                                                                                                                      FSTs
                                                                                                                                                                                                                                                 1.00
                                                                                                                                                                                                                                                                                             100 00
                                                A1347863
                          447261
                                                NM_006691
AW958473
                                                                                      Hs.17917
                                                                                                                      extracellular link domain-containing 1
nudix (nucleoside diphosphate linked mol
KIAA 1233 protein
                                                                                                                                                                                                                                               0.40
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                          447432
                                                                                      Hs.301957
                                                                                                                                                                                                                                                                                             100.00
                                                                                      Hs.18705
Hs.29792
                        447402
                                                 VBU33020
                                                                                                                     KIAA1233 protein
ESTs, Weakly similar to 138022 hypotheti
hypothetical protein FLJ10392
KIAA0758 protein
purino-rich element binding protein A
                                                                                                                                                                                                                                                0.02
                                                                                                                                                                                                                                                                                             642
                          447997
                                                 H00656
10
                          448299
                                                 AA497044
                                                                                       Hs.20887
                                                                                                                                                                                                                                                1 00
                                                                                                                                                                                                                                                                                             79.00
1.56
                                                                                                                                                                                                                                                0.42
                          448782
                                                 AL050295
                                                                                       Hs.22039
                                                                                                                                                                                                                                                                                             11.33
                          450575
                                                 NM_005859
                                                                                       Hs 29117
                                                                                                                                                                                                                                                                                             94.00
                                                                                                                                                                                                                                                 1 00
                                                   AANANAN3
                                                                                       He 60371
                          450584
                          450693
                                                   AW450461
                                                                                       Hs.203965
                                                                                                                                                                                                                                                1 00
                                                                                                                     ES15, Wealthy similar to KIAA1324 protein
DKFZP5640206 protein
novel SH2-containing protein 3
cartilage acidic protein 1
                                                                                                                                                                                                                                                                                             152.00
                                                                                                                                                                                                                                                 1.00
15
                          450715
                                                   AI266484
                                                                                       Hs.31570
                                                                                                                                                                                                                                                 1.00
                                                                                                                                                                                                                                                                                              86.00
                          451103
                                                   DESSUA
                                                                                       He 25956
                                                                                      Hs.26054
Hs.326444
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                          451220
                                                   AF124251
                                                                                                                                                                                                                                                                                             1.91
                                                   743048
                                                                                                                                                                                                                                                 0.54
                          451669
                                                                                                                                                                                                                                                                                             67.00
                          452197
                                                   AW023595
                                                                                       Hs.232048
                                                                                                                       ESTS
                                                                                                                                                                                                                                                 1.00
20
                                                                                                                      purine-rich element binding protein A
epithelial membrane protein 2
                                                                                                                                                                                                                                                 4.53
                                                                                                                                                                                                                                                                                              11.07
                          452331
                                                   AA598509
                                                                                       Hs.29117
                                                                                                                                                                                                                                                 0.72
                                                                                                                                                                                                                                                                                             2 24
                                                   C18825
                          462363
                                                                                       Hs.29191
                          452030
                                                   RF537217
                                                                                       Hs.30343
                                                                                                                                                                                                                                                 1.00
                                                                                                                                                                                                                                                                                             68 00
                                                                                                                      vaniilold receptor-like protein 1
Homo sapiens cDNA FLJ11422 fis, clone HE
                                                                                                                                                                                                                                                                                              170
                          453107
                                                                                       Hs.279746
                                                                                                                                                                                                                                                 0.83
                                                   NM 016113
                                                                                                                                                                                                                                                                                              132.00
                                                                                                                                                                                                                                                 1.00
                          453355
                                                   AW295374
                                                                                       Hs.31412
                                                                                       Hs.28482
                                                                                                                                                                                                                                                   1.00
                                                                                                                                                                                                                                                                                             72.00
25
                                                                                                                       FSTs
                          453390
                                                   AA862496
                                                                                                                       ESTs, Wealdy similar to JCS795 CDEP prot 
gb;CM2-HT0342-091299-050-b05 HT0342 Homo 
up-regulated by BCG-CWS 
Homo saplens, clone MGC:16327, mRNA, com
                                                                                                                                                                                                                                                 1.00
                                                                                                                                                                                                                                                                                             68.00
                          453531
                                                   AA417940
                                                                                                                                                                                                                                                 0.57
                                                                                                                                                                                                                                                                                             2.89
                          454741
456579
456672
                                                   BF154396
                                                                                                                                                                                                                                                   1.00
                                                                                                                                                                                                                                                                                              82.00
                                                                                       He 284205
                                                   AA287827
                                                                                                                                                                                                                                                                                             1.96
                                                                                       Hs.114727
                                                                                                                                                                                                                                                 0.79
                                                   AK002016
30
                          457400
                                                                                                                       cathepsin Z
ESTs, Wealdy similar to ALU4_HUMAN ALU S
gb:HSC1KA072 normalized infant brain cDN
                                                   AF032906
                                                                                        Hs.252549
                                                                                                                                                                                                                                                 1 03
                                                                                                                                                                                                                                                                                              113.00
                          457718
                                                   F18572
                                                                                        Lie 22078
                          459696
                                                E03027
                          TABLE 10B
35
                          Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers
40
                          Pkey
408074
                                                           CAT Number
                                                                                                     R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 Al810530 D31302 AW134897 AA830127 AA046953 Al668930
                                                           103684_1
                                                                                                   CROSSA NATIONALS SEED TI ISOO AWESSIGN 
                          411667
                                                           1253334 1
                                                           1375344_1
                          413533
 45
                           423387
                                                           22779_1
                                                                                                     I I/BD LK 1/3149 (NOUMPA AMBRIST) AUSBUTSN K/ZUZK AUSBUASSE WILLIESD AAN 1882 WOOST I K/ZEWU MI-500 RACISSE RAFTSE
AACSBEES AMBRISTE STATS I FRINGTI FICE ALAZEZERS AND ANDSISSE
ZEISSE ALASSESSE ALSTOSSE AWDALKEZ AUSZYCES NAZSESSE ALTOSELS ALTOSSES ALTOSSES ALTOSSES ALTOSZES I AUSTZASSE AWDALKEZ
ZEISSE ALASSESSES ALSTOSSE AWDALKEZ AUSZYCES NAZSESSES ALTOSZES ALTOSSES ALTOSZES ALT
 50
                                                           23112_1
                            423698
                                                           314437_1
                                                                                                      AA469153 AI718503 AA469225
                            430212
                                                                                                     AA721522 AW975443 T93070
                            436E33
                                                             421802_1
 55
                            430532
453531
                                                             97026 1
                                                                                                      BE154396 AW817959 BE154393
                            454741
                                                             1232559_1
                           TABLE 10C
 60
                           Piesr: Unique number corresponding to an Eos probesel 
Ref: Sequence soutre. The 7 digit numbers in bids column are Genbank Menitiler (G) numbers. "Dunham L et al." refers to the publication entitled "The DNA 
sequence of human chromotome 22" Dunham L et al., Mature (1999, 40;2489-495. 
Indicates DNA stead from which excess were predicted. 
No publics. Indicates DNA stead from which excess were predicted.
 65
                            Pkey
400754
                                                                                                                             Nt_position
144559-144684
                                                                                            Plus
Plus
Plus
Plus
Minus
                                                             7331445
                                                                                                                             90044-90184-91111-91345
                            401045
                                                           8117619
3242744
 70
                            401083
                                                                                                                               33172-33300
53526-53628.56755-55920.57530-67757
                                                             7547175
                            402474
                                                                                                                             114964-115136,115461-115585,115931-116047,117668-117771,118004-118102
                                                             6456148
                            402808
                                                                                            Plus
Minus
Plus
Plus
Minus
Minus
                            403021
                                                           7547270
9665041
9719679
                                                                                                                             120700-120986
                                                                                                                               126609-126773,139988-140205
 75
                            403438
                                                                                                                             90792-90938
                            403687
403764
                                                                                                                             9009-9534
                                                                                                                             118692-118853
                                                             7717105
                                                                                                                             91665-91946
                            404277
                                                             1834458
                                                                                             Plus
Minus
Plus
                            404288
                                                             2769644
                                                                                                                             37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
  80
                             404518
                                                             8151988
                                                                                                                             RAADA RAGOS
                                                                                                                             91057-9118
                            404016
                                                                                             Phie
                                                              7341826
                            405106
                                                             8079395
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405257

85

7329310

73121.73273

7636-8054

5

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TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignent lung disease, and normal lung. These genes were selected from about 59980 probesets on the EostAffymetrix Hutti Generally array.

Table 11B show the accession numbers for those Prey's tacking Unigene(ID's for table 11A. For each probesed we have fetted the gene duster number from which the oliponutacionides were designed. Canne clusters were nomiphed using sequences derived from Gerbank ESTs and nrFVMs. These sequences were clustered based on sequence similarity using Custaring and Afignment's Look (Chabila*Val. Calaban California). The Combant Accession emmohest for requireces comprising each Culture.

10 Table 11C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also lated.

Pkey: ExAcct: UnigenelD: Unigene Title: 15

Unique Eas probasel Identifier number
Exempler Accession number, Genbank accession number
Uniquene genes tile
Average of Insu grunner (including squemous cell cardiormas, adenocardiormas, small cell cardinomas, grandomaticus and cardinold tumora) divided by the
average of formal tung samples
Average of formal tung samples
Average of formal genes tile
Average of

20

20	R2:	Averag	e of non-mailig	nant lung disease samples (including bronchitis, emp	hysema, fibrosi	is, atelectasis, asthma) divided by the average of norm
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
	403329	Cowan	dingundo	Target Exon	1.00	61.00
	408399			NM 003122*:Homo saplens serine protesse	1.00	39.00
25	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
23	407869	AI827976	Hs.24391	hypothesical protein FLJ13612	0.77	1.18
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfol	1.00	10.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
30	409187	AF154830	Hs.50966	carbamoyl-phosphale synthetase 1, mitoch	1.00	1.00
50	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	410076	705387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs-279727	Homo saciens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
35	411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
	412612	NM 000047	Hs.74131	arytsulfatase E (chondrodysplasia puncta	1.02	1.03
	414075	U11862	Hs.75741	amilioride binding protein 1 (amine oxida	0.84	1.07
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
40	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
	420931	AF044197	Hs.100431	small Inducible cytokine B subfamily (Cy	1.00	8.00
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
45	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
50	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422867	L32137	Hs.1584	cartilage of gomeric matrix protein (pse	1.69	3.17
	423472	AF041260	Hs.129057	breast cardnoma amplified sequence 1	48.13	72.00
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
55	424502	AF242388	Hs.149585	lengsin	1.00	1.00 59.00
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino ad	21.35	1.00
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1,00	1.00
	424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	35.00
60	425523	AB007948	Hs.158244	KIAA0479 protein	1.00	83.00
UU	426230 427701	AA367019 AA411101	Hs.241395 Hs.243886	protease, serine, 1 (trypsin 1) nuclear autoantigenic sperm protein (his	7.41	34.00
	428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
65	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
05	429610	AB024937	Hs.211092	LUNX protein: PLUNC (palate lung and nas	1.59	1.69
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430985	AA490232	Hs.27323	ESTs, Weakly similar to 178885 serins/th	0.94	1.28
	431548	AJ834273	Hs.9711	novel protein	5.66	15.00
70	431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
	431986	AA536130	Hs.149018	Novel human gene mapping to chomosome 20	1.19	1.47
	432375	BE536069	Hs.2962	S100 calcium-blading protein P	1.65	1.06
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
75	433819	AW51 1097	Hs.112765	ESTs	3.71	8.00
	434001	AW950905	Hs.3697	serine (or cysteine) proteinese inhibito	29.31	72.00
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L.	1.00	64.00
	434792	AA649253	Hs.132458	ESTs	8.52	44.00
	436217	T53925	Hs.107	fibrinogen-like 1	67.97	31.00
80	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
	437866	AA156781		metallothionein 1E (functional)	3.62	101.00
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
0.5	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
85	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

	we	0 02/0864	143				PCT/US02/12476
	439759	AL359055	Hs.67709	Homo saplens mRNA full length insert cDN	1.00	21.00	
		Al110684	Hs.7645	fibringgen, B beta polypeptide	1.41	99.00	
	441377	BE218239	Hs.202656	ESTs	22.03	1.00	
_	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00	
5		AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99	
		NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87	
		H58373	Hs.332938 Hs.75113	hypothetical protein MGC5370 general transcription factor itIA	1.98	38.00 54.00	
	444931 446102	AV652066 AW168067	Hs.317694	general transcription ractor that	1.00	1.00	
10	446163	AA026880	Hs.25252	Homo saciens cDNA FLJ13603 fis, clone PL	1.00	36.00	
		BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	1.00	11.00	
		AW630534	Hs.76277	Homo saplens, clone MGC:9381, mRNA, comp	1.24	1.16	
		AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1,63	
15	448243 448844	AW369771 AI581519	Hs.52620 Hs.177164	integrin, beta 6 ESTs	15.84 1.00	31.00	
13		AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00	
		W52854	115.23000	hypothetical protein FLJ23293 similar to	1.55	35.00	
		F33868	Hs.284176	transferrin	1.54	1.44	
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00	
20	453464	Al884911	Hs.32989	receptor (catcitonin) activity modifying	1.55	2.45	
	453735	AI066629	Hs.125073	ESTs	1.01	1,30	
	TABLE 11						
	INDUC II						
25	Pkey:			entifier number			
		ber: Gene clust : Genbank a		A.m			
	ALLOSSIUI	. Gollbank a	CC000ION NUM	ludi 3			•
20	Pkey	CAT Numbe	Acces.	slon			
30	410399	11995_1	BE068	889 BE068682 AF044311 AF017256 NM_003087 A	F037207 AF010	126 AA63397	6 AA872836 BE298825 BE299889 Al016464 Al684600 0468480 AA056035 AA055968 AW796957 Al637713
			AISSE	527 AABU4075 AAJU4037 AIT33333 AAS46000 BETI	7634 AAAA3639	AMA 62427 A	A421708 AW265211 AI493266 AA365132 AW966044
	419502	18535_1	Alinza	7704 T74854 T74860 T72098 T73265 T73873 T6918	D T74658 T587	R6 T603R5 T73	3410 T68781 T67845 T67593 T73952 T67864 T60630
			T6836	7 T68401 T53959 T72360 T72099 T60377 T58961 T	71712 172821	T64738 T7464	15 T72037 T68688 T72063 T73258 T72826 T64242
35			T6822	0 T74673 T71800 T68355 T81227 T62738 T69317 T	53850 T64692	T73768 T7398	32 T73382 T68914 T70975 T73400 T60631 T73277
			T7320	3 T70498 T61409 T58925 NM_000508 M64982 T68:	301 T73729 T69	445 T60424 T	167922 T67736 T68716 T67755 T74765 T73819 T58715
			17475	6 T60477 T74863 T61109 T68329 T58850 T71857 T 6 T73787 T56035 T64425 T71870 T60476 T61376 T	73425 153736	168607 15889	36 164309 172031 172079 164305 171906 166107
			1/191	5 1/3/8/ 156035 164425 1/18/0 1604/6 1613/6 1 2 T74644 T63636 T64124 AA663066 T72525 T6777	16/82U 1/1695 10 TERNTR AAN1	1465 443453	78 AV654847 AV654272 AV656001 AI064740 T82897
40			N3359	4 AA344542 AW805054 AI207457 T61743 AA02673	7 H94389 AA38	2695 AA9184	09 T68044 S82092 T39959 Al017721 AA312395
			AA312	2919 T40156 H66239 AV652989 H38728 R98521 AV	655200 R95791	W03250 W00	0913 AA344136 AV660126 R97923 AA343596
			AW47	0774 AV651256 N54417 AA812862 AW182929 Al11			503 H38639 Al277511 AV661108 Al207625 T47810
					1132 (101403 (1	2000 7000	
			AA235	2 770024 770470 T724FC AVEAEE20 AVEE2470 T7	/827166 R9847	5 C20925 AV6	557287 T71959 T71313 T73920 T73333 T61618 T69293
45			T6928	3 T73931 T72178 T72456 AV645639 AV653478 T72	/827166 R9847 1957 T72300 T5	5 C20925 AV6 8906 T71457	T70494 T72956 T70495 T68267 T74407 T85778
45			T6928 AA344 T7047	3 T73931 T72178 T72456 AV645639 AV653478 T72 1726 T27854 T74485 T74101 T73868 T71518 T7230 5 T64751 AA344441 AA343657 AA345732 AA34432	/827166 R9847: /957 T72300 T5 /4 AA343853 T7 /8 AI110639 AA	5 C20925 AV6 8906 T71457 3909 T68070 344603 AF063	T70494 T72956 T70495 T68267 T74407 T85778 T72065 H72149 T73493 T73495 AV645993 R02293 3513 T64696 T68516 T72223 T60507 T67633 R29500
45			T6928 AA34- T7047 T7251	3 T73931 T72178 T72456 AV645639 AV653478 T72 1726 T27854 T74485 T74101 T73868 T71518 T725 5 T64751 AA34444 TA343657 AA345732 AA34432 7 R02292 T60599 T6059 T70452 T74677 R29366	/827166 R9847: /967 T72300 T5 /4 AA343853 T7 /28 AI110639 AA T61277 T74914	5 C20925 AV6 8906 T71457 3909 T68070 344603 AF063 T60352 R296	T70494 T72956 T70495 T68267 T74407 185778 T72065 H72149 T73493 T73495 AV645993 R02293 3513 T64696 T68516 T72223 T60507 T67633 R29500 75 T74843 AV645792 AA344408 T69197 T72057
45	٠		T6928 AA34 T7047 T7251 T6936	3 T73931 T72178 T72456 AV645639 AV653478 T72 5726 T72854 T74465 T74101 T73868 T71518 T7230 5 T647551 AA344441 AA343657 AA345732 AA34432 7 R02292 T60599 T69206 T70452 T74677 R29366 8 T69358 T68258 AV650429 T73341 T61702 T7459	/627166 R9847: /957 T72300 T5 /4 AA343853 T7 /8 AI110639 AA T61277 T74914 /8 T40095 K022	5 C20925 AV6 8906 T71457 3909 T68070 344603 AF063 T60352 R296 72 T40106 AA	T70494 T72956 T70495 T69267 T74407 T65778 T72056 H72149 T73493 T73495 AV645993 R02293 3513 T64696 T68516 T72223 T60507 T67633 R29500 75 T78493 AV645792 AA344408 T69197 T72057 343045 AA341908 AA341907 AA342807 AA341954
	•		T6928 AA34- T7047 T7251 T6936	3 179331 172178 17245 AV645639 AV658478 177 1726 127854 174485 174101 173868 171518 17230 5 164751 AA344441 AA34867 AA346732 AA34432 7 R02292 160599 169206 170452 174677 R29366 8 169358 168258 AV650429 173341 161702 17459 7 1720124 187764 AU64599 AA343901 167833 1779	/827166 R9847: 2957 T72300 T5: 4 AA343853 T7: 28 AI110639 AA T61277 T74914 18 T40095 K022 440 T71770 T6:	5 C20925 AV6 8906 T71457 3909 T68070 344603 AF063 T60352 R296 72 T40106 AA	T7049 T72956 T70495 T62267 T74407 T85778 T72056 H72149 T73493 T73495 AV645993 R02293 3513 T84696 T68516 T72223 T60507 T67633 R29500 75 T74843 AV645792 AA344408 T69187 T72057 343045 AA341906 AA341907 AA342807 AA341954 T72449 T89167 T71289 T68251 AV654844 T64375
45 50	-		T6928 AA34- T7047 T7251 T6938 T5374 AA34	3 173931 172178 17245 AV64533 AV653476 1775 7726 17265 174466 17401 17368 171518 17230 5 184751 AA34441 AA343657 AA345732 AA3437 7 RO2232 160599 189206 170452 174677 R29367 8 183385 186258 AV650429 17341 18707 17459 7 172042 182764 AU64599 AA343080 187832 1727 9234 187898 AU61141 187816 1846762 AV67551 1	/827166 R9847: 1957 T72300 T5: 14 AA343853 T7: 18 AI110639 AA: 161277 T74914: 18 T40095 K022: 140 T71770 T68: 168219 W86031	5 C20925 AV6 8906 T71457 3909 T68070 344603 AF063 T60352 R296 72 T40106 AA 1091 T69108 T T69081 T6423	T70494 T72955 T70495 T69267 T74407 T85778 T72055 H72149 T72493 T73495 XV645993 R02293 3613 T86895 T68916 T72222 T69607 T67633 R29500 75 T74843 AV645792 AA344408 T69197 T72057 343045 AA341908 AA341907 AA342807 AA341994 772449 T69167 T71289 T68251 AV654844 T64375 32 R63198 T62138 AV650539 H67459 T72978
			T6928 AA344 T7047 T7251 T6936 T5374 AA348	3 779931 772176 172455, AV645539 AV553476 177, 7726 17265 174465 17410 17366 17151 187230 5 184751 AA34441 AA34567 AA345752 AA34457 7 R02252 150599 169206 170452 174677 283436 8 159358 169258 AV550429 173341 161702 17459 7 172042 162764 AI064699 AA343060 176733 1772- 5224 161788 AA011414 158036 H48226 AZ07557 1 1593 161909 16191 18191 18191 175001 177801 1768055 1771	/627166 R9847: 1957 T72300 T5 14 AA343853 T7 18 A1110639 AA T61277 T74914 18 T40095 K02 16 K0290 T7270 15 R29036 T727	5 C20925 AV6 8906 T71457 1 3909 T68070 1 344603 AF063 T60352 R296 T60352 R296 T69108 A T69081 T69108 T T69081 T642:	T7049 T7295 T70495 169267 T74407 185778 T72056 172149 T7349 T7349 X4V64599 X02293 913 T64696 T68916 T72223 T60907 T6753 R2950 75 T74943 X4965792 XA34409 T69197 T72057 343045 XA341906 AA341907 AA342807 AA341954 T72444 T59167 T71289 T82925 1 X4956484 T64375 32 R35198 T62198 X4950539 H67459 T72978
	·		T6928 AA34- T7047 T7251 T6936 T5374 AA34- AA34- AA64- T6783	3 17393 1772178 1772455 AV645539 AV655376 777 77256 177256 177456 17746	/627166 R9847: 1957 T72300 T5 44 AA343853 T7 48 A1110639 AA 161277 T74914 48 T40095 K022 440 T71770 T68 68219 W85031 15 R29036 T727 429 T51176 T51 174474 T56068	5 C20925 AV6 8906 T71457 3909 T68070 344603 AF063 T60352 R296 72 T40106 AA 1091 T69108 T T69081 T642: 93 T69122 T6 8866 AV65541	T70494 T72695 T70495 T62627 T74407 T65772 77206 1972149 77349 3 773495 X404999 R02239 1813 T64698 T68916 T72223 T69607 T67533 822950 75 T74943 X045729 X2434440 T69197 T72657 332045 A241909 A241907 A242807 A341994 772445 T6916 T71289 T62515 A49267 A341994 772445 T6916 T71289 T62515 A49267 A341994 772445 T6916 T71289 T62515 A49267 T7271 T46952 24 P63198 T62138 A4926739 H67499 T72789 14 H90425 A3342499 T73666 T67846 T72512 T53835
50	421582	2041_1	T6928 AA34 T7047 T7251 T6936 T5374 AA345 AA697 T6783 A1910	3 179351 172118 172452 N4956559 AV655478 172415 172705 172	/827166 R9847: 9957 T72300 T5 9957 T72300 T5 44 AA343853 T7 48 A110639 AA 161277 T74914 8 T40095 K022 440 T71770 T68 68219 W85031 15 R29036 T727 429 T51176 T51 774474 T55068 1 AA308400 AA5	5 C20925 AV6 8906 T71457 1 3909 T68070 1 344603 AF063 T60352 R296 72 T40106 AA 1091 T69108 T T69081 T642: 93 T69122 T6 8866 AV65541	T70494 T72956 T70495 T62827 T74407 T65778 177056 H72149 T73493 T73495 X469599 R02239 151 3 T64696 T62951 T7232 T62607 T67533 R26950 75 T74694 X045792 A244440 T69197 T72357 3,0005 A,041506 A,047597 A,044207 A,0441594 772440 T6107 T7,024 T607 A,047207 A,0441594 772440 T6107 T7,024 T607 A,047207 A,0441594 772440 T6107 T7,024 T607 A,047207 A,0441594 172440 T6107 T7,024 T607 A,047207 A,0441594 172440 T6107 T7,024 T607 A,047207 A,047207 A,047207 18251 T6107
	421582	2041_1	T6928 AA34* T7047 T7251 T6936 T5374 AA34* AA69; T6783 Al910 AA56	3 179351 172118 172455 N495558 N495558 N153418 172415 172415 172455 N495558 N153418 172475 17251 172475 17251 172475 17251 172475 17251 172475 17251 172475	/827166 R9847: 9957 172300 T5 9957 172300 T5 28 Al110839 AA 161277 174914 88 T40095 K022 440 171770 T68 168219 W86031 15 R29036 T727 429 T51176 T51 774474 T56068 14 AA308400 AA5 110083 M12075	5 C20925 AV6 8906 T71457 3909 T88070 344603 AF063 T60352 R296 72 T40106 AA 1091 T69108 T T69081 T642: 93 T69122 T6 3866 AV65541 506787 AA314 BE074052 AV	TYOUGH T7266 T70465 T06267 T74407 T85778 TYT265 H72149 T77465 T06267 T74407 T85778 151 T1469 T7261 T7416 T7445 T7426 S10220 151 T1469 T7414 T7450 T7465 T7469 T74607 151 T1469 T7469 T7469 T74607 T74607 T7449 T6916 T7428 T08257 T74607 T7449 T7449 T6916 T71289 T08257 T7469 T7449 T7449 T6916 T71289 T08257 T7469 T7478 T696 T6916 T7469 T6916 T7469 T6965 T6768 T77219 T696 T6916 T6916 T7469 T6916 T696 T696 T6971 T7489 T6916 T6916 T7469 T6916 T696 T696 T6971 T7489 T6916 T6916 T6916 T6916 T6916 T6916
50	421582	2041_1	T6928 AA34* T7047 T7251 T6936 T5374 AA34* AA69; T6763 AI910 AA561 BEU7/	3 17933 17218 17245 17245 17245 17245 17245 17245 17245 1724 1725 1725 1725 1725 1725 1725 1725 1725	1827165 R9847; 1957 T72300 T5 14 AA343853 T7 28 A1110639 AA 161277 T74914 18 T40095 K022 140 T71770 T66 168219 W86031 15 R29036 T727 15 R29036 T727 1429 T51176 T6 174474 T56068 14 A3308400 AA5 110083 M12075 1009769 AW050	5 C20925 AV6 8906 T71457 3909 T88070 344603 AF063 760352 R296 72 T40106 AA 10759108 T 169081 T642: 93 T69122 T6 9866 AV65541 806787 AA314 8E074052 AV	TT-0464 T7-2566 T7-0465 109:267 T7-4407 T8-5778 TT-0506 T7-046 T7-0455 T0-2567 T7-0467 T8-5778 TT-0506 T7-046 T7-045 T7-0455 T7-0457 T7-0457 T7-056 T7-046 T7-0457 T
50			T6928 AA344 T7047 T7251 T6936 T5374 AA344 AA693 T6783 Al910 AA566 BE074	3 T7981 T7278 T7245 AV4655 AV66553 AV65547 T72 T7278 T7278 T7278 T7245 AV6553 AV65547 T72 T728 T728 T788 T788 T741 T7388 T758 T758 T15 T8077 AV5572 T758 T758 T758 T758 T758 T758 T758 T758	7827156 R9847: 9957 T72300 T5 44 AA343653 T7 28 A110639 AA 761277 T74914 18 T40095 K022 440 T71770 T66 68219 W86031 15 R29036 T727 429 T51176 T51 774474 T56068 14 AA308400 AA5 110083 M12075 1009769 AW050 124242 A197083	5 C20925 AV6 8906 T71457 3909 T88070 344603 AF063 T60352 R296 72 T40106 AA 1091 769108 T T69081 T642: 93 T69122 T6 8866 AV65541 8160787 AA314 816074052 AW 199 AA85827 9 A1909761 88	TYOUGH T72565 T70465 T06265 T74407 T85778 TYTHOS T17416 T74165 T06265 T74407 T85778 TYTHOS T17416 T74165 T07465 T07465 T07265 T174167 T1565 T17416 T7416 T7416 T74165 T0627 T6753 T02505 T1565 T17416 T17416 T0627 T6753 T06276 T07416 T07416 T07428 T08275 T0746 T0747 T0747 T0747 T07417 T0747
50	421582 437866	2041_1 44433_2	T6928 AA34 T7047 T7251 T6936 T5374 AA34 AA69 T6763 Al910 AA561 BE07- BE07-	3 (7393) 17240 17278 (74456, 3446563) ARGSAN 1777 2772 27725 77456 77461 (77580) 77467 (77580) 7747 2772 27725 77456 77456 7747 (77580) 77467 (77580) 7767 2772 27725 77456 7747 (77580) 7765 7747 (77580) 7767 2772 2772 2772 2772 (77580) 7767 (77580) 7767 (77580) 7772 2772 2772 2772 (77580) 7767 (77580) 7767 (77580) 7772 2772 2772 (77580) 7767 (77580) 7767 (77580) 7767 (77580) 7767 (77580) 7772 2772 2772 (77580) 7767 (77580)	1827156 R9847: 1957 T72300 T5 14 AA343853 T7 18 A110639 AA 161277 T74914 18 T40095 K022 14 O T71770 T68 168219 W85031 15 R29036 T727 1429 T51176 T51 174474 T56058 14 AA308400 AA5 110083 M12075 1009769 AW056 1377 AW44495 13977 AW44495	5 C20925 AV6 8906 T71457 3909 T88070 344603 AF063 T60352 R296 T60352 R296 1091 T69108 T T69081 T642: 93 T69122 T6 3866 AV65541 BE074052 AW 1590 AA85827 9 AJ909751 BE 94 AJ969751	T70484 T7266 T70465 192607 174407 185778 77756 177214 T7265 177465 192607 174407 185778 77756 177214 T7265 177466 792607 174607 185778 715 77464 3475678 247567 24756 24756 185608 185608 185608 18570 185708 185
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50 55 60 65	437866 451807 TABLE 11 Pkey: Ref: Strand: NL position	8865_1 C Unique nu Sequence Indicates I Indicates r	TE928 A344 T7047 T7251 T6936 T5374 A344 A459 T6783 A910 A456 BE077 BE07 A4156 A4853 A4810 W528 AW45 T678 Thuman christopacouros. The of human christopacouros. The of human christopacouros and human christopacouros	3 779931 77276 772456, AV464553 AV665476 1772 772757 77456 774645 AV464553 AV665476 1772 772757 77456 77456 AV66476 AV67476 77586 7758 AV67476 7758 AV67476 AV	R2716s R9847 987 77290 T989 M AA343853 T7 M AA343853 T7 M B A1110839 AB A1110839 AB B R14005 AB A21096 AB B R14005 AB B R14005 AB B R29056 T727 A28 T51176 T5 T74747 T5008 AA308400 AA T009763 AV056 Z4242 AJ8703 A811830 AA58 Z225 AW8522 AJ827 T (G) numbers.	5 C20525 AV6 9906 T71457 "3909 T88070" 39490 T88070" 39450 T760352 R296 72 T40106 AA 9091 T69108 T T89081 T6422 39 T69122 T6 T89081 T6422 39 T69122 T6 T89081 T6422 39 T69122 T6 T6908 30 AA858277 40 AV605254 1805 A8858278 40 AV605254 1805 A8858278 40 AV605254 1805 A8858278 40 AV605254 1805 A8858278 40 AV605254 40 AV60	TT-0444 T7266 T70465 T08269 T74407 T85778 TT-0746 T71246 T71465 T08269 T74407 T85778 TT-07465 T17246 T74407 T74865 AV6936 N02200 16 T7464 AV645792 AV54468 T08197 T72557 16 T7464 AV645792 AV54468 T08197 T72557 AV5064 AV64590 AV41907 AV54297 AV41948 T72449 T08167 T71238 T08251 AV65644 T04375 Z0 261918 T0213 AV65539 H7459 T74697 4655 T02868 T08131 T08651 T07467 T0797 T14692 Z0 261918 T0213 AV65539 H7459 T06467 T0797 T14692 Z0 261918 T0213 AV65539 H4597 AV5751 T08365 Z0 261918 T0213 AV62539 H4597 AV5751 T08365 Z0 261918 T0213 AV62504 T0647 T0647 T0797 T14692 Z0 261918 T0213 AV62504 T0647 T0647 T0797 T14692 Z0 261918 T0713 AV62504 T0766 T0797 T14692 Z0 261918 T0713 AV65504 T0647 T0667 T0797 T14692 Z0 261918 T0713 AV65504 T0667 T0797 T14692 Z0 261918 T0713 AV6504 T0667 T0797 T14692 Z0 261918 T0713 AV6504 T0677 T0797 T0797 T14409 Z0 261918 T0713 AV6504 T0797 T07

WO 02/086443 PCT/US02/12476

TABLE 12A: Genes Distinguishing Squamous Cell Carolnoma from Other Lung Diseases and Normal Lung

Unique Fos probeset identifier number

10

15

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 95800 probesets on the Ecsi/Nlymetrix Hu03 Genechtp array.

Table 128 show the accession numbers for those Play's labbing Unigensity's for table 12A. For each probased we have labed the gene cluster number from which the oligonactuotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence schizarly using Clustering and Alignment Tools (Dooblat wist, California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" oldura.

Table 12C show the genomic positioning for those Pkey's lecking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also fished.

20	Pkey: ExAcon: Unigenell Unigene 1	Exempla t Unigene	r Accession nu number nene title	nommer manuer umber, Genbank accession number s (including squamous cell carcinomas, adenocarcinom	nae email call c	accinomae acanulos	matous and carrinoid himon	s) divided by the
20	R1:	auorooo.	of normal lunn	eamnlos				
	R2:	Average	of non-malign	ant lung disease samples (including bronchills, emphy-	sema, fibrosis, a	delectasis, asthma)) divided by the average of i	ormai lung samples
~-	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2 4.00		
25	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45 3.26	3.22		
	400666			NM_002425:Homo saplens matrix metallopro	26.47	10.50		
	401780			NM_005557*:Homo saplens keratin 16 (foca Tarnet Exon	10.33	4.61		
	401781			NM 002275°:Homo saplens keratin 15 (KRT1	4.13	2.70		
30	401785 401994			Target Exon	61.84	47.00		
50	402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00		
	404996			Target Exon	1.00	1.00		
	407839	AA045144	Hs.161568	ESTs	173.91	108.00		
~~	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17 1.98	8.00 1.24		
35	408522	Al541214	Hs.46320	Small proline-rich protein SPRK [human,	10.04	1.00		
	410561	BE540255 AL044872	Hs.6994 Hs.77910	Homo sapiens cDNA: FLJ22044 fis, clone H 3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00		
	415091 415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00		
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00		
40	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00		
	417366	BE185289	Hs.1076	small proline-rich protein 18 (cornilin)	8.97	3.27		
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00		
	418678	NM_001327	Hs.87225	cancertestis antigen	1.18	1.10		
45	419121	AA374372	Hs.89626	parathyroid hormone-like hormone Inclin, galactoside-binding, soluble, 7	1.00 3.04	1.25		
43	420783 421773	AI659838 W69233	Hs.99923 Hs.112457	ESTs	1.12	1.14		
	421773	L42583	Hs.334309	keratin 6A	51.83	20.25		
	421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91		
	422158	L10343	Hs.112341	protease Inhibitor 3, skin-derived (SKAL	2.37	1.10		
50	422440	NM_004812	Hs.116724	atdo-keto reductase family 1, member B10	47.53	32.00		
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00 1.00		
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20 10.14	51.00		
	423738	AB002134	Hs.132195	airway trypsin-like protease tumor protein 63 kDa with strong homolog	233.42	68.00		
55	424012 424046	AW368377 AF027866	Hs.137569 Hs.138202	serine (or cysteine) proleinase inhibito	1.00	1.00		
"	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00		
	424834	AK001432	Hs.153408	Homo saplens cDNA FLJ10570 fis, clone NT	56.19	12.00		
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00		
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00		
60	427335	AA448542	Hs.251677	Gantigen 7B	51.83 1.00	4.00 1.00		
	428182	BE386042	Hs.293317	ESTs, Wealdy similar to GGC1_HUMAN G ANT ESTs, Wealdy similar to 2017205A dihydro	1.00	16.00		
	428645	AA431400 AW593206	Hs.98729 Hs.98785	Ksp37 protein	1.00	87.00		
	428748 429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18		
65	429538	BE182592	Hs.11261	small profine-rich protein 2A	4.43	2.90		
-	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00		
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00		
	430890	X54232	Hs.2699	glypican 1	1.58	1.40 28.00		
70	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25 4.49	25.00		
70	431846	BE019924	Hs.271580	uroptakin 18 lymphocyte antigen 6 complex, locus D	1.20	1.09		
	433091	Y12642 AW015415	Hs.3185 Hs.127780	ESTs	40.98	27.00		
	434360 434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00		
	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	1.00	38.00		
75	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00		
	436511	AA721252	Hs.291502		16.76	14.00		
	438403	AA806607	Hs.292206	ESTs	1.00	1.00		
	439285	AL133916		hypothetical protein FLJ20093	46.23	139.00 1.00		
90	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61 1.00	1.00		
80	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm ESTs, Weakly similar to DAP1_HUMAN DEATH	1.00 86.55	11.00		
	439706 440325	AW872527 NM_003812	Hs.59761 Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00		
	441525	AW241867	Hs.127728		1.53	1.42		
	443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00		
85	444378	R41339	Hs.12569	ESTs	1.00	1.00		

	we	02/086	443				PCT/US02/12476
		AF081497 AW885727	Hs.279682 Hs.9914	Rh type C glycoprotein ESTs	1.55 47.24	1.26 24.00	
		AVV865727 Al199268	Hs.19322	Homo saciens, Similar to RIKEN cDNA 2010	28.63	1.00	
-	449003	X76342	Hs.389	a'cohol dehydrogenase 7 (class IV), mu o	1.00	1.00	•
5		AA205847	Hs.23016	G protein-coupled receptor	2.58 25.17	27.00 36.00	
		AW970602 AJ591147	Hs.105421 Hs.61232	ESTs ESTs	13.42	1.00	
		NM_002277	Hs.41696	keratin, hair, acidic,1	1,19	1,27	
		AA534296	Hs.20953	ESTs	24.92	25.00	
10	454098 455601	W27953 Al368680	Hs.292911 Hs.816	ESTs, Highly similar to S60712 band-6-pr SRY (sex determining region Y)-box 2	1.26 206.11	1.11 1.00	
	TABLE 12B						
15	Pkey: CAT number Accession:	r: Gene cluste	probeset iden er number ocession numb				
20	Pkey 439285	CAT Number 47065_1	Al 1339	on 16 N79113 AF086101 N76721 AW950828 AA36401 52 N62351 N59253 AA626243 AJ341407 BE175639	3 AW955684 Al34 AA456968 Al358	6341 A1867454 N54784 918 AA457077	4 AI655270 AI421279 AW014882
25	TABLE 120	;					•
23	Pkey: Ref:	Sequence s	source. The 7	ding to an Eos probeset digit numbers in this column are Genbank Identifier	(GI) numbers. *Da	mham I. et al." refers to	the publication entitled "The DNA
	Strand:	sequence o	If numan caror	nosome 22." Dunham I. et al., Nature (1999) 402:48 n which exons were predicted.	5-45U.		
30	NL position			ions of predicted exons.			
	Pkey	Ref 8118496	Strand Plus	Nt_position 17982-18115.20297-20456			
	400666 401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-2	9567,29706-2976	7,30224-30573	
35	401781	7249190	Minus	R3215-R3435 R3531-R3656 R3740-R3901.R4237-R	4393,84955-8503	7,86290-86814	
	401785	7249190	Minus	165776-165996,166189-166314,166408-166669.	167112-167268,1	67387-167469,168634-	168942
	401994 402075	4153858 8117407	Minus	42904-43124,43211-43336,44607-44763,45199- 121907-122036,122804-122921,124019-124161,	1241,46337-4673 124466 124610 1	12 26872-126076	
	404996	6007890	Plus	37999-38145.38652-38998.39727-39872.40557-4			
40							

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TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung lumors and normal lung. These genes were selected from about 59680 probesets on the Ecol/Higmetrix Hu33 Cenechip array.

Table (38 show the accession numbers for those Pkey's ladeing Unigeneit's for table 13A. For each probased we have listed the gase duster number from which the oligonacticulties were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and niRMAs. These sequences were clustered based on sequence shallow using Custoring and Alignment Tools (Double's vist, Coldand California). The Gerbank accession numbers for sequences comprising each duster are fated in the "Accession" country.

Table 13C show the genomic positioning for those Pkay's lacking Unigene I/Vs and accession numbers in table 13A. For each predicted exon, we have listed the genomic

15	Pkey:										
	ExAccn:										
	Unigenel(): Unige	ne number								
	Unigene 1	ille: Unige	ne gene tile								
00	R1:				nomas, small cell	carcinomas, granulomatous and carcinoid tumors) divided by the					
20		avera	ge of normal l	lung samples	Charale	, etelectasis, asthma) divided by the average of normal lung san					
	R2:	Avera	ige of non-ma	agnantiung disease samples (including oxoricitus, en	physema, uprosis,	, attractasts, assumed divided by the average or normal rang sai					
	Pkey	ExAcon	UnigeneID	Unigene Title	R1	R2					
	408562	AJ436323	Hs.31141	Homo sagiens mRNA for KIAA1568 protein,	1.00	230.00					
25	409031	AA376836	Hs.76728	ESTs	1.00	128.00					
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00					
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00					
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00					
	418819	AA228776	Hs.191721	ESTs	1.00	140.00					
30	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00					
		AA464840	Hs.131987	ESTs	1.00	167.00					
		T89832	Hs.170278	ESTs	1.00	141.00					
		AA453800	Hs.192793	ESTs	1.00	138.00					
		AA488988	Hs.293796	ESTs	1.00	133.00					
35		BE041395	113.230130	ESTs. Weakly similar to unknown protein	23.32	941.00					
,,,	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00					
	431728	NM_007351	He 268107	multimerin	1.00	157.00					
	436532	AA721522	113.200101	gb:nv64h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00					
	437960	AI669586	Hs.222194	ESTs	1.00	147.00					
40		AW169287	Hs.22588	ESTs	1.00	141.00					
70		AW298235	Hs.101689	ESTa	1.00	167.00					
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00					
		H25899	Hs.201591	ESTs	1.00	141.00					
	453636	R67837	Hs. 169872	ESTs	1.00	116.00					
45		Al000341	Hs.220491	ESTS	1.00	192.00					
43		AA031956	MS.220491	gb:zk15e04.s1 Soares_pregnant_ulerus_NbH	1.00	154.00					
	TABLE 13	MB		•							
50				h ma							
30	Pkey:	Unique e ber: Gene clu		dentifier number .							
		: Genbank		imbers							
	Pkey	CAT Num	nber Accessio	10							
55	431089	327825	1 BE0413	95 AA491826 AA621946 AA715980 AA666102							
	436532	421802_	1 AA7215	22 AW975443 T93070							
	TABLE 13	С									
60											
	Pkey: Ref:	Unique n	umber corres	ponding to an Eos probesel	r (GI) numbers. T	Dunham I. el al." refers to the publication entitled "The DNA					
	*****	sequence	e of human ch	romosome 22.* Dunham I. et al., Nature (1999) 402:4	89-495.						
65	Strand: Ni_positio			from which exons were predicted, asilions of predicted exons.							
	Pkey	Ref	Strand	Nt_position							
						405ama 4070770					
70	402075	8117407	Plus	121907-122035,122804-122921,124019-12416	1,124455-124510,	1255/2-1260/5					

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TABLE 14A: Preferred Utility and Subcellular Localization for Polential Lung Disease Targets

Table 14A shows the subcellular localization and penterred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, disp symbolizes diagnosis, an symbolizes small molecule, and CTL symbolizes cytotaxic lymphocytic ligand. These genes were selected from 59500 probesels on the ExctAfymetrix Hu03 Centrolip array.

Table 140 show the accession numbers for those Pkey's lacking UniqueniU's for table 14A. For each probasel we have listed the gene dualer number from which the oligonacleotides were designed. Gene clusters were compiled using sequences derived from Cenhank ESTs and mRMAs. These sequences were dualered based on sequences similarly early Custating and Alignment Tools (Double' Vest, Calisand California). The Cenhank excession numbers for sequences comprising each cluster are listed in the "Accession" clumm. 10

Table 14C show the genomic positioning for those Pkey's tacking Unigene ID's and accession numbers in table 14A. For each predicted exon, we have isled the genomic sequence source used for prediction. Nucleoficial locations of each predicted exon are also fished.

15 Pkay: Unique Eos probeset Identifier number
Eu-Loca: Exemplar Accession number, Genbank accession number
Uniquenel Dit. Uniquen pene title
Prat. Utility: Preferred Utility
Prat.Loc: Preferred Visity

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ACCESSON NAME ACCESSON ACCE		Pkey	ExAcon	UnigeneID	Unigene Title	Pref Utility	Pred. Loc
400791	0.5	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
A07891 A07892 A	25		AA242758	Hs.79136			
April							
Accepted							
			AW580227				
April	30	408908	BE296227				
1,000 1,00							
AGSS20							
AUGUSTO MAIL							
102982 AWAPURD AWAPU							
100995 AMP102384 14.727 Inhibits, beta A (activis A, activis A) 3 diag	35						
40007							
400 401 501382		409956	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a		
4101419 D313422 Example D31442		410001	AB041036	Hs.57771			
412140		410407	X66839	Hs.63287	carbonic anhydrase IX		
417719 AV01616 h. 8.16	40	410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
417719 ANOISE 1.47774 AN		412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rabkines	s.m.	
4.14774 202419 th-7.7274 th-7.7274 th-2.0564			AW016610	Hs.816	ESTs	s.m.	nuclear
41 41 41 42 43 43 43 43 43 43 43					plasminogen activator, urokinase	diag	extracellular
4555 45559 ML,050575 47769 47769 47769 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 47779 47769 4					CDC28 protein kinase 1	s.m.	
HISBOT MAL (1993/25) Ex. To 2009 Control Congression Congression Control Congression Control Congression Control Congression Control Congression Control Congression Congres	45			He 295944		CTL & diag	extracellular
418917 189897 14799 187997 14799 187997 14799	15				serine (or cysteine) proteinase inhibito		secreted
display			1188987		protein tyrosina nhosnhatasa, recontor-t	mAb & s.m.	plasma membrane
17704 MHz,005183 ht.90982 meurotential diag extracellular extrac							extracellular
1477299 USS500 hb. 81134 Market			NM 006183				extracellular
17730B 1987727 his. 81992 GAAO/101 game product a.m. mbb & diag mbb & d	50		1166500				extracellular
17738 BE200984 Hs.2016 Tribute Tribu	50						
117433 8EZ70266 hs. B2128 374 oncoheal triplochast dyrespoilers m/b 14827							
1783 2007.208 the 25962 Dymidylate synthistics s.m. embellators c.m. embellat							olasma membrane
1995 1995				Un 82062	flywiddig cynthalaea		endonlasmic reliculum
HISPIN AUGUSTAT HISPIN AUG	55						
418576 MM_C01327 M.1517279 Camparhasis antique (M*-ESO-1) CTL Camparhasis (M*-ESO	33				G protein counted recentor 39		
419121 AA74727 E.189628 Earnthyroid hormonic-like hommone Annual Part Annu					agreed faction antions (NV ESO.1)		
Add							
60 419193 UBSSSS 9 16.89853 Phil.89853 Cythochrom P460, ubdfamly XOV (Marmly 80 Cythochrom P460, ubdfamly XOV (Marmly 80 Cythochrom P460, ubdfamly XOV (Marmly 80 Cythochrom P460, ubdfamly 80							docus membrane
Higher Authority Bernard Higher	60						
149225 AW147011 Nz.288433 neurotinin Nz.28843	oo				ameli ladvelble evideline cultivarily P (C)		
1952 USSSSS 195915 195972 195972 195973 195							
A		419235					
Age							
A A A A A A	65						
Act	05						
A							
22552 AF005962 1:107510 1:107511 12:107511 1							
70 42/1753 EE3144229 Hs.107911 ATP-binding casesiles, sub-tamily 8 (LDIO*) mvhb a s.m. plantam membrane plantam plantam plan							
ATP-binding cases line; sub-family C (CFT) m whò & a.m. plasma membrane (2210) \$75255 h. 14.73 14.	70				secreted inzzied-related protein 4		
March Marc	/υ				ATP-binding cassette, sub-family 8 (ML/RV		
A A A A A A A A A A							
ACCOUNT ACCO		422109					
75 42223 AW141/307 In. 11.4131 CDC/ds (cold dividion cycle 45, Scorevis s.m. nocker child colored 4.418621 Lac 4.418624 La							
422424 A188431 14.296538 procubin differentiation factor diag entracibilitar 42269 AM049770 11.1973							
Address	75				CDC45 (cell division cycle 45, S.cerevis		
ACCOUNTS NATIONARY National Processing Purpose Account National Purpose Account Ac		422424	AJ186431				
422867 1.25127 151, 1584 entitlage ofigoments matrix protein (see day entitlage) entitlage ofigoments matrix protein (see day entitlage) entitlage office of the see day entitlage of the see day entities of the see day entitlage of the		422765					
80 422996 BES-M972 Hs. 12297 ECT2 parktin Eighfeidel del transformi CTL & s.m. 423543 AM9599908 Hs. 1699 Hs. 1695 Hs.							
423534 AM959039 1s. 1690 hepsin-ki-hirding growth factor binding or mAb & disg & s.m. secreted m4b & disg & s.m. s.m.							extracellular
42367.3 BE03056.4 Hs. 1803.4 mash: metallogrollehase 12 (macrophage mAb & diag & s.m. secreted 42361 D13666 Hs. 1803.48 periostin (OSF-2os) mAb & diag secreted mAb & diag secreted diag	80	422956	BE545072	Hs.122579			
42367.3 BE03056.4 Hs. 1803.4 mash: metallogrollehase 12 (macrophage mAb & diag & s.m. secreted 42361 D13666 Hs. 1803.48 periostin (OSF-2os) mAb & diag secreted mAb & diag secreted diag		423634			heparin-binding growth factor binding pr		
423961 D13666 Hs.136348 periostin (OSF-2os) mAb & diag extracellular 424046 AF027866 Hs.138202 serine (or cysteine) proteinase inhibito diag secreted					matrix metalloproteinase 12 (macrophage		
424046 AF027866 Hs. 138202 serine (or cysteine) proteinase inhibito diag secreted			D13666	Hs.136348	periostin (OSF-2os)		
					serine (or cysteine) proteinase inhibito	dlag	
	85			Hs.146329		s.m.	nuclear

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	w	O 02/086	443			
	424502	AF242388	Hs.149585	tengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelafinase B	diag	extracellular secreted
5	425247	NM_005940 U63630	Hs.155324 Hs.155637	matrix metalloproteinase 11 (stromelysin protein kinase, DNA-activated, catalytic	mAb & diag & s.m. s.m.	cytoplasmic
3	425322 425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monocxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
10	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag CTL & s.m.	secreted nuclear
	426427 426514	M86699 BE616633	Hs.169840 Hs.170195	TTK protein kinase bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251877	G antigen 7B	CIL	cytoplasmic
	427747	AW411425	Hs. 180655	serine/threonine kinase 12	s.m.	cytoplasmic
15	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matritysin,	mAb & dlag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479 428484	Y00272 AF104032	Hs.334562 Hs.184601	cell division cycle 2, G1 to S and G2 to solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
20	428664	AK001666	Hs.189095	similar to SALL1 (sai (Drosophila)-like	CTL & s.m.	nuclear
20	428698	AA852773	Hs.334838	KIAA 1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochodria*
0.0	428969	AF120274	Hs. 194689	artemin	diag mAb & s.m.	extracellular plasma membrane
25	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263 429547	AA019004 AW009166	Hs.198396 Hs.99376	ATP-binding cassette, sub-family A (ABC1 ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
30	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515 431846	NM_012152 BE019924	Hs.258583 Hs.271580	endothelial differentiation, lysophospha uroplakin 1B	mAb & s.m. mAb & diag	piasma membrane piasma membrane
	431846	X63629	Hs.271580 Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
35	432201	Al538613 ·	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
55	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	diag	secreted
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	s.m.	cytoplasm
40	437016	AU076916	Hs.5398 Hs.69517	guanine monphosphate synthetase differentially expressed in Fanconi's an	S.M. CTL	ER
40	437044 437789	AL035864 AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	mAb & s.m.	piasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	plasma membrane
45	439606	W79123 BE246502	Hs.58561 Hs.9598	G protein-coupled receptor 87 sema domain, Immunoglobulin domain (Ig),	mAb & s.m. mAb & s.m.	plasma membrane
	439738 440086	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	S.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. carevistae) homolog (E coli Re	s.m.	
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
50	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL dieg	extracellular
	443859 444006	NM_013409 BE395085	Hs.9914 Hs.10086	folkstatin type I transmembrane prolein Fn14	mAb	plasma membrane
	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
55	444381	BE387335	Hs.283713	ESTs, Weakly similar to \$64054 hypotheti	diag	secreted
	444781	NM_014400	Hs.11950	GPI-enchored metastasis-associated prote	mAb & dlag	plasma membrane
	445537	AJ245871	Hs.12844	EGF-tike-domain, multiple 6	mAb & diag	secreted secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag diag	extracellular
60	446921 447033	AB012113 Al357412	Hs.16530 Hs.157601	small Inducible cytokine subfamily A (Cy ESTs	CTL & dlag	secreted
00	447342	Al199268	Hs.19322	Homo saplens, Similar to RIKEN cDNA 2010	CTL	
	448243	AW369771	Hs.52620	Integrin, beta 8	mAb & s.m	plasma membrane
	448844	Al581519	Hs.177164	ESTs	mAb & s.m.	
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose Induc	mAb	plasma membrana
65	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm plasma membrane
	450001	NM_001044 AA009647	Hs.406	solule carrier family 6 (neurotransmitte a disintegrin and metalloproteinase doma	mAb & s.m. mAb & dieg & s.m.	plasma membrane plasma membrane
	450375 450701	H39960	Hs.288467	hypothetical protein XP_098151 (faudino-	mAb & diag & suit.	plasma membrana
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
70	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo saplens cDNA FLJ11041 fis, clone PL	diag	
	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced pro	dlag mAb	extracellular plasma membrane
	452747	BE153855	Hs.61460	tg superfamily receptor LNIR	mAb CTL	piasma memorane nuclear
75	452838 453968	U65011 AA847843	Hs.30743 Hs.62711	preferentially expressed antigen in mela High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
15	457489		Hs.127179	cryptic gene	diag	secreted

TABLE 148

80 Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

Pkey CAT Number Accessio

	wo	02/086443		PCT/US02/12476
	414883	15024_1	AA08243	D AA926959 W76521 W24270 W21526 AA937172 BE267636 H83186 AA46990 N86395 AA001348 BE535736 AA001745 BE566245 5 H72525 H73757 N8796 W80056 H7876 BE559086 W04339 R98127 T55938 BE279271 AW96074 T29812 AA476873 BE297387 J A4177048 NM, 001826 X54941 BE314366 AA908783 JA719075 BE270172 BE259819 AA88955 A1204630 W25234 JW35150
5			AA87203 R75953 A AW61300 N95210 A	SW W72505 1955/0 AL42291 1958(0 AL42291 1958(0 AL522) 1958(0 AL522) 1955(0 AL522) 1955
10			A1494230 A1494211 AA95434 H03266 E	AASSABA ALSSENSE ALSSENSE AASSEZS AARSEZS ALGESSE ALGE
15	450375	83327_1	AA00964	R9/47/0 A/02275 T77551 A011952 H82566 H88573 A/285572 7 A/131254 A/37223 A/195240 SH5940 H5940 A/19526 A/19573 A/285572 3 H03231 H59605 H01642 A/852876 A/1 13758 A/626915 A/746952 A/151014 A/099554 R69067
20	TABLE 140			
20	Pkey: Ref:	Sequence sou	nce. The 7 d	ling to an Eos probeset igit numbers In this column are Genbank Identifier (GI) numbers. "Ounham I. et al." refers to the publication entitled "The DNA socome 2.2" Dunham I. et al., Nature (1999) 402-469-495.
25	Strand: Nt_position:	Indicates DNA	strand from	which exons were predicted. ns of predicted exons.
	Pkey	Ref :	Strand	NL position
30	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 15A: information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAcon, UnigenelD, and Unigene Title for all of the sequences in Table 16.

5 Table 159 show the accession numbers for those Pixer's lacking UniquesiD's for table 15A. For each probesed we have listed the gene cluster number from which the ofigurusdeotices were designed. Censor clusters were complied using sequences defined from Cenhank ESTs and mRNAs. These sequences were clustered based on sequence affinisity using Custating and Alignment Tools (Dootlef wisk, Osatinal California). The Genthank accession numbers for expenses comprising each cluster are listed in the "Accession" obtain.

10 Table 15C show the genomic positioning for those Pkey's backing Uniques ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also Island.

15 Seq ID No: Sequence ID number Unique Eap probasel deriffier number Exchorn: Exchorn: Exemplar Accession number, Genbank accession number Unique ITEL Unique number gene title

20	Seq ID No:	Pkey	ExAcon	UnigenaiD	Unigene Title
	Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase iX
	Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
	Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurolensin
25	Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No. 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2 S100 calcium-binding protein A2
20	Seq ID No: 15 & 16	407788	BE514982	Hs.38991	hypothetical protein FLJ20093
30	Seq ID No: 17 & 18	439285	AL133916	Hs.75517	iaminin, beta 3 (niceln (125kD), kalinin
	Seq ID No: 19 & 20	413753 120486	U17760 AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
	Seq ID No: 21 & 22	425650		Hs.1925	desmodeln 3 (pemphigus vulgaris antigen
	Seq ID No: 23 & 24 Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
35	Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metallogroleinase 12 (macrophage
55	Seq ID No: 29 & 30	452838	U65011	Hs.30743	proferentially expressed antigen in mela
	Seg ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocoliln 3
	Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito
40	Seq ID No: 37 & 38	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq iD No: 41 & 42	431846	BE019924	Hs.271580	uroplakin 1B hypothetical protein MGC4816
	Seq ID No: 43 & 44	418830	BE513731	Hs.88959 Hs.139322	small proline-rich protein 3
45	Seq ID No: 45 & 46	424098 443648	AF077374 Al085377	Hs.143610	ESTs
43	Seq ID No: 47 & 48	311034	BE567130	Hs.311369	ESTs, Highly similar to NKGD_HUMAN NKG2-
	Seq ID No: 49 Seq ID No: 50 & 51	408522	Al541214	Hs.48320	Small proline-rich protein SPRK [human,
	Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 54 & 55	435505	AF200492	Hs.211238	Interleukin-1 homolog 1
50	Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)
	Seq iD No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
	Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
	Seq iD No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A solute carrier family 6 (neurotransmitte
55	Seq ID No: 66 & 67	448733	NM_005629	Hs.187958 Hs.239	forkhead box M1
	Seq ID No: 68 & 69	444371 444371	BE540274 BE540274	Hs.239	forkhead box M1
	Seq iD No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 72 & 73 Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
60	Seq ID No: 76 & 77	422168	AA586894	Hs.112408	\$100 calcium-binding projein A7 (psorias
00	Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
	Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
	Seg ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
65	Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cattonic amino
	Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq iD No: 90 & 91	417389	BE260964	Hs.82045 Hs.1690	midkine (neurite growth-promoting factor heparin-binding growth factor binding pr
	Seq ID No: 92 & 93	423634	AW959908	Hs. 82237	ataxia-telanolectasia group D-associated
70	Seq ID No: 94 & 95	417515 441362	L24203 BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
70	Seq ID No: 96 & 97	425322	U63630	Hs.155637	protein kinase. DNA-activated, catalytic
	Seq ID No: 98 & 99 Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
	Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq iD No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
75	Seg ID No: 106 & 107	417542	J04129	Hs.82269	progestagen-associated endometrial prote
	Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratifin
	Seq iD No: 110 & 111	418004	U37519	Hs.87539	aldehyda dehydrogenase 3 family, member
	Seq iD No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
0.0	Seq iD No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
80	Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m guanine monphosphate synthetase
	Seq ID No: 117 & 118	437016	AU076916 BE613348	Hs.5398 Hs.211579	melanoma cell adhesion molecule
	Seq iD No: 119 & 120	449230 446989	AK001898	Hs.16740	hypothetical protein FLJ11036
	Seq ID No: 121 & 122 Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
85	Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix motalioproteinase 9 (geletinase B
33	OOQ 10 140. 120 @ 120	-24001			

	WO 02/086	443			
	Seq ID No: 127 & 128	414430	Al346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130 Seq ID No: 131 & 132	418462 100668	8E001596 L05424	Hs.85266 Hs.169610	Integrin, beta 4 CD44 antigen (homing function and Indian
	Seq ID No: 131 & 132 Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding grotein 1
5	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 137 & 138 Seq ID No: 139 & 140	418478 418478	U38945	Hs.1174 Hs.1174	cyclin-dependent kinase inhibitor 2A (me cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ 10540
10	Seq ID No: 145 & 146	422765 436481	AW409701 AA379597	Hs.1578 Hs.5199	bacutovirat IAP repeat-containing 5 (sur HSPC150 protein similar to ublquitin-con
	Seq ID No: 147 & 148 Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
15	Seq ID No: 153 & 154	453884 453884	AA355925 AA355925	Hs.36232 Hs.36232	KIAA0186 gene product KIAA0186 gene product
13	Seq ID No: 155 & 156 Seg ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Sea ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877 413129	AF292100	Hs.104613	NM_005365:Homo sapiens melanoma antigen, RP42 homolog
20	Seq ID No: 163 & 164 Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
	Sep ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 169 & 170	416819 451320	U77735 AW118072	Hs.80205	pim-2 oncogene diacylglycerol kinase, zeta (104kD)
	Seq ID No: 171 & 172 Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
25	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
	Seq ID No: 177 & 178	425397 415817	J04088 U88967	Hs.158346 Hs.78867	topolsomerase (DNA) II alpha (170kD) protein tyrosine phosphatase, receptor-t
	Seq ID No: 179 & 180 Seq ID No: 181 & 182	415817	U88967	Hs.78867	omtein tyrosine phosphalase, receptor-t
	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
30	Seq ID No: 185 & 186	415817 415817	U88967 U88967	Hs.78867 Hs.78867	protein tyrosine phosphatase, receptor-t protein tyrosine phosphatase, receptor-t
	Seq ID No: 187 & 188 Seq ID No: 189 & 190	419121	AA374372	Hs.89628	parathyrold hormone-like hormone
	Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
35	Seq ID No: 193 & 194 Seq ID No: 195 & 196	421817 430393	AF146074 BE185030	Hs.108660 Hs.241305	ATP-binding cassette, sub-family C (CFTR estrogen-responsive B box protein
33	Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaete-scute complex (Orosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin I precursor
	Seq ID No: 201 & 202 Seq ID No: 203 & 204	102963 100576	X02404 X00356	Hs.274534 Hs.37058	calcitonin-related polypeptide, beta calcitonin/calcitonin-related polypeptid
40	Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	Seg ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like cancerflestis antigen (NY-ESO-1)
	Seq ID No: 209 & 210 Seq ID No: 211 & 212	418678 418678	NM_001327 NM_001327	Hs.167379 Hs.167379	cancer/testis antigen (NY-ESO-1)
	Sea ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecartex: lissencephaly, X-linked (d
45	Sea ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weathy similar to GGC1_HUMAN G ANT
	Seq ID No: 217 & 218 Seq ID No: 219 & 220	427335 409420	AA448542 , Z15008	Hs.251677 Hs.54451	Gantigen 78 laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II
50	Seq ID No: 223 & 224	438956 404440	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9 NM 021048:Homo sapiens melanoma antigen,
30	Seq ID No: 225 & 226 Seq ID No: 227 & 228	415669	NM 005025	Hs.78589	serine (or cysteine) proteinase inhibito
	Sec ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
	Seq ID No: 231 & 232	320843 429065	BE069288 AI753247	Hs.34744 Hs.29643	Homo sapiens mRNA; cDNA DKFZp547C136 (fr Homo sapiens cDNA FLJ13103 fls, clone NT
55	Seq ID No: 233 Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
	Seg ID No: 236 & 237	330495	1147924	Hs.71642	guanine nucleotide binding protein (G pr
	Seq ID No: 238	413573 428479	AI733859 Y00272	Hs.149089 Hs.334562	ESTs cell division cycle 2, G1 to S and G2 to
	Seq ID No: 239 & 240 Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1 Homo saplens clone N11 NTera2D1 teratoca
	Seq ID No: 245 Seq ID No: 246 & 247	437915 441553	Al637993 AA281219	Hs.202312 Hs.121298	FSTs
	Sen ID No: 248 & 249	331692	A1683487	Hs. 152213	wingless-type MMTV integration site fami
	Sea ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein CDC45 (cell division cycle 45, S.cerevis
65	Seq ID No: 252 & 253 Seq ID No: 254 & 255	422283 448357	AW411307 N20169	Hs.114311 Hs.108923	RAB38, member RAS oncogene family
	Sen ID No: 256 & 257	446292	AFC81497	Hs.279682	Rh type C glycoprotein
	Seq ID No: 258 & 259	416209	AA236776 AF053306	Hs.79078 Hs.36708	MAD2 (mitotic arrest deficient, yeast, h budding uninhibited by benzimidazoles 1
70	Seq ID No: 260 & 261 Seq ID No: 262 & 263	453922 424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito
,,,	Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 266 & 267	429228 409757	Al553633 NM_001898	Hs.326447 Hs.123114	ESTs cystatin SN
	Seq ID No: 268 & 269 Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
75	Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
	Seq ID No: 274 & 275	428969 428969	AF120274 AF120274	Hs.194689 Hs.194689	artemin artemin
	Seq ID No: 276 & 277 Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
	Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
80	Seq ID No: 282	407137	T97307 AA648459	Hs.335951	gb:ye53h05.s1 Soares fetal liver spleen hypothetical protein AF301222
	Seq ID No: 283 & 284 Seq ID No: 285 & 286	412723 450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Sea ID No: 267 & 268	405770			NM 002362:Homo sapiens melanoma antigen,
85	Seq ID No: 289 & 290	439453 414774	BE264974 X02419	Hs.6566 Hs.77274	thyroid hormone receptor Interactor 13 plasminogen activator, urokinase
63	Seq ID No: 291 & 292	414//4	V05418	110.11214	producing and additional and an arrange

	WO 02/086				
	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 297 & 298	437789	Al581344	Hs.127812	ESTs, Wealdy similar to T17330 hypotheti
-	Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
5	Seq ID No: 301 & 302	437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Sea ID No: 303 & 304	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso NM_022342:Homo sapiens kinesin protein 9
	Seq ID No: 307 & 308	403478			NM_022342:Horno sapiens kinesin protein 9
	Seq ID No: 309	441525	AW241867	Hs.127728	ESIS
10	Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presentlins associated rhombold-like pro
	Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
15	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidaling monooxyg
	Seg ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
	Seq ID No. 326 & 327	403329			unnamed protein product (Homo sapiens)
	Seq ID No: 328 & 329	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.
20	Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to \$41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
	Sea ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
25	Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
20	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease Inhibitor 3, skin-derived (SKAL
30	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
	Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372 D86407	Hs.89626 Hs.54481	parathyroid hormone-like hormone low density lipoprotein receptor-related
	Seq ID No: 356 & 357	409459		HS.04481	endogenous retroviral protease
35	Seq ID No: 358 & 359	330493 417866	M27826 AW067903	Hs.82772	collagen, type XI, alpha 1
33	Seq ID No: 360 & 361				SRY (sex determining region Y)-box 4
	Seq ID No: 362 & 363	418113	Al272141	Hs.83484 Hs.5398	guanine monphosphate synthetase
	Seq ID No: 364 & 365	437016	AU076916	Hs.252587	pitultary tumor-transforming 1
	Seq ID No: 366 & 367	429612 440704	AF062649 M69241	Hs.162	Insulin-like growth factor binding prote
40	Seq ID No: 368 & 369 Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
40		431565	AF161470	Hs.260622	butyrate-Induced transcript 1
	Seq ID No: 372 & 373 Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (comifin)
	Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
45	Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,
	Sea ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
50	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 394 & 395	418738	AW388533	Hs.6682	solute carrier family 7, (cationic amino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
55	Seq ID No: 400 & 401	423961	D13666	Hs.136348	periostin (OSF-2os)
	Seq ID No: 402 & 403	414812	X72755	Hs.77367	monokine induced by gamma interferon
	Seq ID No: 404 & 405	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq 1D No: 406 & 407	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
60	Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Wealdy similar to S64054 hypotheti
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adlican
	Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
65	Seq ID No: 420 & 421	-450098	W27249	Hs.8109	hypothetical protein FLJ21080
	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	lg superfamily receptor LNIR
	Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
70	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	starviocalcin 2
70	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324 Hs.298241	matrix metalloproteinase 11 (stromelysin
	Seq ID No: 432 & 433	432201	AI538613	HS.238241	Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899 Hs.323733	ESTs; hypothetical protein for IMAGE:447 gap function protein, beta 2, 26kD (conn
75	Seq ID No: 438 & 439	431211	M86849	Hs.323733 Hs.157601	ESTs
75	Seq ID No: 440 & 441	447033	Al357412		
	Seq ID No: 442 & 443	447033	Al357412	Hs.157601	ESTs ESTs
	Seq ID No: 444 & 445	447033	Al357412	Hs.157601 Hs.333893	
	Seq ID No: 446 & 447	115522 410418	BE614387 D31382	Hs.63325	c-Myc target JPO1 transmembrane proteaso, serine 4
80	Seq ID No: 448 & 449 Seq ID No: 450 & 451	410418	D31382 AB033025	Hs.50081	Hypothetical protein XP 051880 MIAA119
80	Seq ID No: 450 & 451 Seq ID No: 452 & 453	409041	AB033025 AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119 Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
	Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrilin 2 (congenital contractural ara
85	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP anlagon
33	OCQ 10 110. 400 tt 401				

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	W O 02/080				
	Seq ID No: 462 & 463 Seq ID No: 464 & 465	437852 402075	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa ENSP00000251056*:Plasma membrane calcium
	Seq ID No: 466 & 467	421110	AJ250717	Hs.1355	cathepsin E
_	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
5	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282 425852	AF019225 AK001504	Hs.114309 Hs.159651	apolipoprotein L death receptor 6, TNF superfamily member
	Seq ID No: 476 & 477	425852 439738	BE246502	Hs. 159651 Hs. 9598	sema domain, immunoglobulin domain (Ig),
10	Seq ID No: 478 & 479	427747	AW411425	Hs.180655	serine/threonine kinase 12
10	Seq ID No: 480 & 481 Seq ID No: 482 & 483	420281	Al623693	Hs.323494	Predicted cation efflux nump
	Seq ID No: 484 & 485	405932	7402000		C15000305:gi 3806122 gb AAC69198.1 (AF0
	Seq ID No: 486 & 487	405932			C15000305:glj3805122[gb]AAC69198.1] (AFU
	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
15	Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist
	Sea ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4 KAA0877 protein
20	Seg ID No: 498 & 499	444471 413063	AB020684 AL035737	Hs.11217 Hs.75184	chitinase 3-like 1 (cartilage glycoprote
20	Seq ID No: 500 & 501	433800	AI034361	Hs.135150	lang type-I cell membrane-associated gly
	Seq ID No: 502 & 503 Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM 007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
25	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80962	neurotensin
	Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
30	Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 522 & 523	425650 423673	NM_001944 BE003054	Hs.1925 Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 524 & 525	418663	AK001100	Hs.41690	desmocallin 3
	Seq ID No: 526 & 527 Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
55	Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uropiakh 1B
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protesse inhibitor 3, skin-derived (SKAL
40	Sea ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
40	Seq ID No: 540 & 541	437044 428484	AL035864 AF104032	Hs.69517 Hs.184601	differentially expressed in Fanconi's an solute carrier family 7 (cationic amino
	Seq ID No: 542 & 543	428484 429211	AF052693	Hs.198249	gap junction protein, bela 5 (connexin 3
	Seq ID No: 544 & 545 Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connextn 3
45	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progestagen-associated endometrial prole
7.5	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
50	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	Integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762 Hs.58581	hypoxla-inducible protein 2 · G protein-coupled receptor 87
	Seq ID No: 564 & 565	439606 404877	W79123	ns.3030 i	NM 005365:Homo saptens melenoma antigen,
	Seq ID No: 566 & 567	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
55	Seq ID No: 568 & 569 Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaturonan synthase 3
55	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Sea ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
	Sea ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074 NM_001327	Hs.108660 Hs.167379	ATP-binding cassette, sub-family C (CFTR cancer/testis antigen (NY-ESO-1)
	Seq ID No: 586 & 587	418678		Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589	418678 409420	NM_001327 Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
05	Seq ID No: 590 & 591 Seq ID No: 592 & 593	332180	AF134160	Hs.7327	daudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Sea ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor.
	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
70	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	arternia
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 608 & 609	428969	AF120274	Hs.194689 Hs.288467	artemin hypothetical protein XP_098151 (leucine-
75	Seq ID No: 610 & 611	450701 450701	H39960 H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701 414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 614 & 615 Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
	Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocolin 2
80	Seq ID No: 620 & 621	457489	Al693815	Hs.127179	cryptic gene
30	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	FSTs
	Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreading antig
	Sea ID No: 626 & 627	407242	M18728		oh-Human conspecific crossreacting actio
	Seg ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting antig
85	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type I transmembrane protein Fn14

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	wo	02/0864	143			PCT/US02	/12476
	Seq ID No: 6 Sea ID No: 6	632 & 633 634 & 635	429597 422109	NM_003816 S73265	Hs.2442 Hs.1473	a disintegrin and metallioproteinase doma gastrin-releasing peolide	
	Seq ID No: 6		419235	AW470411	Hs.288433	neurotrimin	
5	Seq ID No: 6	638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose Induc	
2	Seq ID No: 6	540 & 641	419216	AU076718	Hs. 164021	small inducible cytokine subfamily B (Cy	
	Seq ID No: 6		431462 448243	AW583672 AW369771	Hs.256311 Hs.52620	granin-like neuroendoorine peptide precu Integrin, beta 8	
	Seq ID No: 6 Seq ID No: 6	644 & 645	426427	M86699	Hs.169840	TTK protein kinase	
	Seq ID No: 6		445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	
10	Seq ID No:		422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	
10	Seq ID No:	652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product	
	Seq ID No:		446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	
	Seg ID No: 6		453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	
	Seq ID No: 1	658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (asteogenic	
15	Seq ID No:		425776	U25128	Hs.159499	parathyroid hormone receptor 2	
	Seq ID No:		425776	U25128	Hs.159499	parathyroid hormone receptor 2	
	Seq ID No:		431515 419452	NM_012152 U33635	Hs.258583 Hs.90572	endothelial differentiation, lysophospha PTK7 protein lyrosine kinase 7	
	Seq ID No:		432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	
20	Seq ID No:	670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	
20	Seq ID No:	672 & 673	432653	N62096	Hs.293186	ESTs, Weakly similar to JC7328 amino acl	
	Seq ID No:	674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	
	Seq ID No:	676 & 677	410001	AB041036	Hs,57771	kallikrein 11	
25	Seq ID No:		426501	AW043782	Hs.293616	ESTs	
25	Seq ID No:		408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	
	Seq ID No:		445413 422424	AA151342 AI186431	Hs.12677 Hs.296638	CGI-147 prolein prostate differentiation factor	
	Seq ID No:		428330	L22524	Hs.2256	matrix metalloproleinase 7 (matrilysin,	
	Sea ID No:	688 A 689	420610	AI683183	Hs.99348	distal-less homeo box 5	
30	0041011111			,			
	TABLE 15B						
	Pkey:	Unique Eo	s probesel i	dentifier number			
	CAT numbe	r: Gene dust	er number				
35	Accession:	Genbank a	ocession nu	mbers			
	Pkey	CAT Numb	or Acce	ession			
	309931	AW341683					
	330493	33264_5	M27	826 R78416 AA3	07645 AW957879	9 AW957800 AA633529 H03662	
40	439285	47065_1	AL13	33916 N79113 A	-086101 N76721 A	AW950828 AA364013 AW955684 Al346341 Al867454 N54784 Al655270 Al421279 AW0	14882
			AA7	75552 N62351 N	59253 AA626243	Al341407 BE 175639 AA456968 Al358918 AA457077	
	450375	83327_1	AAOO	09647 AA131254	AA374293 AW95	54405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 AB52876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067	HU4021 HU1532
	451320	86576_1	AMI	18072 41631982	115734 A 22241	95 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T0351:	7 R88265
45	431320	00070_1	Al12	4088 AA224388	AI084316 AI3546	66 T33652 AI 140719 AI 720211 T03490 AI 372637 T15415 AW 205836 AA 630384 T03515	T33230
			AA01	17131 AA443303	T33623 Al22255	6 T33511 T33785 AI419606 D55612	
	TABLE 15C						
50						•	
	Pkey:	Unique nur	nber corres	ponding to an Ed	s probeset	O A List 10 COn	n DNA
	Ref:	Sequence	source. The	e 7 digit numbers	in this column an	 Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "Th Nature (1999) 402:489-495. 	IS DITA
	Strand:	sequence o	or numan cr	romosome 22.	were predicted.	remute (1999) 402.409-495.	
55	Nt position:	Indicates n	ucleotide oc	sitions of predic	ed exons.		
			остольно р				
	Pkey	Ref	Strand	Nt_position			
	402075	8117407	Plus			921,124019-124161,124455-124610,125672-126076	
60	403329	8518120	Plus	96450-965			
60	403478	9958258	Plus	116458-11			
	404440 404877	7528051 1519284	Plus Plus	80430-815 1095-2107	01		
	404877	2735037	Plus	61057-620			
	405770	7767812	Minus	123525-12			
65	*****						

Table 16

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001216
Coding sequence: 43..1422

-	couring acde						
		11	21	31	41	51	
	†	1.	î.	1	7.	ĩ*	
	<u> </u>	ACCGTGTGCT	L	!	I management	2000000000	60
10	GCCCGTACAC	ACCUTGIGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCIGIGCCCC	120
IU	AGCCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCCC	240
	AGTGAAGAGG	ATTCACCCAG	AGAGGAGGAT	CCACCCGGAG	AGGAGGATCT	ACCTGGAGAG	300
	GAGGATCTAC	CTGGAGAGGA	GGATCTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
15	TOTOTALACT	TAGAGGATCT	ACCTACTOTT	GAGGCTCCTG	GAGATCCTCA	AGAACCCCAG	420
	AATAATGCCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGCGAC	480
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGGGTGTC	CCCAGCCTGC	GOGGGCCGCT	TCCAGTCCCC	GGTGGATATC	540
	OCCCCCTGGC	TOGCOGCCTT	OTCOCCCCCCCC	CENTRACTOR	TOGRACTOCT	GGGCTTCCAG	600
	COCCCCCAOC	TCCCAGAACT	CIGCCCGGCC	A A CR A TOCOCCO	ACACTOTOCA	ACTOACCCTG	660
20	CICCOGCOGC	TCCCAGAACI	GCGCC1GCGC	MUNITORIC	ACCOCCOCCOCCO	CCACCOCCAT	720
20	CCTCCTGGGC	TAGAGATGGC GGGCTGCAGG	TCTGGGTCCC	GGGCGGGAGT	ACCUGGCTCT	GCAGCIGCAI	780
	CTGCACTGGG	GGGCTGCAGG	TOGTCCGGGC	TOUGAGCACA	CTGTGGAAGG	CCACCGTTTC	
	CCTGCCGAGA	TCCACGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCTTG	840
	GGGCGCCCGG	GAGGCCTGGC	CCTCTTCGCC	GCCTTTCTGG	AGGAGGGCCC	GGAAGAAAAC	900
	AGTGCCTATG	AGCAGTTGCT	GTCTCGCTTG	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
25	CAGGTCCCAG	GACTGGACAT CTCTGACTAC	ATCTGCACTC	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
	TATGAGGGGT	CTCTGACTAC	ACCIGCCCTGT	GCCCAGGGTG	TCATCTGGAC	TGTGTTTAAC	1080
	CAGACAGTGA	TGCTGAGTGC	TARGUAGUTO	CACACCCTCT	CTGACACCCT	GTGGGGACCT	1140
	action and a	GGCTACAGCT	CARCEMCCCA	COCACGCACC	CTTTTCAATTCC	GCGAGTGATT	1200
	GGTGACTCTC	GGCIACAGCI	ACTUAL CACO	ACTROCTOCCO	CTTTCACCC	ACTOCACCTG	1260
30	GAGGCCTCCT	TCCCTGCTGG	MGIGGMCAGC	AGICCICGGG	mpococomcom	MATCCAGCTO.	1320
50	AATTCCTGCC	TGGCTGCTGG CGTTCCTTGT	TGACATCCIA	GCCCIGGIII	TIGGCCICCI	TITIOCIOIC	1380
	ACCAGCGTCG	CGTTCCTTGT	GCAGATGAGA	AGGCAGCACA	GAAGGGGAAC	CAAAGGGGT	
	GTGAGCTACC	GCCCAGCAGA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGGAGAA	1440
	TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGGTA	ACTGTCCTGT	CCTGCTCATT	1500
	ATGCCACTTC	CTTTTAACTG	CCAAGAAATT	TTTTAAAATA	ATATTTATA	AT	
35							
	Seg ID NO:	2 Protein s	seguence:				
	Protein Ac	cession #: 2	IP 001207				
	1	11	21	31	41	51	
40	†	î	i*	i	î"	ī	
40		PLLIPAPAPG		1	DOMONDON C	OGGCGERRANT	60
	MAPLCPSPWL	SPREEDPPGE	LIVQUUSUU	LLMPVNPQKL	PRINCEDSPIN	GOODO TOTAL	120
							180
	DPQEPQNNAH	RDKEGDDQSH	WRYGGDPPWP	RVSPACAGRF	QSPVDIRPQL	AAFCPALRPL	
	ELLGFQLPPL	PELRLRNNIGH	SVQLTLPPGL	EMALGPGREY	RALQLHLHWG	AAGRPGSEHT	240
45	VEGHRFPAEI	HVVHLSTAFA	RVDEALGRPG	GLAVLAAFLE	EGPEENSAYE	QLLSRLEEIA	300
	EEGSETQVPG	LDISALLPSD	PSRYFOYEGS	LTTPPCAQGV	IWTVFNQTVM	LSAKQLHTLS	360
	DTLWGPGDSR	LOIMPRATOR	THOMPTONON			BACDITALUE	420
					ALL VOLUCE	JOIOD ALDERY	420
		FLVQMRRQHR			REI TOMOCE	JOIGE ALIGNATURE TO	420
50	GLLPAVTSVA	FLVQMRRQHR	RGTKGGVSYR		Aut vgmtocu	Augumut	420
50	GLLFAVTSVA Seq ID NO:	FLVQMRRQHR 3 DNA seque	RGTKGGVSYR ence	PAEVAETGA	Aur Volkocu	AND ADDRESS	420
50	GLLPAVTSVA Seq ID NO: Nucleic Ac	FLVQMRRQHR 3 DNA seque id Accession	RGTKGGVSYR ence n #: BC0139	PAEVAETGA	Ans Vonco	AND ADDRESS	420
50	GLLPAVTSVA Seq ID NO: Nucleic Ac	FLVQMRRQHR 3 DNA seque	RGTKGGVSYR ence n #: BC0139	PAEVAETGA	Aus VQuitoca		
50	GLLPAVTSVA Seq ID NO: Nucleic Ac	FLVQMRRQHR 3 DNA seque id Accession uence: 438-	RGTKGGVSYR ence n #: BC0139 1391	PAEVAETGA 23			
	GLLPAVTSVA Seq ID NO: Nucleic Ac	FLVQMRRQHR 3 DNA seque id Accession	RGTKGGVSYR ence n #: BC0139	PAEVAETGA	41	51	
50 55	Seq ID NO: Nucleic Ac Coding seq	FLVQMRRQHR 3 DNA seque id Accession uence: 438-:	RGTKGGVSYR ence 1 #: BC0139 1391	PAEVAETGA 23	41 	51 	
	Seq ID NO: Nucleic Ac Coding sequents	3 DNA seque id Accession mence: 438-:	RGTKGGVSYR ence 1 #: BC0139 1391 21 1 TGTTCAAAAA	PAEVAETGA 23 31 GTATCAGGAG	41 TIGTCAAGGC	51 AGAGAAGAGA	60
	GLLPAVTSVA Seq ID NO: Nucleic Acc Coding seq AGCGGGGTTG GTGTTGCAA	FLYOMERQUE 3 DNA seque id Accession uence: 438- 11 TCTATTAACT AAGGGGGAAA	RGTKGGVSYR ence 1 #: BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT	PAEVAETGA 23 31 GTATCAGGAG GCCTCTTTAA	41 TIGTCAAGGC	51 AGAGAAGAGA GAGAGAAGA	60 120
	GLLPAVTSVA Seq ID NO: Nucleic Acc Coding seq AGCGGGGTTG GTGTTGCAA	FLYOMERQUE 3 DNA seque id Accession uence: 438- 11 TCTATTAACT AAGGGGGAAA	RGTKGGVSYR ence 1 #: BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT	PAEVAETGA 23 31 GTATCAGGAG GCCTCTTTAA	41 TIGTCAAGGC	51 AGAGAAGAGA GAGAGAAGA	60 120 180
55	GLLPAVTSVA Seq ID NO: Nucleic Ac: Coding sequence AGCGGGGTTG GTGTTTGCAA AGAGGAGAGA AGAGGAGAGAA AGAGGAGAGAA AGAGGAG	FLYOMERQUE 3 DNA sequid Accession uence: 438-: 11 1 TCTATTAACT AAGGGGGAAA GAAAGGAAGG	RGTKGGVSYR ence n #: BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT GAGAGAAGTTTGCT GAGAGAAGTAGTAGGA	PAEVAETGA 23 31 GTATCAGGAG GCCTCTTAA TGAGCCCAG	41 TTGTCAAGGC GACTAGGACT GCTTAAGCCT TAGGGAGGGA	51 AGAGAAGAGA GAGAAAAAA CCACAAAAAA CCACATTTTT	60 120
55	GLLPAVTSVA Seq ID NO: Nucleic Ac: Coding sequence AGCGGGGTTG GTGTTTGCAA AGAGGAGAGA AGAGGAGAGAA AGAGGAGAGAA AGAGGAG	FLYOMERQUE 3 DNA sequid Accession uence: 438-: 11 1 TCTATTAACT AAGGGGGAAA GAAAGGAAGG	RGTKGGVSYR ence n #: BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT GAGAGAAGTTTGCT GAGAGAAGTAGTAGGA	PAEVAETGA 23 31 GTATCAGGAG GCCTCTTAA TGAGCCCAG	41 TTGTCAAGGC GACTAGGACT GCTTAAGCCT TAGGGAGGGA	51 AGAGAAGAGA GAGAAAAAA CCACAAAAAA CCACATTTTT	60 120 180
	GLLPAVTSVA Seq ID NO: Nucleic Ac: Coding sequence AGCGGGGTTG GTGTTTGCAA AGAGGAGAGA AGAGGAGAGAA AGAGGAGAGAA AGAGGAG	FLYOMERQUE 3 DNA sequid Accession uence: 438-: 11 1 TCTATTAACT AAGGGGGAAA GAAGAAAGG	RGTKGGVSYR ence n #: BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT GAGAGAAGTTTGCT GAGAGAAGTAGTAGGA	PAEVAETGA 23 31 GTATCAGGAG GCCTCTTAA TGAGCCCAG	41 TTGTCAAGGC GACTAGGACT GCTTAAGCCT TAGGGAGGGA	51 AGAGAAGAGA GAGAAAAAA CCACAAAAAA CCACATTTTT	60 120 180 240 300
55	GLLPAVTSVA Seq ID NO: Nucleic Ac: Coding seq 1 AGCGGGGTTG GTGTTTGCAA AGAGGAGAG TAATAATAAC TGATCCTGAT TCCTCGGGA	FLVQMRRQHR 3 DNA seque id Accession uence: 438-1 11 TCTATTAACT AAGGGGAAA GAAAGAAAGG AATCATCGGC TCCAGTTTGC GCCCTGGGGT	RGTKGGVSYR ence n #: BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT GAGAGAAGTT GGCGGCAGGA CTCTCTCTTTT CCCGACACCC	PAEVAETGA 23 31 GTATCAGGAG GCCTCTTTAA TGAGCCCAG TCGGCCAGAG TTTTCCCCCA CCGCCCGCCT	41 TTGTCAAGGC GACTAGGACT GAGGAGGGA AATTATTCT COCCTCCTCC	51 AGAGAAGAGA GAGAGAAAAA GCGCTTTTTT CGCCCCCGT	60 120 180 240 300 360
55	GLLPAVTSVA Seq ID NO: Nucleic Ac: Coding seq:	PLVQMRRQHR 3 DNA sequid Accession uence: 438-: 11 1 TCTATTAACT AAGGGGAAA GAAAGAAGGC TCCAGTTTGC GCCCTGGGCT CCCCAAAGTC	RGTKGGVSYR ence 1 #: BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT GAGAGAAGTCTCTCTTT CCCGACACCCC CCGGCGGGGGGGGGG	PAEVAETGA 31 GTATCAGGAG GCCTCTTAA TGAGCCCAG TCGGCCAGAG TTTCCCCA CGCCCGCCT CGAGGGTCGG	41 TIGTCAAGGC GACTAGGACT GCTTAAGCCT GAGGAGGGAA AATTATTCTT CCCCTCCTCC CGGCCGCCGGCGCCGGCGCCGCCGCCGCCGCCGCCGGCGC	51 AGAGAAGA GAGAGAAAGA TTCCAAAAAA GGGCTTTTT CGCCTGATTT TCTCCCCCG GGGGCCGGGC	60 120 180 240 300 360 420
55	GLLPAVTSVA Seq ID NO: Nucleic Ac: Coding seq 1 AGCGGGGTTG GTGTTTGCAA AGAGGAGAA TAATAATAAC TQATCCTGAT TCCTCGCGGA CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCG	PLVQMRRQHR 3 DNA sequid Accession usnce: 438-: 11	RGTKGGVSYR ence n #: BC0139 1391 21 TGTTCAAAAA GTAGTTTCCT GGCGCAGGA CTCTCTTT CCCGACACCC CCGCCGCGCC	PAEVAETGA 31	41 TTGTCAAGGC GACTAGGACT GCTTAAGCCT GAGGAGGAA AATTATTCTT CCCTCCTCC CGCCCCCCG GGTGAAGCCG	51 AGAGAAGAG GAGAGAAAGA TTCCAAAAAA GCGCTTTTT TCTCCCCCG CGGGCCCGGC	60 120 180 240 300 360 420 480
55	GLLPAVTSVA Seq ID NO: Nucleic Ac: Coding seq 1 AGCGGGGTTG GTGTTTGCAA AGAGGAGAA TAATAATAAC TQATCCTGAT TCCTCGCGGA CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCGGGGGCACAG CCG	PLVQMRRQHR 3 DNA sequid Accession usnce: 438-: 11	RGTKGGVSYR ence n #: BC0139 1391 21 TGTTCAAAAA GTAGTTTCCT GGCGCAGGA CTCTCTTT CCCGACACCC CCGCCGCGCC	PAEVAETGA 31	41 TTGTCAAGGC GACTAGGACT GCTTAAGCCT GAGGAGGAA AATTATTCTT CCCTCCTCC CGCCCCCCG GGTGAAGCCG	51 AGAGAAGAG GAGAGAAAGA TTCCAAAAAA GCGCTTTTT TCTCCCCCG CGGGCCCGGC	60 120 180 240 300 360 420 480 540
55	GLLPAVTSVA Seq ID NO: Nucleic Ac: coding seq coding seq flags acceptation acce	PLVQMRRQHR 3 DNA sequid Accession usnce: 438-: 11	RGTKGGVSYR PINCE 1 #: BC0139 1391 21	PAEVAETGA 31 GTATCAGGAG GCCTCTTTAA TGAGCCCCAG TCGGCCAGGAG TCTTCCCCA CGGCGGCT CGAGGGTCGG TGGAGACGGA CCACCGCGGC TGGAGACGGA	41 TIGTCAAGGC GACTAGGACT GAGGAGGGAA AATTATICTT COCTOCTOC CUGCCOCCOG GCTGAAGCCG GCGGCCGGC GCGGCCGGC CATGGATGTGG	51 AGAGAAGAGA GAGAAAGA TTCCAMAAAA GCGCTTTTT TCTCCCCCC GGGCCCGGC CCGGGCCCGGC GGCAACCAGA TCCCCCCGGGC	60 120 180 240 360 420 480 540 600
55	GLLPAVTSVA Seq ID NO: Nucleic Ac: Coding seq 1 AGCGGGTTG GTGTTTGCAA AGAGGAGAGA TAATAATAAC TGATCCTGAT TCCTCGCGGA CCGGGCCCCACAG AGCAAACTTC AAAACTACCAACACCCA AGCGGCCCAACAG AGCAAACTTC AAAACAGCCCA AGCGGCCCAACAG AGCAAACTTC AAAACAGCCCA AGCGGCCCAACAG AGCAAACTTC AAAACAGCCCA AGCGGCCCAACAG	PLVQMRRQHR 3 DNA sequid Accession usnce: 438-: 11 TATATTAACT AAGGGGAAA GAAGAAAGG CCCCGCAT CCCCAAAGTC CCCCAAAGTC CGCCGCAT GGGGGGGGGG	RGTKGGVSYR ence n #: BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT GAGAGAAGT TCTCTCTTTCCCGACACATCA CCGACACACATCA GGCGGCAACT AAAGGGCCCA AAGGGGCCCAACT AAAGGGCCCA	PAEVAETGA 31. GTATCAGGAG GCCTCTTTAA TGAGCCCAG TTTTCCCCCA CGGCGGCT CGAGGGTCGG TGAGAGCGGAG CCACCGCGCT TGAGAGCGGAG AGATGCCT TGAATGCCT TGAATGCCT AGATGCACAA	41.	51 AGAGAAGAGA GAGAGAAGA TTCCAAAAAA GCGCTTTTT GCCTGATTT TCTCCCCCG GGGACCGGG GCCACCAGA TCCGCGGGG AGCAGCAGA AGCAAGGGC	60 120 180 240 300 360 420 480 540 600
55	GLLPAVTSVA Seq ID NO: Nucleic Ac: Coding seq 1 AGCGGGGTTO GTGTTTGCAA AGAGGAGAA TAATAATAC TCATCGGGGA TCCTCGGGGCCAA AGCGGGGCCAA AGAGGGGGCCAA AGGGGGCCAA AGGGGGCCAA AGGGGGCCAA AGGGGGCCAA	PLVQMRRQHR 3 DNA sequid Accession usince: 438-: 11	RGTKGGVSYR Ence i #: BC0139 21 TGTTCAAAAA TGAFTTGCT GGCGCAGGA CTCTCTTT TCCGAACACC CCGGCAGGA GGCGGGGAC TACAACATGA GGCGGCAACT AAGCGGCCAA TAGAGCCCA GAGAACCCC TTGTCGGCAAC TTGTCGGCAAC TTGTCGGCAAC TTGTCGGCAA	PAEVAETGA 31 GTATCAGGAG GCTCTTTAA TGAGCCCAG TCGGCCAGAG TTTTCCCCA CCGCCGCCT CGAGGGTC3G CCACCGCGCC TGAGAGACGCA CCACCGCGCC TGAATGCCT AGATGACAGA	41.	51 AGAGAAGAGA GAGGAAGA GAGCTTTTT TCTCCCCCG GGGCCCGGC CCGGGCCCGG GGCAACCAGA TCCCGCGGGC AGCAAGCGCC	60 120 240 300 360 420 540 600 600
55	GLLPAVTSVA Seq ID NO: Nucleic Ac. coding seq 1 AGCOGGGTTG GTGTTTGCAA AGAGGAGAA TAATAAT TCCTCGCGGA CCGCGCACAG AGCAGCACAG AGCAGCAG AGCAACATC AAACAGCCC AGCGGGCAA TGGGGCCCAACAG AGGGGCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGCCCCCAACAG AGGGCCCCAACAG AGGCCCCCAACAG AGGCCCCCCAACAG AGGCCCCCCAACAG AGGCCCCCCAACAG AGCCCCCCCAACAG AGGCCCCCCAACAG AGGCCCCCCCAACAG AGGCCCCCCCAACAG AGGCCCCCCCC	PLVQMRRQHR 3 DNA sequida dacession da Accession de Access	RGTKGGVSYR BINCE 1 #; BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT GGCGGCAGGA CTCTCTCTTCT CCCGACACCC CCGGCAGGGC TACAACATGA AGGGGCAACT AAGCGGCCCA TGTTCGGAGA	PAEVAETGA 23 31 GRATCAGGAG GCCTCTTTAA TGAGGCCCAGG TCGGCCAGGA TCTTCCCCA CGCCGCCT TGAGGGTCGG TGAGAGAGGAA CCACGGGGG TGAATGCCT AGATGCACAA CGAGAGAAGGA	41 TTGTCAAGGC GACTAGGACT GATAAGCCT GAGGAGGGAA AATTATTCT CCCCTCCTCC CGGCCGCCGG GCGGCCGGC CATGGTGTGG CTCGGAGACC CTCGGAGACC CTCGGAGATC CCCGTTCATC	51 AGAGAAGAGA GAGGAAGAA GCGCTTTTTT TCTCCCCCCG GGGCCGGGC CGGGCCGGC GGCACCAGA GCAAGGCCA AGCAAGGCC ACCAAGGCCAA ACCAGGCCGACAGGCCAACAGGCAACAGGCCA	60 120 180 240 360 420 480 540 660 720
55 60 65	GLLPAVTSVA Seq ID NO: Nucleic Ac. coding seq 1 AGCOGGGTTG GTGTTTGCAA AGAGGAGAA TAATAAT TCCTCGCGGA CCGCGCACAG AGCAGCACAG AGCAGCAG AGCAACATC AAACAGCCC AGCGGGCAA TGGGGCCCAACAG AGGGGCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGGCCCCAACAG AGGCCCCCAACAG AGGGCCCCAACAG AGGCCCCCAACAG AGGCCCCCCAACAG AGGCCCCCCAACAG AGGCCCCCCAACAG AGCCCCCCCAACAG AGGCCCCCCAACAG AGGCCCCCCCAACAG AGGCCCCCCCAACAG AGGCCCCCCCC	PLVQMRRQHR 3 DNA sequida dacession da Accession de Access	RGTKGGVSYR BINCE 1 #; BC0139 1391 21 TGTTCAAAAA GTAGTTTGCT GGCGGCAGGA CTCTCTCTTCT CCCGACACCC CCGGCAGGGC TACAACATGA AGGGGCAACT AAGCGGCCCA TGTTCGGAGA	PAEVAETGA 23 31 GRATCAGGAG GCCTCTTTAA TGAGGCCCAGG TCGGCCAGGA TCTTCCCCA CGCCGCCT TGAGGGTCGG TGAGAGAGGAA CCACGGGGG TGAATGCCT AGATGCACAA CGAGAGAAGGA	41 TTGTCAAGGC GACTAGGACT GATAAGCCT GAGGAGGGAA AATTATTCT CCCCTCCTCC CGGCCGCCGG GCGGCCGGC CATGGTGTGG CTCGGAGACC CTCGGAGACC CTCGGAGATC CCCGTTCATC	51 AGAGAAGAGA GAGGAAGAA GCGCTTTTTT TCTCCCCCCG GGGCCGGGC CGGGCCGGC GGCACCAGA GCAAGGCCA AGCAAGGCC ACCAAGGCCAA ACCAGGCCGACAGGCCAACAGGCAACAGGCCA	60 120 180 240 300 360 420 540 600 720 780
55	GLIPATTSVA Seq ID NO: Nucleie Ac. Coding seq AGCGGGTTG GTGTTTGCAB AGAGGAGAGA TAATAATAAC CCCGCGGGCC CCGCGCACAG AGCAGCGCACAG AGCAGCGCAAAA TGGGGCGCA AAACAGCCC AGCGGCGCAAAA TGGGGCGCAAAA TGGGGCTTACA AAAACAACAAC AGCGGCAAAA	FLVQMRRQHR 3 DNA sequid Accession usence: 438-1 11. TCTATTAACT AAGGGGRAAA GAAAAAAAAGG AATCATGGG TCCCCAAAGTC CCCCCAATGGGGGGGACCGGGTGAACTGATGGCCCAGGGGGAACCTGATGCCCAGATGAACTCAGCCCAGATGAACTCAGCGCAAGCCCAGCCCATGAAACTCATGAGGCCCAGGCCCAGCCCATGAAACTCATGAGGCCCAGCTCATGAAGCCCAGCCCATGAAACTCATGAACCTATGAAGCAGCCCAGCCCATGAAACTCATGAACCTATGAAACTCATGAAACTCACAGCAACCCAGCCAAGAACTAGAACAGCAAGCA	RGTKGGVSYR RICE 1 #; BC0139 21	23 31 GTATCAGAG GCCTCTTAA TGAGCCCCA TCGGCCCCAC CCGCCGCCT TGAGGGTCGG TGAGAGCGGA CCACCGCGCT TGAGAGCGGA AGATCACAA AGACGCACA TGAGAAAGCG ACCCGGATAA ACACGCTGCC	41 	51 	60 120 180 240 360 420 480 600 720 780 840
55 60 65	GLIPATTSVA Seq ID NO: Nucleie Ac. Coding seq AGCGGGTTG GTGTTTGCAB AGAGGAGAGA TAATAATAAC CCCGCGGGCC CCGCGCACAG AGCAGCGCACAG AGCAGCGCAAAA TGGGGCGCA AAACAGCCC AGCGGCGCAAAA TGGGGCGCAAAA TGGGGCTTACA AAAACAACAAC AGCGGCAAAA	FLVQMRRQHR 3 DNA sequid Accession usence: 438-1 11. TCTATTAACT AAGGGGRAAA GAAAAAAAAGG AATCATGGG TCCCCAAAGTC CCCCCAATGGGGGGGACCGGGTGAACTGATGGCCCAGGGGGAACCTGATGCCCAGATGAACTCAGCCCAGATGAACTCAGCGCAAGCCCAGCCCATGAAACTCATGAGGCCCAGGCCCAGCCCATGAAACTCATGAGGCCCAGCTCATGAAGCCCAGCCCATGAAACTCATGAACCTATGAAGCAGCCCAGCCCATGAAACTCATGAACCTATGAAACTCATGAAACTCACAGCAACCCAGCCAAGAACTAGAACAGCAAGCA	RGTKGGVSYR RICE 1 #; BC0139 21	23 31 GTATCAGAG GCCTCTTAA TGAGCCCCA TCGGCCCCAC CCGCCGCCT TGAGGGTCGG TGAGAGCGGA CCACCGCGCT TGAGAGCGGA AGATCACAA AGACGCAGAAACC AGAGAAACG ACCCGGATAA ACACGCTGCC	41 	51 	60 120 180 240 360 420 480 600 720 780 840
55 60 65	GLIPAVTSVA Seq ID NO: Nucleic Roc. Coding sequence 1 ASCGGGGTTG GTGTTTGCAA AGRGGAGATA TATAATAAC TATACTGTAT TCCTCGGGA CCGGGCCAA AGCGGGGCCAA AGCGGGGCCAA AGCGGGCCCAA AGCGGCTCGA AGCGGCTCGA AGCGGCTCGA AGCGGCTCGA AGCGGCTCGA	FLVQMRRQHR 3 DNA sequated and access ac	RGTKGGVSYR BINCE In #: BC0139 1391 21 TGTTCARARA GRAGTAGGA GRAGGAGGA CTCTCTCTT GCGGCAGGA CTCTCTCTT TACARCAGGAGGA CTCTCTCTT TACARCAGGAGGA TTCTCGGGAGA GGGGGCACC GGGGGGAGCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC GGGGGCACCT AGGGGGCACCT AGGGGGCACCT AGGGGGCACCT AGGGGGCACCT AGGGGGCACCT AGGGGGGAACCCC AGGAACCCC AGGAACCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCC AGGAACCCC AGGAACCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCC AGGAACCCC AGGAACCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCCC AGGAACCC AGGAACCCC A	PAEVAETGA 23 31 GEATCAGGAG GCCTCTTTAA TGAGCCCCAG TCGGCCCAGAG TTTCCCCCA CGGCCT CGAGGGTCGG CTGAGAGCGAA CCACGGGGC TGAATGCCT AGATGCCT AGATGCCT AGATGCCT TGAGGGCCC TGGGGGCCC TGGGGCCC TGGGGCCC TGGGGCCCC TGGGGCCCC TGGGGCCCC TGGGGCCCC TGGGGCCCC TGGGGCCCC TGGGCGCCC TGGGGCCCC TGGGGCCCC TGGGCGCCCC TGGGCGCCCC TGGGCGCCCC TGGCGCCCC TGGGCGCCCC TGGGCCCCC TGGCGCCCC TGGCGCCCC TGGCGCCCC TGGCGCCCC TGCCCCCC TCCCCCC TCCCCCC TCCCCCC TCCCCCC TCCCCCC	41 TTGTCAAGGC GACTAGGACT GCTTAAGCCT GGGGGGGGAA AATTATTCTT CGGCCCCCG GGCGGCCGGC GCTGAAGCCG GCGGCCGGC CATGGTGTGG CCGGTGAT TAAATACCGG GGGGGTTAC CGGGGGCTAC CGGGGGCGC CGGGGGCGCGC CGGGGGCGCGC CGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	51 AGAGAAGAG GAGAGAAAGA TTCCAAAAAA GGGCTTTTT CDCCTGATTT TCTCCCCCC CGGGCCCGC CGGGCCCGC GGCAACCAGA TCCCGCGGGG AGCAAGCGC GACAAGGCT CCCGGGCGGA CTGGCCCCCG GGCTGAACC GGCTGAACCAGA GACCAGGCTAACC GACCAGGCTAACC GGCTGAACCAGA AGCATGATGC	60 120 180 240 300 360 420 540 600 720 780
55 60 65	GLIPATTSVA Seq ID NO: Nucleic Ac. Coding seq 1 AGCGGGGTTG GTGTTTGCAA AGAGGAGGAG TAATAATAAC TUATCCTGAT TUCTCGCGGACC AGCAAACTCC AGCGGGCCCA AGCACACG AGCACACG AGCACACG AGCACACG AGCACACG AGCACACG AGCACCACG AGCACACG AGCACCACG	FLVQMRRQIR 3 DNA sequidad Accession uence: 438-: 11	RGTKGGVSYR since a #: BC0139 1391 21 i TGTTCAAAAA GTAGTTTGCT GAGAGAACCC CCGCCAGGA CTCTCTGTTT TACAACAATGA GGCGGCAACA CCGCCGGGGC AAGCACCC AAGCAGCACC AAGCAGCACC CCGCCGGGGCAACA TGAAGAGCACC AAGCAGCACC CCGCCGGGGCAACA TGAAGAGCACC AAGCAGCACC AAGCATGAAG ATGAAGGACC AAGCATGAAG CAAGCACCC CAAGCATGAAGC CAAGCACCCC CAAGCACCCC CAAGCACCCC CAAGCACCCC CAAGCACCC CAAGCACCCC CAAGCACCCC CAAGCACCCCC CAAGCACCCCC CAAGCACCCCC CAAGCACCCCC CAAGCACCCCCC CAAGCACCCCCCC CAAGCACCCCCCC CAAGCACCCCCCC CAAGCACCCCCCCC	23 21 21 21 21 21 21 21 21 21 21 21 21 21	41 	51 AGAGRAGAGA GAGAGAAGA TTCCAAAAAA GCSCTTITTT GCCTGATTT TCTCCCCCC GCGCCCGGC GCGCCGGC GACAGGCTA ACCACGCGGC AACAAGGCTA ACCACGCGGA ACCACGCGGA ACCACGCGGA ACCACGCGGA ACCACGCGGA ACCACGCGGA ACCACGCGA ACCACGCGGA ACCACGCGAAACC AGCATGATGA	60 120 240 300 420 480 600 720 780 800 900 900
55 60 65	GLIPATTSVA Seq ID NO: Nucleic Ac. Coding seq I AGGGGGGTTG GTGTTTGCAA AGAGGAGAGA TUATCCTGAT TCTTCGGGA AGGGGGCA AGGGGGCA AGGGGGCA AGGGGGCA AGGGGCACAG AGGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCAATAG AGGGCACAG AGGGCACAG AGGACCAGCT	FLVQMRRQIR 3 DNA sequidad Accession usince: 438-: 11 11 11 12 13 15 17 17 17 17 17 17 17 17 17 17 17 17 17	ROTKOGVSYR since an # BCO139 1391 21 1 TOTALANA GOOGRAGH GOOGRAGH GOOGRAGH GOOGRAGH TAGANACT GOOGRAGH GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH CONTROL GOOGRAGH CONT	23 31 CARTER OF THE PROPERTY OF THE PROPER	41 TESTCAAGGE GACTAGGACT GCTTAAGCET GCTTAAGCET GCTTAAGCET GGCTGCGCGGGGGGGGGCGGGCGGGCGGGCGGGCGGGC	51 IGAGAAAGA GAGAAAGA TTOCAMAAA GAGCTTTTT TCTCCCCCC GAGGACGGGC COGGGCCGGC GGCAACAGA TCCCGCGGG GACACAGA TCCCGCGGG GACAGGGC GACAGGGG TCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGA TCCCCCCC GACAGGGA GACAGGGA GACAGGGA GACAGGGA GACAGGGA GACAGAGA GACAGA GACAGAGA GACAGA GACAGAGA GACAGA GACAGA GACAGAGA GACAGA	60 120 180 300 420 480 540 600 672 780 840 960 1020
55 60 65 70	GLIPATTSVA Seq ID NO: Nucleic Ac. Coding seq I AGGGGGGTTG GTGTTTGCAA AGAGGAGAGA TUATCCTGAT TCTTCGGGA AGGGGGCA AGGGGGCA AGGGGGCA AGGGGGCA AGGGGCACAG AGGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCACAG AGGGCAATAG AGGGCACAG AGGGCACAG AGGACCAGCT	FLVQMRRQIR 3 DNA sequidad Accession usince: 438-: 11 11 11 12 13 15 17 17 17 17 17 17 17 17 17 17 17 17 17	ROTKOGVSYR since an # BCO139 1391 21 1 TOTALANA GOOGRAGH GOOGRAGH GOOGRAGH GOOGRAGH TAGANACT GOOGRAGH GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH TAGANACT GOOGRAGH CONTROL GOOGRAGH CONT	23 31 CARTER OF THE PROPERTY OF THE PROPER	41 TESTCAAGGE GACTAGGACT GCTTAAGCET GCTTAAGCET GCTTAAGCET GGCTGCGCGGGGGGGGGCGGGCGGGCGGGCGGGCGGGC	51 IGAGAAAGA GAGAAAGA TTOCAMAAA GAGCTTTTT TCTCCCCCC GAGGACGGGC COGGGCCGGC GGCAACAGA TCCCGCGGG GACACAGA TCCCGCGGG GACAGGGC GACAGGGG TCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGGA TCCCCCCC GACAGGGA TCCCCCCC GACAGGGA GACAGGGA GACAGGGA GACAGGGA GACAGGGA GACAGAGA GACAGA GACAGAGA GACAGA GACAGAGA GACAGA GACAGA GACAGAGA GACAGA	60 120 180 240 360 420 540 660 720 840 900 1020 1040
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5	AAATGGCCAT TTCCATTTTG	GCAGGTTGAC	ACCUTTGGTA	ATTTATAATA	CCTTTTGTTC	GATCCCAACT	2220
,	TTCCATTTC	TTCAGATAAA	AAAAACCATG	AAATTACTGT	GTTTGAAATA	TTTTCTTATG	2280
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	GTATATATTT	GAACTAATAT	CATCCTTATA	ACAGGTACAT	TTTCAACTTA	AGTTTTTACT	2460
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	ARRARACAA	AAAAAAAAA	CAAAAAACAA	AAACAGAAAA	AACAAAAAA	AAAACAAAAC	2580
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20	!		GGGNSTAAAA	CONCERNE	TAND DIVINE RIMES	MGDGUDDKMY	60
20	MANAMETERY	PPGPQQTSGG	T.I. CETTEVEDE	THEATRIPAL	HWKEHDDAKA	RPRRKTKTLM	120
	ORNERMINE DOG	T. I. D. CONCHA	LLSETEKRPF SGVGVGAGLG	AGVINORMDSY	AHMNGWSNGS	YSMMODOLGY	180
							240
	GRANKSEYES	SPRVVTSSSH	SRAPCQAGDL	RDMISMYLPG	AEVPEPAAPS	RLHMSQHYQS	300
25	GPVPGTAING	TLPLSHM					
	Seq ID NO:	5 DNA seque	ence				
	Nucleic Ac:	id Accession	ı #: U91618				
20	Coding sequ	uence: 29-5	11				
30			21.		41	51	
	1	11	21.	31	41	1	
	1		GCTGAAAGAT	CATOCCACCA	ATCABABTCC	AGCTTGTATG	60
							120
35	CATGCTACTC	CTGGCTTTCA	TGACCAATAT	GCATACATCA	BAGATTAGTA	AAGCACATGT	180
33							240
	ACCORDERACES A	ACACCACAGAG	TTCATGAAGA	GGAGCTTGTT	GCAAGAAGGA	AACTTCCTAC	300
	TOCTTTAGAT	CCCTTTAGCT	TTCATGAAGA TGGAAGCAAT	GTTGACAATA	TACCAGCTCC	ACAAAATCTG	360
							420
40	MCACS BARAS	CCRARCGARG	AACTCATAAA	GAGAAAATT	CCTTATATTC	TGAAACGGCA	480
	COTOTATOAG	BATABACCCA	GAAGACCCTA	CATACTCAAA	AGAGATICTI	ACTATTACTG	540
							600
	ATTATATTTG	TGTGAAAATG	TGACAAACAC	ACTTATCTGT	CTCTTCTACA	ATTGTGGTTT	660
	ATTATATTTG	TCTGAAAATG	TGACAAACAC	TTAGACTAAG	CTCTTCTACA TGTTTTCAAA	ATTGTGGTTT TAAATCTAAA	660 720
45	ATTATATTTG	TCTGAAAATG	TGACAAACAC CTAATAGAAA AAATGGGGCC	TTAGACTAAG	CTCTTCTACA TGTTTTCAAA	ATTGTGGTTT TAAATCTAAA	
45	ATTATATTTG	TCTGAAAATG	TGACAAACAC	TTAGACTAAG	CTCTTCTACA	ATTGTGGTTT TAAATCTAAA	
45	ATTATATTTG	TCTGAAAATG	TGACAAACAC	TTAGACTAAG	CTCTTCTACA	ATTGTGGTTT TAAATCTAAA	
45	ATTATATTG ATTGAATGTG TCTTCAAAAA	TGTGAAAATG TTTTTCTGCA AAAAAAAAAA	TGACAAACAC CTAATAGAAA AAATGGGGCC	TTAGACTAAG	CTCTTCTACA TGTTTTCAAA	ATTGTGGTTT TAAATCTAAA	
	ATTATATTG ATTGAATGTG TCTTCAAAAA	TGTGAAAATG TTTTTCTGCA AAAAAAAAAA 6 Protein	TGACAAACAC CTAATAGAAA AAATGGGGCC sequence:	TTAGACTAAG	CTCTTCTACA TGTTTTCAAA	ATTGTGGTTT TAAATCTAAA	
45	ATTATATTG ATTGAATGTG TCTTCAAAAA	TGTGAAAATG TTTTTCTGCA AAAAAAAAAA	TGACAAACAC CTAATAGAAA AAATGGGGCC sequence:	ACTIATCIGI TIAGACTAAG GCAATT	TOTTTCAAA	TAAATCTAAA	
	ATTATATTG ATTGAATGTG TCTTCAAAAA	TGTGAAAATG TTTTTCTGCA AAAAAAAAAA 6 Protein	TGACAAACAC CTAATAGAAA AAATGGGGCC sequence:	TTAGACTAAG	CTCTTCTACA TGTTTTCAAA	ATTGTGGTTT TAAATCTAAA 51	
	ATTATATTG ATTGAATGTG TCTTCAAAAA Seq ID NO: Protein Ac	TGTGAAAATG TTTTTCTGCA AAAAAAAAAA 6 Protein cession #:	TGACAAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564	ACTEATORY TTAGACTAAG GCAATT	CTCTTCTACA TGTTTCAAA	TAAATCTAAA	720
50	ATTATATTIG ATTGRATGIG TCTTCAAAAA Seq ID NO: Protein Ac	TGTGAAAATG TTTTTCTGCA AAAAAAAAAA 6 Protein cession #:	TGACAAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564	ACTIATORY TTAGACTAAG GCAATT	41	S1	720
	ATTATATTG ATTGAATGTG TCTTCAAAAA Seq ID NO: Protein Ac	TGTGAAATG TTTTTCTGCA AAAAAAAAA 6 Protein Cession #:	TGACAAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564 21 SLCSDSEEEM	ACTEATCHOT TTAGACTAAG GCAATT 31 KALEADFLIN	41 METSKISKAR	51 VPSWKMTLLN	720
50	ATTATATTG ATTGAATGTG TCTTCAAAAA Seq ID NO: Protein Ac	TGTGAAATG TTTTTCTGCA AAAAAAAAA 6 Protein Cession #:	TGACAAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564 21 SLCSDSEEEM	ACTEATCHOT TTAGACTAAG GCAATT 31 KALEADFLIN	41 METSKISKAR	51 VPSWKMTLLN	720
50	ATTATATTG ATTGAATGTG TCTTCAAAAA Seq ID NO: Protein Ac 1	TOTGAAAATG TTTTTCTGCA ARAAAAAAAA 6 Protein cegsion #: 11 CMLLLAFSW PARETGEVHE NDKNGKEEVI	TGACAACAC CTAATAGAAA AAATGGGCC sequence: AAB50564 21 SLCSDSEEM EELVARRKLP KRKIPYILKR	ACTEATCHOT TTAGACTAAG GCAATT 31 KALEADFLIN	41 METSKISKAR	51 VPSWKMTLLN	720
50	ATTATATTG ATTGATGTG TCTTCAAAAA Seq ID NO: Protein Ac 1 MAGMKIQLV YCSLVNNIMS LIQEDILDTG Reg ID NO:	TOTGARANTG TITTTCTGCA ARAAAAAAAA 6 Protein cegsion #: 11 CMILLIAPSSW PARETGEVHE NDKNGKERVI 7 DNA segu	TGACARACAC CTAATAGAA ARATTGGGCC sequence: AAB50564 21 SLCSDSEEEM EELVARRKLP KRKIPYILKR	ACTIATCROFT TTAGACTAAG GCAATT 31 KALEADFLIN TALDGFSLER QLYENKPRRE	41 METSKISKAR	51 VPSWKMTLLN	720
50	ATTAATTG ATTGAAAAA Seq ID NO: Protein Ac MAGMKIQLV VCSLVNNINS LIQEDILDTG Seq ID NO: MUCLeic Ac	TOTRADATE TITTTCTGCA ARABARARA 6 Protein cession #: 11 CMLLLAPSSW PARETGEVHE NDKNKEEVI 7 DNA sequ id Accessio	TGACAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564 21 SLCSDSEEEM SELVARRKLP KRKUPYILKR ence n #; NM_006	ACTIATCROFT TTAGACTAAG GCAATT 31 KALEADFLIN TALDGFSLER QLYENKPRRE	41 METSKISKAR	51 VPSWKMTLLN	720
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50	ATTATATTE ATTGATATOR TCTTCAAAAA Seq ID NO: Protein Ac 1 	TOTRADATE TITTTCTGCA ADARAGNAA 6 Protein cession #: 11 CMLLLAPSSW PARETGEVHE NDKNKEEVI 7 DNA sequ id Accessio	TGACAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564 21 SLCSDSEEEM SELVARRKLP KRKUPYILKR ence n #; NM_006	ACTIATCROFT TTAGACTAAG GCAATT 31 KALEADFLIN TALDGFSLER QLYENKPRRE	41 METSKISKAR	51 VPSWKMTLLN	720
50	ATTATATTE ATTGAAAAA Seq ID NO: Protein Ac 1 MMAGMKIQLV VCSLWANIMS LIQEDILDIG Seq ID NO: Nucleic Ac Coding seq 1	6 Protein cession #: 11 CMLLLAPSW PARETGEVHE NDKNGKESVI 7 DNA sequ ild accession uence: 109-	TGACAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564 21 SLCSDSBEEM EELVARRKLP KRKIPYILKR ence ence n #: nM_006 2940	ACTIATION TRAGACTANG GCAATT 31 KALEADFLIN TALLOGFSLER QLYENKPRRE	41 HETSKISKAH WLTIYQLIKI YILKRDSYYY	S1 VPSNKMTLLN CHSRAFQKWE	60 120
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50	Seq ID NO: Protein Ac MAGNICIAN Seq ID NO: Protein Ac MAGNICIAN MAGNICIAN MAGNICIAN MUCIELO AC Coding seq 1 ACCTARAACC	6 Protein cession #: 11 PARETGEVHE NDKNOKESVI 7 DNA sequ (id Accession unence: 109- 11 TITCAAGTICE CRESSIONALITY	TGACAACCA CTAATAGAAA AAATGGGGCC sequence: AAB50564 21 1 SLCSDSEEM EELVARRKLP KRKIPYILKR ence n #: NM_006 2940 21 1 AGGAGAAAC CTYMACTGGAC CTYMACTGGAC CTYMACTGGAC CTYMACTGGAC CTYMACTGGAC CTYMACTGGAC CTYMACTGGAC CTYMACTGGAC	31 KALEADPLIN TALDGESLEN GLYENKPRES	41 HETSKISKAH METIYQLEKI YILKEDSYYY	51 VPSWEMTLLN CHSRAPQRIVE	60 120 60 120
50 55 60	ATTATATTIC ATTGATATO TCTTCAAAAA Seq ID NO: Protein Ac 1 	6 Protein cession #: 11 CMLLLAPSW PARETGEVE NOKINGKEEVI 7 DNA sequid Accession unce: 109- 11 TTUCAAGTYC CAGGGTCAGT	TGACAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564 21 SLCSDSBEEM SELVARRKLP KRKIPYILKR ence n #1 NM_006 2940 21 AGGAAGAAAAC GTGAAGGAAAAC	31 KALEADPLIN TALOGESLER QLYENKPRES 536.2	41 HETSKISKAB MLTIYQLHKI YILKRDSYYY 41 CATATTGAAA	51 VPSWEMTLLIN CHSRAFQHWE	60 120 60 120
50 55 60	ATTATATTIC ATTGATATO TCTTCAAAAA Seq ID NO: Protein Ac 1 	6 Protein cession #: 11 CMLLLAPSW PARETGEVE NOKINGKEEVI 7 DNA sequid Accession unce: 109- 11 TTUCAAGTYC CAGGGTCAGT	TGACAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564 21 SLCSDSBEEM SELVARRKLP KRKIPYILKR ence n #1 NM_006 2940 21 AGGAAGAAAAC GTGAAGGAAAAC	31 KALEADPLIN TALOGESLER QLYENKPRES 536.2	41 HETSKISKAB MLTIYQLHKI YILKRDSYYY 41 CATATTGAAA	51 VPSWEMTLLIN CHSRAFQHWE	60 120 60 120 180 240
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50 55 60 65	ATTATATTO ATTGAMAA Seq ID NO: Protein Ac LIEUTONIANA Seq ID NO:	TOTICALANTO TITTETCEGA ARAAARARA 6 Protein cossion #: 11 CMLLLAPSN PARENGENE TO NINNAESUT 7 DNA sequ id Accessio uence: 109- 11 TITCALAFTE CARGETTCH CARGETTCH TTCTTCAGGAG ATCCTCAGGT ATCCTCAGGAG ATCCTCAGGT ATCCTCAGGAG	TGACAAACAC CTANTAGANA ANATGGGGCC sequence: AABS0564 21 SLCBDSBEEM EBLVARREIP RRRIPTILGE ence in in NM_006 21 AGCANGANAC GTUAGTGANA CCTACTGANA ACCTGRAGAT	31 31 31 31 31 31 31 31 31 31 31 31 31 3	41 METSKISKAN METSKISKAN METSKISKAN CATATTGAAA 41 CATATTGAAA TCTACAACAT TCCTGGTTGC AATGGGTATAA TCTACAACAT	TANATOTAGATT TANATOTAGATT TANATOTAGATT S1	60 120 60 120 180 240 300 360
50 55 60	ATTATATTO ATTGATATO ATTGATATO TCTTCRAMAA Seq ID Noi- Probein Ac 1	6 Protein cession #: 11 11 12 13 14 14 15 16 17 17 18 17 17 18 18 18 18 19 18 18 18 18 18 18 18 18 18 18 18 18 18	TGACAAACAC CTAATAGAAA AAATGGGGCC sequence: AAB50564 21 SLCSDSEEME ERLVARRED, KRRIPYILKR ence ence n # 1 MM_006 2940 21 AGEMGAAACA GTGAAGTGAAC TGAAGTGAAC TGAAGTGAAC TGAAGTGAAC CTAATTGAAC CTATTTAAT CCTATTTAAT CCTATTTAAT	31 KALEADFLITT TALDGPSLER GLYENKPRE 536.2	41	51 VESWENTILIN CHISRAPQUINE S1 ACCTGACACA GACCYAAGG CTTAAGGTTACT TGAGTTGCT TTTCAGAATT TTTCAGAATT	60 120 60 120 180 240 300 360 420
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50 55 60 65 70	Seq ID No: Protein Ac Seq ID No: Protein Ac I MAGMRKIQLW VCSLUMNIAS LIGEBILDM Seq ID No. LIGEBILDM Seq ID	6 Protein cossion #: 11 11 11 11 11 11 11 11 11	TGACAAACAC CTAATAGAA AAATGGGCC sequence: AAMS0564 ABS0564 ABS0564 BELCEDSHEEM ESLAMSHEEP RERIFITLEM 1	31 RALEADFLTS STANDARD CONTROL STANDAR	41 1 1 1 1 1 1 1 1 1	S1 VSSSEMTILLA S1 ACCTGACACA ACCCAMAGG CTTANGTTCA AAATCATAAA AAACAAGAA AAAGACAAAAG AAGACAAAGAA AAGACAAAGAA AAGACAAAGAA AAGACAAAGAA AAGACAAAGAA AAGACAAAGAA AAGACAAAGAA AAGACAAAGAA AAGACAACAACAAGAA AAGACAACAACAAGAA AAGACAACAACAAGAA AAGACAACAACAAGAA AAGACAACAACAAGAA AAGACAACAACAACAACAAGAA AAGACACAACAACAACAACAACAACAACAACAACAACAAC	600 120 120 120 120 140 140 140 140 140 140 140 140 140 14
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50 55 60 65 70	AFTATATTATATATATATATATATATATATATATATATA	6 Probein 6 Probein 11 11 12 13 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16	TGACAAACAC CTAATAGAAA AAATGGGGC EGQUEAC 21 21 ELCSDSEEDE ERLVARREN ERLYARREN ERLYAREN ERLYARREN	31 SALEADPLITA FALEADPLITA FAL	41 HETSKISKAN MULTIVICHEN LOTATION AUTOMATIC A	S1 S1 VPENENTLLIN CHISRAPGINE S1 ACCTGGCACACA ACCTGGCACAAGG CTTANGTON TOGATTGCTT TTTCAAGAAA AGAGGAATTT TTTTTAAGAAA AGGCCAGGCC	60 120 60 120 60 120 60 60 60 60 60 60 60 60 60 60 60 60 60
50 55 60 65 70 75 80	PATRATATTA ATTGARATTA	6 Probein cession #: 11 11 11 11 11 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18	TGACAAACAC CTAATAGAAA AAATGGGGC ### CONTROL ### CONTROL	31 STANDARD TO THE CONTROL OF THE CO	41 41 41 41 41 41 41 41 41 41 41 41 41 4	SI I VESWATILIAN CHISRAPGINE SI I I ACCURACACA ACCURANGE THRAGGANAT THRAGGANAT ACCURACY ACCUR	600 1200 600 1200 600 600 7200 800 8400 9600 9600 10200 10200 10200 10200 10200 10200 120000 12000 12000 12000 12000 12000 12000 12000 12000 12000 12000 120
50 55 60 65 70	Seq ID No. Protein Ac ATTACATATA ATTACATATA ATTACATATA ATTACATATA ATTACATATA ATTACATACA	6 Probein cossion #: 111 11	TGACAAACAC CTAATAGAAA AAATGGGGC sequence: AAASSSS44 21 21 21 31 31 31 31 31 31 31 31 31 31 31 31 31	31 11 17. ALCHART ST. THARKTHAN GOART ST. ALL	41 41 41 41 41 41 41 41 41 41 41 41 41 4	SI CONTROLL CONTROL CONTROLL CONTROLL CONTROLL CONTROL CONTROL CONTROL CONTROL CONTROLL CONTROL CONTROL CONTROL	60 120 60 120 60 180 240 300 300 420 480 650 660 660 660 600 660 1020 720 730 1020 1020 1020 1020 1020 1020 1020 10
50 55 60 65 70 75 80	Seq ID No. Protein Ac ATTACATATA ATTACATATA ATTACATATA ATTACATATA ATTACATATA ATTACATACA	6 Probein cossion #: 111 11	TGACAAACAC CTAATAGAAA AAATGGGGC sequence: AAASSSS44 21 21 21 31 31 31 31 31 31 31 31 31 31 31 31 31	31 11 17. ALCHART ST. THARKTHAN GOART ST. ALL	41 41 41 41 41 41 41 41 41 41 41 41 41 4	SI I VESWATILIAN CHISRAPGINE SI I I ACCURACACA ACCURANGE THRAGGANAT THRAGGANAT ACCURACY ACCUR	60 120 60 120 60 180 240 300 300 420 480 650 660 660 660 600 660 1020 720 730 1020 1020 1020 1020 1020 1020 1020 10

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CTGGGTTCAT CTGCAGCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500

	TTCTTTGTTC	CAGATATATC	AAACTCCAAT	AGCATGATTG	ATGCTTTCAG	TAGAATTTCC	1560
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5	ATGTTTCTAG	TTACGTGGCA	GGCCAGTGGT	CCTCCTGAGA	TTATATTATT	TGATCCTGAT	1740
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10			ATTTTATCCC				2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100
	GTTATAAAAA	ATGATGGAAT	TTACTCGAGG	TATTTTTTCT	CCTTTGCTGC	AAATGGTAGA	2160
	TATAGCTTGA	AAGTGCATGT	CAATCACTCT	CCCAGCATAA	GCACCCCAAC	CCACTCTATT	2220
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15	GCTCCAAGGA	AATCAGTAGG	CAGAAATGAG	GAGGAGCGAA	AGTGGGGCTT	TAGCCGAGTC	2340
	AGCTCAGGAG	GCTCCTTTTC	AGTGCTGGGA	GTTCCAGCTG	GCCCCCACCC	TGATGTGTTT	2400
			CCTGGAAGCT				2460
	TGGACAGCAC	CTGGAGAAGA	CTTTGATCAG	GGCCAGGCTA	CAAGCTATGA	AATAAGAATG	2520
	AGTAAAAGTC	TACAGAATAT	CCAAGATGAC	TTTAACAATG	CTATTTTAGT	AAATACATCA	2580
20	AAGCGAAATC	CTCAGCAAGC	TGGCATCAGG	GAGATATTTA	CGTTCTCACC	CCAGATTTCC	2640
	ACGAATGGAC	CTGAACATCA	GCCAAATGGA	GAAACACATG	AAAGCCACAG	AATTTATGTT	2700
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	CCTCTGTTTA	TTCCCCCCAA	TTCTGATCCT	GTACCTGCCA	GAGATTATCT	TATATTGAAA	2820
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25	CATACTTTAA	GCAGGAAAAA	GAGAGCAGAC	AAGAAAGAGA	ATGGAACAAA	ATTATTATAA	2940
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30	GCAAAGGGAA	GGGTAAAGTC	GGACCAGTGT	CAAGGAAAGT	TTGTTTTATT	GAGGTGGAAA	3240
	AATAGCCCCA	AGCAGAGAAA	AGGAGGGTAG	GTCTGCATTA	TAACTGTCTG	TGTGAAGCAA	3300
	TCATTTAGTT	ACTITGATTA	ATTTTTCTTT	TCTCCTTATC	TGTGCAGTAC	AGGTTGCTTG	3360
	TTTACATGAA	GATCATGCTA	TATTTTATAT	ATGTAGCCCC	TAATGCAAAG	CTCTTTACCT	3420
	CTTGCTATTT	TOTTATATAT	ATTTCAGATG	ACATCTCCCT	GCTAATGCTC	AGAGATCTTT	3480
35	TTTCACTGTA	AGAGGTAACC	TTTAACAATA	TGGGTATTAC	CTTTGTCTCT	TCATACCGGT	3540
	TTTATGACAA	AGGTCTATTG	AATTTATTTG	TNTGTAAGTT	TCTACTCCCA	TCAAAGCAGC	3600
			GGTTATTATG	GAATGATAGT	TATAGCCCCN	TATAATGCCT	3660
	TACCTAGGAA	. A					
40							

40 Seq ID NO: 8 Protein sequence: Protein Accession #: NP_006527.1

	1	11	21	31	41	51	
45	MTORSTAGET	CNUKEVTLLV	ALSSELPFLG	AGVQLQDNGY	NGLLIAINPO	VPENONLISM	60
	TKEMITEASE	YLFNATKRRV	PPRNIKILIP	ATWKANNISK	IKQESYEKAN	VIVTDWYGAH	120
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	KPFYINGONO	IKVTRCSSDI	TGIFVCEKGP	CPOENCIISK	LFKEGCTFIY	NSTQNATASI	240
	MEMOSLSSVV	EFCNASTHNO	EAPNLQNQMC	SLRSAWDVIT	DSADFHHSPP	MNGTELPPPP	300
50	TESLVOAGDK	VVCLVLDVSS	KMAEADRLLQ	LQQAAEFYLM	QIVEIHTFVG	IASFDSKGEI	360
	RAOLHOINSN	DDRKLLVSYL	PTTVSAKTDI	SICSGLKKGF	EVVEKLNGKA	YGSVMILVTS	420
	GDDKLLGNCL	PTVLSSGSTI	HSTALGSSAA	PNLEELSRLT	GGLKFFVPDI	SNSNSMIDAP	480
	SRISSGTGDI	FOOHIQLEST	GENVKPHHQL	KNTVTVDNTV	GNDTMFLVTW	QASGPPEIIL	540
	FDPDGRKYYT	NNFITNLTFR	TASLWIPGTA	KPGHWTYTLN	NTHHSLQALK	VTVTSRASNS	600
55	AVPPATVEAF	VERDSLHFPH	PVMIYANVKQ	GFYPILNATV	TATVEPETGD	PVTLRLLDDG	660
	AGADVIKNDG	IYSRYFFSFA	ANGRYSLKVH	VNRSPSISTP	AHSIPGSHAM	YVPGYTANGN	720
	IONNAPRKSV	GRNEEERKWG	PSRVSSGGSF	SVLGVPAGPH	PDVPPPCKII	DLEAVKVEEB	780
	LTLSWTAPGE	DFDOGOATSY	BIRMSKSLON	IQDDFNNAIL	VNTSKRNPQQ	AGIREIFTFS	840
	POISTNGPEH	OPNGETHESH	RIYVAIRAMD	RNSLQSAVSN	IAQAPLFIPP	NSDPVPARDY	900
60	LILKGVLTAM	Gridiicrii	VVTHHTLSRK	KRADKKENGT	KLL		

Seq ID NO: 9 DNA sequence Nucleic Acid Accession #: Eos sequence

65	Coding sequ	ence: 336-6	32				
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70	CCTGGGTGGG	CTCAGGGGCT	GCCCTTGACC	TGGCCTAGAG	CCCTCCCCCA	GCTGGTGGTG	120
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	CAGGGTTTGG	TGGGATCAGG	TTGAGGCAGG	TTTGGTTTCC	TTAAAATGCC	AAGTTGGGGG	240
	CCAGTGGGGC	CCACATATAA	ATCCTCACCC	TGGGAGCCTG	GCTGCCTTGC	TCTCCTTCCT	300
	GGGTCTGTCT	CTGCCACCTG	GTCTGCCACA	GATCCATGAT	GTGCAGTTCT	CTGGAGCAGG	360
75	CGCTGGCTGT	GCTGGTCACT	ACCTTCCACA	AGTACTCCTG	CCAAGAGGGC	GACAAGTTCA	420
	AGCTGAGTAA	GGGGGAAATG	AAGGAACTTC	TGCACAAGGA	GCTGCCCAGC	TTTGTGGGGG	480
	AGAAAGTGGA	TGAGGAGGGG	CTGAAGAAGC	TGATGGGCAG	CCTGGATGAG	AACAGTGACC	540
	AGCAGGTGGA	CTTCCAGGAG	TATGCTGTTT	TCCTGGCACT	CATCACTGTC	ATGTGCAATG	600
	ACTTCTTCCA	GGGCTGCCCA	GACCGACCCT	GAAGCAGAAC	TCTTGACTTC	CTGCCATGGA	660
80	TCTCTTGGGC	CCAGGACTGT	TGATGCCTTT	GAGTTTTGTA	TTCAATAAAC	TTTTTTTTTCTC	720
	TGTTGATAAT	ATTTTAATTG	CTCAGTGATG	TTCCATAACC	CGGCTGGCTC	AGCTGGAGTG	780
	CTGGGAGATG	AGGGCCTCCT	GGATCCTGCT	CCCTTCTGGG	CTCTGACTCT	CCTGGAAATC	840
	TCTCCAAGGC	CAGAGCTATG	CTTTAGGTCT	CAATTTTGGA	ATTTCAAACA	CCAGCAAAAA	900
0.5		GAGATAGGTT	GCTGACTTTT	ATTTTGTCAA	ATAAAGATAT	TAAAAAAGGC	960
85	AAATACCA						

Seq ID NO: 10 Protein sequence:

		/086443 ession #: 3	IP_005969.1				
5	1 MMCSSLEQAL GSLDENSDQQ	11 AVLVTTPHKY VDFQEYAVPL	21 SCQEGDKFKL ALITVMCNDF	31 SKGEMKELLH FQGCPDRP	41 KELPSFVGEK	51 VDEEGLKKIM	60
10	Nucleic Ac	11 DNA sequid Accession lence: 336-6	#: Eos sec	fuence			
15	CCTGGGTGGG GAGCTGGCAC CAGGGTTTGG	11 CCCGGTCCAG CTCAGGGGCT TCTCTGGGAG TGGGATCAGG	GCCCTTGACC GGAGGGGGCT TTGAGGCAGG	TGGCCTAGAG GGGAGGGAAT TTTGGTTTCC	CCCTCCCCCA GAGTGGGAAT TTAAAATGCC	GCTGGTGGTG GGCAAGAGGC AAGTTGGGGG	60 120 180 240
20	GGGTCTGTCT CGCTGGCTGT	CCACATATAA CTGCCACCTG GCTGGTCACT GGGGGAAATG ACCATGTGCT	GTCTGCCACA ACCTTCCACA AAGGAACTTC	GATCCATGAT AGTACTCCTG	GTGCAGTTCT CCAAGAGGGC	CTGGAGCAGG GACAAGTTCA TTTGTGGGGC	300 360 420 480 540
25	CCAGCAGGTG TGACTTCTTC	ACCATGTGCT AAACCAGAGC GATGAGGAGG GACTTCCAGG CAGGGCTGCC GCCCAGGACT	AGTATGCTGT CAGACCGACC	GCTGATGGGC TTTCCTGGCA CTGAAGCAGA	CTCATCACTG ACTCTTGACT	TCATGTGCAA TCCTGCCATG	600 660 720 780 840 900
30	TCTCTCCAAG	ATATTTAAT TGAGGGCCTC GCCAGAGCTA TCGAGATAGG	TGCTTTAGGT	CTCAATTTTG	GAATTTCAAA	CACCAGCAAA	960 1020 1080
35	Seq ID NO: Protein Acc	12 Protein ession #: 1	sequence:	•	•		
40	1 MMCSSLEQAL VHLFNPVIGD	11 AVLVTTPHKY LRNQSPEGKS	SCOEGDKPKL SCOEGDKPKL DCPKITQHWR	31 SKGEMKELLH KWMRRG	41 KELPSFVGHS	51 REPCAVRAFR	60
45	Nucleic Ac	13 DNA sequ ld Accession mence: 58-35	#: Eos sed	Tuence			
	1	11	21	31	41	ș1	
50	ATGTGCAGTT TGCCAAGAGG GAGCTGCCCA	CATGTGGGGG CTCTGGAGCA GCGACAAGTT GCTTTGTGGG AGAACAGTGA	GGCGCTGGCT CAAGCTGAGT GGAGAAAGTG	GTGCTGGTCA AAGGGGGAAA GATGAGGAGG	CTACCTTCCA TGAAGGAACT GGCTGAAGAA	CAAGTACTCC TCTGCACAAG GCTGATGGGC	60 120 180 240
55	CTCATCACTG ACTCTTGACT TATTCAATAA CCCGGCTGGC	TCATGTGCAA TCCTGCCATG ACTTTTTTTG TCAGCTGGAG CTCCTGGAAA	TGACTTCTTC GATCTCTTGG TCTGTTGATA TGCTGGGAGA	CAGGGCTGCC GCCCAGGACT ATATTTTAAT TGAGGGCCTC	CAGACCGACC GTTGATGCCT TGCTCAGTGA CTGGATCCTG	CTGAAGCAGA TTGAGTTTTG TGTTCCATAA CTCCCTTCTG	360 420 480 540 600
60	GAATTTCAAA AAATAAAGAT	CACCAGCAAA ATTAAAAAAG	AAATTGGAAA GCAAATACCA	TCGAGATAGG	TTGCTGACTT	TTATTTTGTC	660
65	Protein Acc 1 MMCSSLEQAL	14 Protein cession #: 1 11 AVLVTTFHKY VDFQEYAVPL	IP_005969.1 21 SCQEGDKFKL	31 SKGEMKELLH FQGCFDRP	41 Kelpsyvgek	51 VDEBGLKKLM	60
70	Nucleic Aci	15 DNA sequ Ld Accession Lence: 62-35	a #: Eos sec	quence			
75	1 GGAGGGTGTG CATGATGTGC	11 CCGCTGAGTC AGTTCTCTGG GAGGGCGACA	21 ACTGCCTGGG AGCAGGCGCT	31 CATCTGGGCC GGCTGTGCTG	41 TGGAACCTCG GTCACTACCT	51 GCCACAGATC TCCACAAGTA	60 120
80	CAAGGAGCTG GGCACTCATC CAGAACTCTT	CCCAGCTTTG GATGAGAACA ACTGTCATGT GACTTCCTGC	TGGGGGAGAA GTGACCAGCA GCAATGACTT CATGGATCTC	AGTGGACTTC CTTCCAGGGC TTGGGCCCAG	GAGGGGCTGA CAGGAGTATG TGCCCAGACC GACTGTTGAT	AGAAGCTGAT CTGTTTTCCT GACCCTGAAG GCCTTTGAGT	180 240 300 360 420
85	TTTGTATTCA ATAACCCGGC TCTGGGCTCT	ATAMACTITT TGGCTCAGCT GACTCTCCTG CAAACACCAG	TTTGTCTGTT GGAGTGCTGG GAAATCTCTC	GATAATATTT GAGATGAGGG CAAGGCCAGA	TAATTGCTCA CCTCCTGGAT GCTATGCTTT	GTGATGTTCC CCTGCTCCCT AGGTCTCAAT	480 540 600 660

WO 02/086443 TGTCAAATAA AGATATTAAA AAAGGCAAAT ACCA

Seq ID NO: 16 Protein sequence: Protein Accession #: NP_005969.1

5 10

> Seq ID NO: 17 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 939-2372

15		d Accession lence: 939-2		ruence			
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	CGCGGGGGGCA	GGGCACGCGT	TCGCGCACAC	CCTAGCACAC	ATGAACACGC	GCAAGAGCTG	240
	AACCAAGCAC	GGTTTCCATT	TCAAAAAGGG	AGACAGCCTC	TACCGCGATT	GTAGAAGAGA	300
25	CTGTGGTGTG	AATTAGGGAC	CGGGAGGCGT	CGAACGGAGG	AACGGTTCAT	CTTAGAGACT	360
25	AATTTTCTGG	AGTTTCTGCC CGGCGGCGGC	CCTGCTCTGC	GTCAGCCCTC	ACGICACTIC	GCCAGCAGTA	420 480
	GCAGAGGCGG	CTACGCGCTC	ACTOCCCCCC	COTTACCACCA	CCTCGACCC	AGGCCCCCCC	540
		AGGCGCCGGA					600
	AACAAGGAAT	CTGCGCCCCA	GAGAGTCCCG	GGAGCGCCGC	COGTCGGTGC	CCGGCGCGCC	660
30	GGGCCATGCA	GCGACGGCCG	CCGCGGAGCT	CCGAGCAGCG	GTAGCGCCCC	CCTGTAAAGC	720
	GGTTCGCTAT	GCCGGGGCCA	CTGTGAACCC	TGCCGCCTGC	CGGAACACTC	TTCGCTCCGG	780
	ACCAGCTCAG	CCTCTGATAA	GCTGGACTCG	GCACGCCCCC	AACAAGCACC	GAGGAGTTAA	840
	GAGAGCCGCA	AGCGCAGGGA	AGGCCTCCCC	GCACGGGTGG	GGGAAAGCGG	CCGGTGCAGC	900 960
35	GCGGGGACAG	GCACTCGGGC CATGGCGCGG	TGGCACTGGC	TGCTAGGGAT	GTCGTCCTGG	TRANSTIGG	1020
33	ATGGACCCGC	CATGGCGCGG	TOTALLA	GCAGTGCCTC	TOTATOTA	TGCAGCGACC	1080
	CTTCTCTGG	CATCGTGGCA	TTTCCGAGAT	TOGRECCTAA	CAGTGTAGAT	CCTGAGAACA	1140
	TCACCGAAAT	TTTCATCGCA	AACCAGAAAA	CCTTAGAAAT	CATCAACGAA	GATGATGTTG	1200
	AAGCTTATGT	GGGACTGAGA	AATCTGACAA	TTGTGGATTC	TGGATTAAAA	TTTGTGGCTC	1260
40	ATAAAGCATT	TCTGAAAAAC	AGCAACCTGC	AGCACATCAA	TTTTACCOGA	AACAAACTGA	1320
	CGAGTTTGTC	TAGGAAACAT	TTCCGTCACC	TTGACTTGTC	TGAACTGATC	CTGGTGGGCA	1380 1440
	ATCCATTTAC	ATGCTCCTGT TCAGGATTTG	GACATTATGT	GGATCAAGAC	CONCORRE	CCCCCCCA	1500
	ACCTCCAGACAC	ACCCAATTGT	COTTOCCTOR	CTCCAAATCT	CARGACIATI	AACCTCACTG	1560
45	TECHCOLOGI	AAAGTCTATC	ACATTATCCT	GTAGTGTGGC	AGGTGATCCG	GTTCCTAATA	1620
	TGTATTGGGA	TGTTGGTAAC	CTGGTTTCCA	AACATATGAA	TGAAACAAGC	CACACACAGG	1680
	GCTCCTTAAG	GATAACTAAC	ATTTCATCCG	ATGACAGTGG	GAAGCAGATC	TCTTGTGTGG	1740
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50	CTATCACATT	TCTCGAATCT	CCAACCTCAG	ACCACCACTG	GTGCATTCCA	TTCACTGTGA	1860
30	AAGGCAACCC	CAAACCAGCG TACTAAAATA	CTTCAGTGGT	TCTATAACGG	GGCAATATTG	MATGAGTCCA	1920 1980
	RATACATCIG	CACTCACATG	PACATOTTACCA	ATCACACGGA	BATACCCACGC	PATGAGTATG	2040
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	ACCATCACTT	TGGGACTTGG	TAGTATTATT	ANANGGTTAT	TTCCTTCACT	GTCAATAAAA	3000
	GTCCAAATGT	TTAGCTTAGG	TCTGAGAGTC	AAACAATGTT	AAGGATTGTC	TTARAGTTCC	3060
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	GGCATAGTCA	ATTTCAGAAT	AACTAAGAGT	GGAATATATG	CATATGGTGA	AATTATAACC	3240
	TIGCCCITTI	TTATTTGCCC	TCTGCGATCC	ACCTGCTTTT	TAGAAGTCTG	CCGAGTGAGA	3300 3360
75	AGGCCACAGT	ATCTCATGCT GAATGGCTGG	GTTTGCATTA	CAGAMCIGO	BOATTOTAG	AAGGATAGTC	3420
13	CCCCCTACAA	CATACTCTCA	TACTOCYCO	TTTTCATGGG	TAGGAAAGCT	TGTCCTGACC	3480
	CCAGCAGCAA	AGAGGTGGCA	GGTCGCTAAT	GAATATATGC	TTTATAATGT	CCTTCTTCAT	3540
	TOTTCAGAGG	GCAGCCTTAG	AGCTGTGGAT	TTCTGCATCC	CCCCTGAGTC	TGACCCATGG	3600
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80	CAGGCAGTAT	GCTTGTCCTG	AAGAGAGGTT	TGGCTATCCC	CACCCCACCC	CACCCCACCC	3720
	TGTTCCTTTT	TTATCAGGAG	GACTTCAGAG	CCAGGCCTGC	AGCATTTTGT	11GAAAACAC	3780 3840
	AATCAGCTCT	GACAGTTAGA	CATGCACACA	TOCACA A A TO	CIGOMITOGA	AACATTGATG	3900
	TOTATAGATT	TTTAACTAGT	CCAACACACAGT	CAGAAACATT	GTTTTGAATC	CTCTGTAAAC	3960
85	CARGGCATTA	ATCTTAATAA	ACCAGGATCC	ATTTAGGTAC	CACTTGATAT	AAAAAGGATA	4020
	TCCATAATGA	ATATTTTATA	CTGCATCCTT	TACATTAGCC	ACTAAATACG	TTATTGCTTG	4080
	ATGAAGACCT	TTCACAGAAT	CCTATGGATT	GCAGCATTTC	ACTTGGCTAC	TTCATACCCA	4140

	****	1006443					
		/086443				a amummaa	4200
	TCCTAACTCC	AGGGGCAGTT ATTTGAATGT	AAGGGCAGCT	GGCCCCCAAT	GTGGGGAGGT	CCGAACATTT	4260
	TOTGAATTCC	CATTTTCTTG	TTCCCCGCCTA	AATGACAGTT	TCTGTCATTA	CTTAGATTCC	4320
5	GATCTTTCCC	AAAGGTGTTG TGAAATTCAA	ATTTACAAAG	AGGCCAGCTA	ATAGCAGAAA	TCATGACCCT	4380 4440
,	GAGAATCAGC	CATTTGGTAC	AAAAAAGATT	TTTAAAGCTT	TTATGTTATA	CCATGGAGCC	4500
	ATAGAAAGGC	TATGGATTGT	TTAAGAACTA	TTTTAAAGTG	TTCCAGACCC	AAAAAGGAAA	4560 4620
	AATAAAAAA	AAGGAATATT AGAGAAGTGG	TGTACCCAAC	AGCTAGAAGG	ATTGCAAGGT	CAGTTGACAT	4620
10	CTCCTAGGGA	ATGATGAAAA	CAGCAGGCTA	T			
	Protein Acc	18 Protein ession #: 0	AAS3571				
1.5							
15	1	11	21	31	41	51	
	MSSWIRWHGP	AMARLWGFCW	LVVGPWRAAF	ACPTSCKCSA	SRIWCSDPSP	GIVAPPRLEP	60
	NSVDPENITE	IFIANQKRLE SRKHFRHLDL	IINEDDVEAY	VGLRNLTIVD	SGLKFVAHKA	PLKNSNLQHI .	120
20	SKNTPLANIA	IPNCGLPSAN	LAAPNLTVEE	GKSITLSCSV	AGDPVPNMYW	DVGNLVSKHM	240
	NETSHTOGSL	RITNISSDDS	GKQISCVAEN	LVGEDQDSVN	LTVHFAPTIT	PLESPTSDEH	300
	WCIPFTVKGN	PKPALQWPYN EKQISAHPMG	GAILNESKYI	CTKIHVTNHT	BYHCCLQLON	THINNIGHT	360 420
	DVTDKTGREH	LSVYAVVVIA	SVVGPCLLVM	LFLLKLARHS	KEGMKGEVLE	HKIPLDG	
25						•	
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85	A A C C A C C C C C C C C C C C C C C C	CONTRACTOR CONTRACTOR	CACACCCATC	GAGGAGCTCC	GCCACCAAGC	CCGGCAGCAG	3240
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		1	acras arens	CDITANCETER	LONCOTOTA	KDETYCTOVG	60		
	MRPFFLICFA	DEGUNAQUA	CSRGACIPPY	DIDDANGELEE	IMMUST OF DE	DEPENTATION			
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20	MERCGIMPAG	MLIERSSDEG	KIWKVIQIDA	MCISTERV	THE PART A PULLOOP	CAMBBERANA			
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	VSQLRLQGSC	PCHGHADRCA	PRPGASAGPS	TAVQVRDVCV	CUCCHACAGENC	POPULOPPOOL			
	PWRPAEGQDA	HECORCDCNG	HSETCHFDPA	VFAASQGAYG	GVCDNCKDRT	DI CKOCIMOT			
25	HYFRNRRPGA	SIGELCISCE	CDPDGAVPGA	PCDPATGGCA	CKBAVQGERC	DISCUSSION OF THE			
25									
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Seq ID NO: 21 DNA sequence Nucleic Acid Accession #: NM_003722 Coding sequence: 145-1491

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	ANDUOUNGCIG	AGGGACAGAT	BCCCCCCCCCCCC	ACTCATTTCA	TTCGAGTAGA	COCCAACAGO	844
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80	TTTGTGAGAA	CTTGCATTAT	TTGTGTCCTC	CCCTCATGTG	TAGGTAGAAC	ATTTCTTAAT	216
	GCTGTGTACC	TGCCTCTGCC	ACTGTATGTT	GGCATCTGTT	ATGCTAAAGT	TTTTCTTGTA	222
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	CACCAGCACT	GTATTTTCTG	TCACCAAGAC	AATGATTTCT	TGTTATTGAG	GCTGTTGCTT	2760
5	TTGTGGATGT	GTGATTTTAA	TTTTCAATAA	ACTITICAT	CTTGGTTTAA	AAGAAA	
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15	PQGAVIRAMP	VYKKAEHVTE	VVKRCPNHEL	SREFNEGQIA	PPSHLIRVEG	NSHAQYVEDP	240 300
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	Nucleic Ac	id Accession	ience	944.1			
	Coding seg	uence: 84-30	083				
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	Sea In No.	24 Protein	semience:				
85	Protein Ac	Cession #:	MP 001935.1				
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20 Seq ID NO: 25 DNA sequence Nucleic Acid Accession #: Eos sequence coding sequence: 56-1642

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	GGMCTCTTTT	ATCTTTGGGC	CACAACTOCC	ACAGGGATCC	TTCTTCAACC	AADTOTOAAT	480
	CONCINCONS	AAGGATGTAC	TCABAGGGCA	GAACTGGCTC	ATCTATACAT	ATGGAGTCAC	540
35	MATERIA CONTRACTOR	AAAACCCACA	CONTECNACE	TACCATCAAC	GATGGAGGGA	TTCTCCCCCG	600
55	TAACTCAGGG	CTGATCTTCA	AMACCCTCCA	ACCCCAACTT	CATCCAACAC	CTCATCTCAA	660
	GICCCIGGCG	TCCAATGAGG	#ANGCCICCA	AGRICACIONALI	CAGATCCGAC	AGGAGGAAAT	720
	GCCCTTGCTC	TCCCTGCTAA	AMOCACCOCT	CCAACAGCAG	CAGATCCCAC	CTTCCTTCAA	780
	GAAGAUGCIG	TACATCGAAA	ALGGNOGCCI	TA CCT CCT CC	ACCEPACION	GTGCCATTGC	840
40	GAGGAGIGIC	TCTATCAGTC	ACTOCION COMO	CACTACCCAC	CTCCATCAAA	CARGECATOG	900
40	TGGGCTCTCT	CCAGACACTG	AGTGTACCAG	CAGTAGCCAG	* A CAMPOCOTE	CONGIGUE	960
	ATGGGCACAG	TTTGAGATCT	CCCCACTACC	COTTTNUCAC	CTATTACAAC	CCCCTACCCA	1020
	GATCTCATTC	AGGCAGACTT	MCANCONACT MCCOCCONA MC	COLCORAGE	THE THORNE	COTTANCTORA	1080
	ACAGCGCAAG	TGGATTCATG	TGCGGCTATG	TOAGGATCAA	MAIGGCANIC	TARACTOR	1140
45	AGATCTCAAC	CAGAGCTTTG	TGCAAGATGC	TOMOGRAGICA	100MAGCICC	TANAMIGI GOO	1200
43	TCGTAAGAAC	ATCAGGATCC	CCAGCACCCA	CCTCAACCAG	AMCTCCAGCC	CONTRACTOR	1260
	CATCITCICA	CTCTGTGATC	TACACCUTCA	GGGGGAAGGA	GATATAGICC	COMMICAG	1320
	CGAGCTGTCA	GAAGCAGGAA	TGGCTGGCTC	AGAGGGGCTGC	MANGATCAGA	MONOTOGICAL	1380
	ACGGTTGAAG	CAAAACCAGC	ACATTACACAC	PARCONCAL	ACCCIGGGCC	TCCCTCACAC	1440
50	TGCCCTTCGT	CGAGTGTTCC	MGAACCGGIC	CACAGOGG	COCCOMMOCM	CCATCATTOT	1500
30	CAAGTTGACT	CCCTGTGCAT	AAGGITICIT	CACAGGCCGA	CATCTCCCCA	BOTTOTORGO	1560
	CAATGIGAAT	CAGGTGACTT	CINCCINIGA	CACCTATGCA	ACTGGGGATTC	CATCCCTGC	1620
	CATIGCIAGE	CAAGGAACAT	PODGETTOCCC	WATCH COURT	CTTACACAAA	GCCCCTAAGG	1680
	ACTOGREGAT	CCTTGATGAT	CATATTONA	ATGRACCTGA	CATCTCCATG	TATGGCAAAG	1740
55	CAGACACAGG	ACAAGTTGTG	CARCCOATCA	ACACACTOCT	TTTGAAGGAA	CCACACGAAA	1800
55	AGGAGCICCI	GGAGATGCAT	CTCCCACATC	AAATTYCCAA	TGAGATGGTA	GAACAGATGC	1860
	AGCTACAGCT	ACAGTGGTGC	*COCONGATO	TOTAL CACCOCA	BARCCARCTA	TTGGAGGAAA	1920
	AACAGCGGGA	AAAACTAAAT	AUTOMOCITE	ACTOR CTORC	PARCOLLIA	CAAGAAGAGA	1980
	TGTATGAAGA	GGATGAAAAG	ATCCTCAMOG	MACA ACCORD	CTTCCACCAA	GCCAGACAAC	2040
60	TTCAGGAGCG	CCATCAGCAA	MITONAGAGE	BATTO CCCCT	ACCECCATCA	CAAAGGTTGG	2100
00	AGTCAGTGGC	CTCCACCCAG	CAGGGGGGG	ACCOUNTABLE	TA A ATTA CAC	CACTOCAAAG	2160
	CAGCITCIGC	CTCTACCACT	CABCATCAGG	ATANCTATOR	CAAAATTTA	GAACCACCAC	2220
	CAGAGCTAAA	GCCCTTCACC	ATTORNOTTOC	ACABGAAGTT	AGRAGAGGGC	CAGAAGAATA	2280
	CCICAGCCAA	GCGGACAGAG	CHECKEGIGG	THYCHOLOGIC	TOTOCANTON	GCAGAGAGAG	2340
65	TANGGCIGIT	CAGCACTGGG	CIICAGOOAC	TIGGIGAGIC	CTTCACTACT	TYPEDATERCA	2400
03	CITOTIOCCA	ACAGGACCAG	ACTOTOCOM	PACTECAGAR	CARCATGGTG	CTAGTGAAAC	2460
	TCTTAATCAA	GAAGAAGGCA	ACTUIOGUIG	OFFICERCATE	TOTAL	TTGAAACTCC	2520
	TGGACCTTCG	TTCTGCCAAA	PACCOCCULATION OF THE	CTACCARCCA	CCANANTCAC	CARCCARACC	2580
	AAGGCCAGGT	AGGGAAGAAA	ACT WAS COLCUITED	GIACCAACCA	TOTOTALO	CONNECTRO	2640
70	AACAACCACC	AGACTGCAGC	CONTICCTIC	CONTROCTO	CTCACCCCCT	TOTOCTTTAC	2700
70	AAAUCTCAAC	GCCTTTTGGC	CCTTATGCCC	and common	CICACOCCI	CACCACTCAG	2760
	TCAAATCTGG	TGGGTCAGCT	AAAAAGTACT	ACCEPTAGE	CONTRACTOR	CTTTACCATA	2820
	GGCCCTGAGG	TATATCAGCT	ACTO TOCTOR	COLON CALCADO	CTTTTTTT	ACTIONION	2880
	TATCAGGAAT	TATATCCAGG	ATGUARTACT	CAUACACTAG	TOTAL COMMENTS	MCITIGIAI	2940
75	TATAACCACC	ACAGTTATAT	CATGITIGITG	A TTTTTTTTT	TIMOTIATA	PATTICIAT	3000
13	GCACACAAAA	CATTARACA	TAMMATATT	CCCDCDCDCD	BR TILLIFEATIG	WITCHMI	2000
	GTAGCAAAAT	CATTAAAACA	AALLATAAAA	GOGNCHUHAN	. ^^		

Seq ID NO: 26 Protein sequence: Protein Accession #: Eos sequence 80

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	1	11	21	31	41	51	
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	MSOGILSPPA	GLLSDDDVVV	SPMFESTAAD	LGSVVRKNLL	SDCSVVSTSL	EDKQQVPSED	60
	SMEKVKVYLR	VRPLLPSELE	RQEDQGCVRI	ENVETLVLQA	PKDSFALKSN	ERGIGOATHR	130
85	PTFSQIFGPE	VGQASFFNLT	VKEMVKDVLK	CONMITALA	VINSORTHTI	QGTIKDGGIL	180
	PRELALIPNS	LOGOLHPTPD	LKPLLSNEVI	WLDSKQIRQE	EMERLSLLING	GLQEEELSTS	240
	LKRSVYIESR	IGTSTSFDSG	IAGLSSISQC	TSSSQLDETS	HRWAQPDTAP	LPVPANIRFS	300

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	WO 02/						
	VGRKNQSPAS GERLKEAGNI	ELLYDLLEPP THLMQNSSRS NTSLHTLGRC YDETLHVAKF	HSIFSIRILH IAALRONOON	LQGEGDIVPK RSKONLVPFR	ISELSLCDLA DSKLTRVFOG	GSERCKDOKS	360 420 480
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	Nucleic Ac:	27 DNA sequid Accession ence: 13-14	#: Eos sec	Ineuce .			
10	1	11	21	31	41	51	
		CAATGAAGTT	-	I	PCCCCP CAMC	TTCTCCACCT	60
	CTTCCCCTGA	ACAGCTCTAC	AAGCCTGGAA	AAAAATAATG	TGCTATTTGG	TGAAAGATAC	120
	TTAGAAAAAT	TTTATGGCCT	TGAGATAAAC	AAACTTCCAG	TGACAAAAAT	GAAATATAGT	180
15	GGAAACTTAA	TGAAGGAAAA	AATCCAAGAA	ATGCAGCACT	TCTTGGGTCT	GAAAGTGACC	240
	GGGCAACTGG	ACACATCTAC TCAGGGAAAT	CCTGGAGATG	ATGCACGCAC	CTCGATGTGG	AGTCCCCGAT	300 360
	AGAATCAATA	ATTACACACC	TGACATGAAC	CGTGAGGATG	TTGACTACGC	AATCCGGAAA	420
••	GCTTTCCAAG	ATTACACACC TATGGAGTAA	TGTTACCCCC	TTGAAATTCA	GCAAGATTAA	CACAGGCATG	480
20							540 600
	AAAGGTGGAA	TCCTAGCCCA ACGAATTCTG	GACTACACAT	TCAGGAGGCA	CARACTTGTT	CCTCACTGCT	660
	CTTYCA CCAGA	TYGGCCATTC	CTTAGGTCTT	GGCCATTCTA	GTGATCCAAA	GGCCGTAATG	720
0.5	TTCCCCACCT	ACAAATATGT CCCTGTATGG	TGACATCAAC	ACATTTCGCC	TCTCTGCTGA	TGACATACGT	780
25	GGCATTCAGT	CTCTCTGTGA	AGACCCAAAA	GAGAACCAAC	GCTTGCCAAA	TCCTGACAAT	840 900
	AAGATCTTTT	TCTTCAAAGA	CAGGITTCTTC	TGGCTGAAGG	TTTCTGAGAG	ACCAAAGACC	960
	AGTGTTAATT	TAATTTCTTC	CTTATGGCCA	ACCTTGCCAT	CTGGCATTGA	AGCTGCTTAT	1020
30	GAAATTGAAG	CCAGAAATCA	AGTTTTTCTT	TTTAAAGATG	ACAAATACTG	GTTAATTAGC	1080
30	AATTTAAGAC	CAGAGCCAAA TTGATGCAGC	TTATCCCAAG	AGCATACATT	ATAGGACCTA	CTTCTTTGTA	1200
							1260
	CTGATTACCA	AGAACTTCCA ACTATTTCTT	AGGAATCGGG	CCTAAAATTG	ATGCAGTCTT	CTACTCTAAA	1320
35	AACAAATACT	ACTATTTCTT	CCAAGGATCT	AACCAATTTG	AATATGACTT	CCTACTCCAA	1380 1440
33	TGGTTTTTGT	TAGTTCACTT	CAGCTTAATA	AGTATTTATT	GCATATTTGC	TATGTCCTCA	1500
	GTGTACCACT	TAGTTCACTT ACTTAGAGAT	ATGTATCATA	AAAATAAAAT	CTGTAAACCA	TAGGTAATGA	1560
							1620 1680
40	CTCTACTATT	AAGTTTGAAA TGCTTCCTAA	CATCCTTGGA	CTGAGAAATT	ATACTTACTT	CTGGCATAAC	1740
10	TAAAATTAAG	TATATATATT	TTGGCTCAAA	TAAAATTG			
	Seq ID NO:	28 Protein	sequence:				
	Protein Ac	reggion # · I	tos semience				
45	Protein Ac	cession #:	Sos sequence				
45	Protein Ac	cession #:	Zos sequence	31	41	51	
45	1 MKPLLILLLO	cession #: - ATASGALPLN	21 ESTSLEKNNV	31 LPGERYLEKP	YGLEINKLPV	TKMKYSGNLM	60
	1 MRPLLILLLQ	11 ATASGALPLN	21 STSLEKNNV	31 LPGERYLEEP BCGVPDVHHP	YGLEINKLPV REMPGGPVWR	TKMKYSGNLM KHYITYRINN	120
45 50	1 MRPLLILLLQ	11 ATASGALPLN	21 STSLEKNNV	31 LPGERYLEEP BCGVPDVHHP	YGLEINKLPV REMPGGPVWR	TKMKYSGNLM KHYITYRINN	120 180
	1 MRPLLILLLQ KEKIQEMQHF YTPDMNREDV LAHAFGPGSG	11	21	31 LFGERYLEKF RCGVFDVHHF KINTGMADIL NLFLTAVHEI LDNDINGSPIA	YGLEINKLPV REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDDNLSEDA	TKMKYSGNLM KHYITYRINN PHAPDGKGGI DPKAVMFPTY VTTVGNKIPP	120 180 240
	1 MRPLLILLLQ KEKIQEMQHF YTPDMNREDV LAHAFGPGSG	11	21	31 LFGERYLEKF RCGVFDVHHF KINTGMADIL NLFLTAVHEI LDNDINGSPIA	YGLEINKLPV REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDDNLSEDA	TKMKYSGNLM KHYITYRINN PHAPDGKGGI DPKAVMFPTY VTTVGNKIPP	120 180 240 300 360
50	1 KEKIQEMQHF YTPDMNREDV LAHAFGPGSG KYVDINTFRL PKDRPFWLKV EPNYPKSIHS	11 ATASGALPLN LGLKVTGQLD DYAIRKAFQV IGGDAHFDED SADDIRGIQS SERPRTSVNL PGFPNFVKKI	21 21 STSLEKNNV TSTLEMMEAP WSNVTPLKPS EPWITHSGGT LYGDPKENOR ISSLWPTLPS DAAVPNPRPY	31 	YGLEINKLPV REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDPNLSFDA RNQVPLFKDD WRYDERRQMM	TKMKYSGNLM KHYITYRINN PHAPDGKGGI DPKAVMFPTY VTTVGNKIPP	120 180 240 300
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50	I MKPLLILLLQ KEKTQEMQHF YTPDMNREDV LAHAFGPGSG KYVDINTFRL PKDRPFWLKV EPNYPKSIHS MFQGIGPKID Seg ID NO:	11	21 SSTSLEKNNV TSTLEMMHAP WSNVTPLKPS EFWTHESGT LYGDPKENOR ISSLWPTLPS DAAVPNRFY YPPOGSNOFE	31 	YGLEINKLPV REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDPNLSFDA RNQVPLFKDD WRYDERRQMM	TKMKYSGNLM KHYITYRINN PHAPDGKGGI DPKAVMFPTY VTTVGNKIPP	120 180 240 300 360
50	1 KEKIQEMQHF YTPMNREDV LAHAFGPSGG KYVDINTFRL PKDRPFWLKV EPNYPKSIHS NFQGIGPKID Seg ID NO: Nucleic Ac	11	21	31 	YGLEINKLPV REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDPNLSFDA RNQVPLFKDD WRYDERRQMM	TKMKYSGNLM KHYITYRINN PHAPDGKGGI DPKAVMFPTY VTTVGNKIPP	120 180 240 300 360
50	1 KEKIQEMQHF YTPMNREDV LAHAFGPSGG KYVDINTFRL PKDRPFWLKV EPNYPKSIHS NFQGIGPKID Seg ID NO: Nucleic Ac	11	21	31 	YGLEINKLPV REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDPNLSFDA RNQVPLFKDD WRYDERRQMM	TKMKYSGNLM KHYITYRINN PHAPDGKGGI DPKAVMFPTY VTTVGNKIPP	120 180 240 300 360
50 55	1 KEKIQEMQHF YTPMNREDV LAHAFGPSGG KYVDINTFRL PKDRPFWLKV EPNYPKSIHS NFQGIGPKID Seg ID NO: Nucleic Ac	11	21	31 	YGLEINKLPV REMPGGPVWR VVFARGAHGD GHSLGLGHSS LCDPNLSFDA RNQVPLFKDD WRYDERRQMM	TKMKYSGNLM KHYITYRINN PHAPDGKGGI DPKAVMFPTY VTTVGNKIPP	120 180 240 300 360
50 55	MRPLITLLO KEKTQEMQHF YTPONNREDV LAHARGPGSG KYVDINTFRL EDNYPKSINS NFQGIGPKID Seq ID NO. Nuclaic Ac Coding seq	11 ATASGALPLM LGLKVTGQLD DYALTKAPQLD USGDAHFDED SADDIRGIQS SERPRTSVNL PGFNNFVKKI AVFYSKNKYY 29 INA seq id Accession uence: 236.	21 STSLEKNNV TSTLEKNNV TSTLEMBLAP SENTIFICAP SEPWITESGGT LYGDPKENQR ISSLWPILPS DAAVENPRPY YPFQGSNQFE LICICE a #: NM_0061 1.765	31 LFGERYLEKF RCGYPDVHHP KINTOMADIL NLPITAVHEI LENPDNISEPA GIERAYETEA RTYPPVDNQY YDFILQRITK	YGLEINKLPV YGLEINKLPV YGRAGAGG GHSLGLGAG GHSLGLGAG GHSLGLSAG GHSLGLSAG GHSLGLSAG GHSLGLSAG MYDERGOM TLKSNSWPGC	TIMKYSCHLM KHYITTRINN PHAPDERGGI DPKAVMPPTY VTTVGNKIPP KYMLISNLRP DPGYPKLITK	120 180 240 300 360 420
50 55 60	MRPLLILLO KEKTQEMQHF YTFDNNREDV LAHARGPGSG KYVDINTFRL ENVPKSINS NFQGIGPKID Nclaic Ac Coding seq GCTTCAGGGT COSSECCO	11. I ATASGALPIN LGLKYTGOLD DYARRANGV IGGDAHPDED SADDIRGIGS SERRITSVIK PGFNNFVIK AVFYSKNKY 29 INA seq id Accession mence: 236. 11. ACAGGTCCCCC	ZOS SEQUENCE 21 SSTSLEXNNV TSTLEMBEAP SSNTPLKPS EPWTHSGGT LYGDPKENGR LYGDPKENGR LYGDPKENGR LYGDPKENGR LYGDPKENGR 4: NM_0061 1765 21 CSCAGOCAGA	31 	YGLEINKLPV YGLEINKLPV YGRAGAGG GHSIGLGES LCDPNLSPDA RNQVPLFROM WIYDERROM TLKSNSWFGC	TOWKYSCHLM KHYITYRINN FILAPDERGGI DPRAVMPPTY VTTVGNKIPP KYMLISNLRP DPGYPKLITK	120 180 240 300 360 420
50 55	MRPLLILLO KEKTQEMQHF YTFDNNREDV LAHARGPGSG KYVDINTFRL ENVPKSINS NFQGIGPKID Nclaic Ac Coding seq GCTTCAGGGT COSSECCO	11. I ATASGALPIN LGLKYTGOLD DYARRANGV IGGDAHPDED SADDIRGIGS SERRITSVIK PGFNNFVIK AVFYSKNKY 29 INA seq id Accession mence: 236. 11. ACAGGTCCCCC	ZOS SEQUENCE 21 SSTSLEXNNV TSTLEMBEAP SSNTPLKPS EPWTHSGGT LYGDPKENGR LYGDPKENGR LYGDPKENGR LYGDPKENGR LYGDPKENGR 4: NM_0061 1765 21 CSCAGOCAGA	31 	YGLEINKLPV YGLEINKLPV YGRAGAGG GHSIGLGES LCDPNLSPDA RNQVPLFROM WIYDERROM TLKSNSWFGC	TOWKYSCHLM KHYITYRINN FILAPDERGGI DPRAVMPPTY VTTVGNKIPP KYMLISNLRP DPGYPKLITK	120 180 240 300 360 420
50 55 60	MEPLIJILLIA KEKIGEMGER TYPDINNEEDV LAHARGPGSG KYVDINTFRL FEDRFFWLKV EDNYPKSIHS MEPGIGPKID Seq ID NO: Nucloid a Coding seq GCTTCAGGGT GGTTCAGGGT COGGACACCC ACTCTTCAG	11 11 11 12 13 14 15 16 17 17 18 17 18 17 18 18 18 18 18 18 18 18 18 18 18 18 18	ZOS SEQUENCE 21 SSTSLEKNNV TSTLEMBEAP KSNVTPLKPS EPWTHSGN LYGDPKENGR LYGD	31 	YGLEINKLPV REMPGGPVWR VVPARGARGO GRSIGLGHSS LCDPNLSPBA WRYDEFRAD W	TOWKYSCHLM KHYITYRIMN FHAPDGROGI DPEAVMFPTY VTTVGHKIPF KYMLISHLED DPGYPKLITK 51 AGCACCGCTC GGTGTGGTGA ACAAGTGACT TCAAAATGGA	120 180 240 300 360 420
50 55 60	MEPLIJILLO MERCIGEMORE TYPDNOREDV LMHARGPOSG KYVDINTERL PKDRPFWLKV ENNYRSINS NEGGIGPKID Seq ID NO: NUClaic Ac coding seq CGTTCAGGGT CGGGACACCT ACTCTCTGGG ACGACTGGG ACGACTGGG ACGACTGGG ACGACGGGG ACGACGGG ACGACGGGG ACGACG	11 ATASGALPLM LGLKVTGQLD DYALRKARGV LGGDAHFDED SADDIRGIGS SERPETSVIN FGFNHFVKKI AVFYSRNKYY 29 INA seq id Accession wence: 236. 11 ACAGGTCCCC CACCGGTTC AATACCAAGGG TTGTGSGGGTT	21 21 25 SEQUENCY 25 STATEMENTA 26 STATEMENTA 26 STATEMENTA 27 STATEMENT	31 LPGERYLEKP RCGYDVHEN RCGYDVHEN KINTGMADIL ILPIDNOSE GIEAAYETEA RTYPFUDNOY TOPFILORITK 31 AGCCGGGCCT CCTGTCAACA TGAGGCCAGC TGAGGCCAGC CCGATACATC	YGLEINKLPV REMPGGPVMF VPFARGANGD GHSLGLGHSS LCDPALSPICATION WR IDERROMM TLKSNSWFGC 41 GCAGCCCCTC GCAGTTGGCA CTAGTGGCA CTAGTGGCA CTAGTGGCA	TOMKYSCNIM KHYITYRINN HHAPDGGGI DPKAVMPPTY VTTYGNKIPP KYMLISNIRP DPGYPKLITK 51 AGGACCGCTC GGTGTGGTGA ACAAGTGACT TCAAAATGGA	120 180 240 300 360 420 60 120 180 240 300
50 55 60 65	1 REPLITILLA REFUGEMENT TYPONNREDV LAHARGOSSE KYVDINTFRL FEDREFWIKV SenyleKitis NEGGIGPKID Seq ID NO; Coding seq I GCTTCAGGGT COGGRACACC ACTCTCTCAG AGGACCTAGA ACGAAGGCT CCCACGGGA ACGACGCC CCCACGGGA ACGACGCC CCCACGGGA ACGACGCC CCCACGGGA ACGACGCC CCCACGGGA ACGACGCC CCCACGGCA ACGACGCC	TOTOTOGGGCT CHARGAGE 11 11 12 13 14 15 16 16 17 17 17 17 17 17 17 17 17 17 17 17 17	20 sequenci 21 21 25 STSLEENNV SSTSLEENNV SSTSLEENNV SSTSLEENNV SSTSLEENNV SSTSLEENNV SSTSLEENNV SSTSLEENNV 15 SEMPTHESO 16 DAAWSHRFFY YFFQGSNOVE LIGHT SSLEENNV 21 21 21 21 21 21 21 21 21 21	31	YGLEINKLPV REMPGGPVMF VPFARGANGD GHSLGLGHSS LCDPNLSPV REMPGDFVMF VFFARGANGD TLKSNSWFGC 41 GCAGCCCCTC GCAGCTCCCC GCAGTTGGCCA CTAGGTGGCCA AGGATGAGG TCTCTTCAGG	I TKMKYSGNLM KHYITTRINN HHAPDGRGI DPKAVMPPTY VTTYGNKIPP KYMLISNIRP DPGYPKLITK 51 I AGGACCGCTC GGTGTGGTGA ACAAGTGACT TCAAAATGGA CCTGGCCAT GGTGGCCAA	120 180 240 300 360 420 60 120 180 240 300 360 420
50 55 60	THE PROPERTY OF THE PROPERTY O	11 11 12 13 14 15 17 17 18 17 18 17 18 17 18 17 18 17 18 18 18 18 18 18 18 18 18 18 18 18 18	20 sequenci 21 21 3 STSLEENNY 3 STSLEENNY 4 SSTSLEENNY 4 SSTSLEENNY 4 SSTSLEENNY 4 SSTSLEENNY 4 SSTSLEENNY 5	31 LOGRRYLEKP ROSVEDHIP KROSVEDHIP KROSVEDHIP KRITONADIL NEPLITAVHEI LEPRENSEER RTTFPUNDIG YOPFLICRITK 115.1 31 AGCOGGGCT CCTOTCAGAC ACTOTCAGAC CCCATTCAGAC CCTACCACCA CCTCCCACA CCTCCCACA CCTCCCACA CCTCCCACA CCCATTCAGAC CCTCCCACA CCTCCCACA CCCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CATTCAGAC CCATTCAGAC CCATTCAGAC CATTCAGAC CATTCAGA	YGLEINKLPV REMPSGEVWR VEPARGARGD GHSLGLGHSS LCDPNLSPD MYDERGDW MYDERGDW TLKSNSWFGC 41	TKWKYSGNLM KHYITTRINN FHAPDGRGGI DPRAVMFPTY VTTYGNRIP KYMLISNLRP DPGYPKLITK 51 AGCACGCTT GGGTGGACAG TGTAGACAG TGTAGACAG CCCTGCACA CAGCCTTTCA CAGCCTTCA CAGCCTTCA CAGCCTTTCA CCTGCACAC CAGCCTTTCA CCTGCACAC CAGCCTTTCA	120 180 240 300 360 420 60 120 180 240 360 420
50 55 60 65	THE PROPERTY OF THE PROPERTY O	11 11 12 13 14 15 17 17 18 17 18 17 18 17 18 17 18 17 18 18 18 18 18 18 18 18 18 18 18 18 18	20 sequenci 21 21 3 STSLEENNY 3 STSLEENNY 4 SSTSLEENNY 4 SSTSLEENNY 4 SSTSLEENNY 4 SSTSLEENNY 4 SSTSLEENNY 5	31 LOGRRYLEKP ROSVEDHIP KROSVEDHIP KROSVEDHIP KRITONADIL NEPLITAVHEI LEPRENSEER RTTFPUNDIG YOPFLICRITK 115.1 31 AGCOGGGCT CCTOTCAGAC ACTOTCAGAC CCCATTCAGAC CCTACCACCA CCTCCCACA CCTCCCACA CCTCCCACA CCTCCCACA CCCATTCAGAC CCTCCCACA CCTCCCACA CCCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CCATTCAGAC CATTCAGAC CCATTCAGAC CCATTCAGAC CATTCAGAC CATTCAGA	YGLEINKLPV REMPSGEVWR VEPARGARGD GHSLGLGHSS LCDPNLSPD MYDERGDW MYDERGDW TLKSNSWFGC 41	TKWKYSGNLM KHYITTRINN FHAPDGRGGI DPRAVMFPTY VTTYGNRIP KYMLISNLRP DPGYPKLITK 51 AGCACGCTT GGGTGGACAG TGTAGACAG TGTAGACAG CCCTGCACA CAGCCTTTCA CAGCCTTCA CAGCCTTCA CAGCCTTTCA CCTGCACAC CAGCCTTTCA CCTGCACAC CAGCCTTTCA	60 120 180 360 420
50 55 60 65	1 MEPLIJLLIQ RESCUENCE RES	ression #: 1 Thread.plm Ldi.wrtqub Ldi.wrtq	205 sequence. 20	31 LAGSTYLEEF RECYPOYATE RECYPO	YGLBINKLPV REMPGGVVR REMPGGVVR VVPARGAHEG GRISLIGHSS LLCPINLEPIN RAYOPELPRID HRYDERGOPH TLKSNSWPGC 41	I TROMEYSCALLM KHYLITELING HIAPDERGOI DERAVMEPTY ENTRY OF STREET O	60 120 180 360 420 60 120 180 240 360 420 420 540 660
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50 55 60 65	1 REPLILILIO RESCUENCIA PLANTINE PROPERTIES PROPERTIE	cession #: 1 Thread.plm Ldiavitqua Ldiavitq	205 sequence. 205 sequence. 207 september 20	31 LAGSTYLEEF RECYPOINTS LAGSTYLEEF RECYPOINTS LAGSTYLEEF RECYPOINTS LAGSTYLEEF RECYPOINTS LAGSTYLEEF RETYPOINTS LAGSTYLEEF RECYPOINTS L	TUGETINELPY REMICEGEVE REMICEGEVE VEYARGARGE GISTALICHES LEDPHISPES REMICEGE GISTALICHES LEDPHISPES REMICEGE GISTALICHES LEDPHISPES REMICEGE GISTALICHES REMICEGE GISTALICHES REMICEGE	I TORKYSGILM RIYLTYRINN FRINDERSGI DPKANFETY VYTTGIKLE VYTTGIKLE SI AGCAGGGCC GGTGTGGTGA ACAGGGCCA GGGTTTGAAATGGA TGTGAAATGAC TGTAAAATGGA CAGGGCTGAAAGGAC CAGGCTTGA CAGGGCCAG GGGTTGGTGAAAGAGA CAGGGCTGAAAGAGAAGAC CAGGGCTGAAAGAGAAGAC CAGGGCTGAAAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	50 120 240 300 420 420 600 120 240 300 420 420 420 600 720 660 720
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50 55 60 65 70	1 HOPALILLAGE RECEIVED HIS PROPERTY OF THE PRO	TATOCARACCA TATOCA	231	11 LPGRSYLERP REGERENCE STATE	TOTAL PURPOSE OF THE PROPERTY	I TOMETSGELLE STORYTSGELLE STOR	240 300 420 360 420 60 120 360 420 360 420 540 540 560 660 600 660 600 600 600 600 600 60
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50 55 60 65 70	1 INSTALLILLIAN INSTALLIAN	LI L	231	11 LPGRAYLERP RECYPOYORS IN THE PROPERTY OF TH	YGLEINKLPV ROMPAGEVAR ROMPAGEVAR GRISGAGGES LODNKLSPRA ROMPAGEVAR GRAGGCCCTC GCAGCTTGGC GCAGCTCGC GCAGCTTGGC GCAGCTCGC GCAGCTTGGC GCAGCCCTC GCAGCTTGGC GCAGCCCTC GCAGCATGGC GCAGCCCTC GCAGCATGGC GCAGCCCTC GCAGCATGGC GCAGCCCTC AGCATGGGC AGCATGGC CCTCAGGG AGCATGGC GCAGCCCTC AGCATGGC CCTCAGGG AGCATGGC CCTCAGGC AGCATGGC CTGGCCCAGA AGCATGCC CTGGCCCAGA AGCATGCC TTGGCTCGGA CTGGCCCAGA CTGGCCCAGA CTGGCCCCAG AGCATGCC TTGGCTCGGC GAAGGTCCTC TTGGCTCGGC GAAGGCCCTC TTGGCTCGGC GAAGGCCCTC TTGGCTCGGC GAAGGCCCTC TTGGCTCGGC GAAGGCCCTC TTGGCTCGGC GAAGGCCCTC CTGGCCCCAGC CTGGCCCCCC GAAGGCCCTC TTGGCTCGGC CTGGCCCCCC CTGGCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCCC	TOMEYSBALM BRITATERIAN BRITA	120 120 240 330 360 420 60 120 120 120 120 120 120 120 120 120 12
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		CTCCTGCAGC					1560
	CTTGCAGAGT	CTCCTGCAGC	ACCTCATCGG	GCTGAGCAAT	CTGACCCACG	TGCTGTATCC	
	TGTCCCCCTG	GAGAGTTATG	AGGACATCCA	TGGTACCCTC	CACCIGGAGA	GGCTTGCCTA	1620
	TCTGCATGCC	AGGCTCAGGG	AGTTGCTGTG	TGAGTTGGGG	CGGCCCAGCA	TGGTCTGGCT	1680
-	TAGTGCCAAC	CCCTGTCCTC	ACTGTGGGGA	CAGAACCTTC	TATGACCCGG	AGCCCATCCT TTCTGCATAC	1740
5	GTGCCCCTGT	TTCATGCCTA	ACTAGCTGGG	TGCACATATC	AAATGCTTCA	TTCTGCATAC	1800
							1860
	ACABATGTTC	AGTGTGAGTG	AGGARACAT	GTTCAGTGAG	GARARARCAT	TCAGACAAAT	1920
	GTTCNGTGAG	CAAAAAAAAGG	CONSCRIPTION	GATAGGCAGA	TOTTGACTTG	AGGAGTTAAT	1980
	CTCATCTTC	AGTGTGAGTG GAAAAAAGG GGGAGATACA	TCTTATAGAG	TTAGAAATAG	AATCTGAATT	TCTALAGGGA	2040
10	GIGAICITIG	DOGADALACA	TCTTATAGAG	TIMOMMING	CONTRACTOR CONTRACTOR	CERRACESEC	2100
10	GATTCTGGCT	TUGGAAGTAC	ATGTAGGAGT	TAMICCCIGI	GIAGACIGII	GTAAAGAAAC	2100
	TGTTGAAAAT	AAAGAGAAGC	AATGTGAAGC	AAAAAAAAA	AVAVVVVVV		
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	GCTTCAGGGT	ACAGCTCCCC	CGCAGCCAGA	AGCCGGGGCCT	GCAGCGCCTC	AGCACCGCTC	60
	CCCCACACCC	CACCCGCTTC	CCAGGCGTGA	CCTGTCAACA	GCBACTTCGC	GGTGTGGTGA	120
20	ACTICTICAC	CARARACCAT	TTTTATT	ACTUTURAN	GTGCGTGGCA	ACABGTGACT	180
20	CACACCTORG	GAAAAACCAT AATCCAAGCG	TITIONITALI	TCACCCCACC	CTANGECCE	TCAAAATGGA	240
	GAGACCTAGA	AATCCAAGCG	TIGGNGGTCC	TGAGGCCAGC	CIAAGICGCI	TOROUNIOUM	300
	ACGAAGGCGT	TIGIGGGGTT	CCATTCAGAG	CCGATACATC	AGCATGAGTG	TGTGGACAAG	360
	CCCACGGAGA	CFTGTGGAGC	TGGCAGGGCA	GAGCCTGCTG	AAGGATGAGG	TGTGGACAAG CCCTGGCCAT CAGCCTTTGA CCTGCCTCCC	
25	TGCCGCCCTG	GAGTTGCTGC	CCAGGGAGCT	CTTCCCGCCA	CTCTTCATGG	CAGCCTTTGA	420
25	CGGGAGACAC	AGCCAGACCC	TGAAGGCAAT	GGTGCAGGCC	TGGCCCTTCA	CCTGCCTCCC	480
	TCTGGGAGTG	CTGATGAAGG	GACAACATCT	TCACCTGGAG	ACCTTCAAAG	CTGTGCTTGA	540
	TGGACTTGAT	GTGCTCCTTG	CCCAGGAGGT	TCGCCCCAGG	AGGTGGAAAC	TTCAAGTGCT	600
	GGATTTACGG	AAGAACTCTC	ATCAGGACTT	CTGGACTGTA	TGGTCTGGAA	CTGTGCTTGA TTCAAGTGCT ACAGGGCCAG	660
	TCTGTACTCA	TTTCCAGAGC	CAGAAGCAGC	TCAGCCCATG	ACARAGARGO	GAAAAGTAGA	720
30	TOGETTTGAGE	ACRGREGERG	AGCAGCCCTT	CATTCCAGTA	GAGGTGCTCG	TAGACCTGTT	780
	CCTCAAGGAA	GOVERNITOR	ATCAATTCTT	CTCCTACCTC	ATTGAGAAAG	TGAAGCGAAA	840
	COLUMNOON	OUTOCOTOTO	COMOUNTAGE	CONCARCATE	TTTCCAATCC	CCATCCAGGA	900
	GARARATOTA	CIACUCCIGI	OCTOTIONOM.	COLOMONII	Chachman	AACTICA CITTIC	960
	TATCAMGATG	ATCCTGARAA	TOGIGCAGCI	GGACICIAII	CONTRACTOR	ACAGGGCCAG GAAAAGTAGA TAGACCTGTT TGAAGCGAAA CCATGCAGGA AAGTGACTTG TGATTAATCT	1020
35	TACCTGGAAG	CTACCCACCT	IGGCGMAATT	TICICCITAC	CIGGGCCAGA	IGNITATION	1080
33	GCGTAGACTC	Crecrerece	ACATCCATGC	ATCTTCCTAC	ATTICCCCGG	AGAAGGAAGA AGGCTCTCTA ACGTGATGAA	1080
	GCAGTATATC	GCCCAGTTCA	CCTCTCAGTT	CCTCAGTCTG	CAGIGCCIGC	AGGCTCTCTA	1140
	TGTGGACTCT	TTATTTTTCC	TTAGAGGCCG	CCTGGATCAG	TTGCTCAGGC	ACGTGATGAA	1200
							1260
	GTCCCAGAGT	CCCAGCGTCA	GTCAGCTAAG	TGTCCTGAGT	CTAAGTGGGG	TCATGCTGAC CCCTCCAGGA	1320
40	CGATGTAAGT	CCCGAGCCCC	TCCAAGCTCT	GCTGGAGAGA	GCCTCTGCCA	CCCTCCAGGA	1380
							1440
	GAGCCACTGC	TCCCAGCTTA CTCCTGCAGC	CAACCTTAAG	CTTCTACGGG	AATTCCATCT	CCATATCTGC	1500
	CTTCCACACT	CTCCTGCAGC	ACCTCATOGG	CCTCACCAAT	CTGACCCACG	TGCTGTATCC	1560
							1620
45	TCTGCATGCC TAGTGCCAAC GTGCCCCTGT	AGGCTYCAGGG	ACTTOCTOR	TGAGTTGGGG	CGGCCCAGCA	TOGTCTGGCT	1680
43	TCTGCATGCC	AGGCTCAGGG	VOLLOCIOIO	CACAACCTTC	TATCACCCCC	ACCCCATCCT	1740
	INGIGCCANC	CCCIGICCIC	ACTOTOGGGA	moca di Tito	TATOACCCOO	TECTOCATAC	1800
	GIGCCCCIGI	TICAIGCCIA	ACTAGCTGGG	TOCACATATE	ANATOCITOS	-CECTOCATAC	1860
	TTGGACACTA	AAGCCAGGAT	GIGCATGCAT	CITGAAGCAA	CHANGCAGCC	ACAGTTTCAG TCAGACAAAT AGGAGTTAAT	1920
50	ACAAATGTTC	AGTGTGAGTG	AGGAAAACAT	GITCAGIGAG	GAAAAAACAT	TCAGACAMAT	1920
30	GTTCAGTGAG	GAAAAAAAGG	GGAAGTTGGG	GATAGGCAGA	TGTTGACTTG	ACCAGTTAAT	1980
	GTGATCTTTG	GGGAGATACA	TCTTATAGAG	TTAGAAATAG	AATCTGAATT	TCTAAAGGGA	2040
	GATTCTGGCT	TGGGAAGTAC	ATGTAGGAGT	TAATCCCTGT	GTAGACTGTT	TCTAAAGGGA GTAAAGAAAC	2100
	TGTTGAAAAT	AAAGAGAAGC	AATGTGAAGC	AAAAAAAAA	AAAAAAA		
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	i cochaarena	acrerence:	COMPONE	decement	TOTAGGGGG	GCCCGGCATC	60
	GGCAGGICIC	GCTCTCGGCA	cccrcccac	GCCCGCG11C	COCTOOCCCT	GCATCTGCTG	120
	CCGATGGCCG	managed a	TOGGCGCTCC	Chacococa	PARACONCE	PCALFORIA	180
65	CTGACCCTCG	TGATCTTCAG	TCGTGATGGT	GAAGCCTGCA	AAAAAGGIGAI	ACTIMATOIA	240
00	CCTTCTAAAC	TAGAGGCAGA	CAAAATAATT	GGCAGAGITA	MITTGGMAGA	ACTTAATGTA GTGCTTCAGG	240
	TCTGCAGACC	TCATCCGGTC	AAGTGATCCT	GATTTCAGAG	TTCTAAATGA	TGGGTCAGTG	300
	TACACAGCCA	GGGCTGTTGC	GCTGTCTGAT	AAGAAAAGAT	CATTTACCAT	TGGGTCAGTG ATGGCTTTCT GAAGAAGGTA ATGGGCACCT	360
	GACAAAAGGA	AACAGACACA	GAAAGAGGTT	ACTGTGCTGC	TAGAACATCA	GAAGAAGGTA	420
	TCGAAGACAA	GACACACTAG	AGAAACTGTT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
70	ATTCCTTGCT	CTATGCAAGA	GAATTCCTTG	GCCCCTTTCC	CATTGTTTCT	TCAACAAGTT TGGAGTTGAT	540
	GAATCTGATG	CAGCACAGAA	CTATACTGTC	TTCTACTCAA	TAAGTGGACG	TGGAGTTGAT	600
							660
	CCTGTGGATC	GTGAAGAATA	TGATGTTTTT	GATTTGATTG	CTTATGOTTC	AACTGCAGAT AAATGACAAC TAGACCTGGT	720
	CCATATTC	CACATONICA	CCTCCCACTA	CYCATCACCC	TAGAGGATCA	ABATGACAAC	780
75	CHARLICAL	manage and	* * COUNTY TO A TO	TTTCAACTT	TOGRANGER	TAGACCTGGT	840
,,	CACCCTGTTT	TCACAGAAGC	MALLIATAAT	1110000111	COCK CACETAG	CCPARACCIOGI	900
	ACTACAGTGG	GGGGGTTTG	TUCCACAGAC	MUAGATUAAC	COGACACAAT	GCATACGCGC	900
	CIGAAATACA	GCATTTTGCA	GCAGACACCA	AUGTCACCTG	GGCTCTTPTC	TGTGCATCCC	960
				TATTTGGACA	GAGAGGTTGT	AGACAAGTAC	1020
00	AGCACAGGCG	TAATCACCAC					1080
80	ACTACAGTGG CTGAAATACA AGCACAGGCG TCATTGATAA			GGCCAGTTTT		MOOCHCAICA	
				GGCCAGTTTT	CCACTTTCAG	ACAAAATGCT	1140
-				GGCCAGTTTT GATAATGCAC AATGTGGAAA	CCACTTTCAG TCTTACGAAT	ACAAAATGCT ACCTATAGAA	1140 1200
00	TCATTGATAA ACTTGTATCA TATGAAGCAT	TGAAAGTACA TAACAGTAAC TTGTAGAGGA	AGACATGGAT AGATTCAAAT AAATGCATTC	GATAATGCAC AATGTGGAAA	CCACTTTCAG TCTTACGAAT	ACAAAATGCT ACCTATAGAA	1140 1200 1260
	TCATTGATAA ACTTGTATCA TATGAAGCAT	TGAAAGTACA TAACAGTAAC TTGTAGAGGA	AGACATGGAT AGATTCAAAT AAATGCATTC	GATAATGCAC AATGTGGAAA	CCACTTTCAG TCTTACGAAT	ACAAAATGCT ACCTATAGAA	1140 1200
	TCATTGATAA ACTTGTATCA TATGAAGCAT GATAAGGATT GAAAATGGAC GTAAAGCCAC	TGAAAGTACA TAACAGTAAC TTGTAGAGGA TAATTAACAC ATTTCAAAAT TGAATTATGA	AGACATGGAT AGATTCAAAT AAATGCATTC TGCCAATTGG CAGCACAGAC AGAAAACCGT	GATAATGCAC AATGTGGAAA AGAGTCAATT AAAGAAACTA CAAGTGAACC	CCACTTTCAG TCTTACGAAT TTACCATTTT ATGAAGGTGT TGGAAATTGG	ACAAAATGCT ACCTATAGAA AAAGGGAAAT TCTTTCTGTT AGTAAACAAT	1140 1200 1260 1320
	TCATTGATAA ACTTGTATCA TATGAAGCAT GATAAGGATT GAAAATGGAC GTAAAGCCAC GAAGCGCCAT	TGAAAGTACA TAACAGTAAC TTGTAGAGGA TAATTAACAC ATTTCAAAAT TGAATTATGA	AGACATGGAT AGATTCAAAT AAATGCATTC TGCCAATTGG CAGCACAGAC AGAAAACCGT TATTCCCAGA	GATAATGCAC AATGTGGAAA AGAGTCAATT AAAGAAACTA CAAGTGAACC GTGACAGCCT	CCACTTTCAG TCTTACGAAT TTACCATTTT ATGAAGGTGT TGGAAATTGG TGAACAGAGC	ACAAAATGCT ACCTATAGAA AAAGGGAAAT TCTTTCTGTT AGTAAACAAT CTTGGTTACA	1140 1200 1260 1320 1380 1440
.85	TCATTGATAA ACTTGTATCA TATGAAGCAT GATAAGGATT GAAAATGGAC GTAAAGCCAC GAAGCGCCAT	TGAAAGTACA TAACAGTAAC TTGTAGAGGA TAATTAACAC ATTTCAAAAT TGAATTATGA	AGACATGGAT AGATTCAAAT AAATGCATTC TGCCAATTGG CAGCACAGAC AGAAAACCGT TATTCCCAGA	GATAATGCAC AATGTGGAAA AGAGTCAATT AAAGAAACTA CAAGTGAACC GTGACAGCCT	CCACTTTCAG TCTTACGAAT TTACCATTTT ATGAAGGTGT TGGAAATTGG TGAACAGAGC	ACAAAATGCT ACCTATAGAA AAAGGGAAAT TCTTTCTGTT AGTAAACAAT CTTGGTTACA	1140 1200 1260 1320 1380 1440
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	TCATTGATAA ACTTGTATCA TATGAAGCAT GATAAGGATT GAAAATGGAC GTAAAGCCAC GAAGCGCCAT	TGAAAGTACA TAACAGTAAC TTGTAGAGGA TAATTAACAC ATTTCAAAAT TGAATTATGA	AGACATGGAT AGATTCAAAT AAATGCATTC TGCCAATTGG CAGCACAGAC AGAAAACCGT TATTCCCAGA	GATAATGCAC AATGTGGAAA AGAGTCAATT AAAGAAACTA CAAGTGAACC GTGACAGCCT	CCACTTTCAG TCTTACGAAT TTACCATTTT ATGAAGGTGT TGGAAATTGG TGAACAGAGC	ACAAAATGCT ACCTATAGAA AAAGGGAAAT TCTTTCTGTT AGTAAACAAT	1140 1200 1260 1320 1380 1440

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CTCACTATAT ACTATGAGG AAGAGATCT CCAGCTGOTT CTGTGGGCTG CTGCAGTGAA AAGCAGGAAG AAGATGGCCT TGACTTTTTA AATAATTTGG AACCCAAATT TATTACATTA GCAGAAGCAT GCACAAAGAG ATAATGTCAC AGRICCIACAA TIAGGICTIT GICAGACATI CIGAGGITI CCAAAAAIAA TATIGTAAAG TICAATTICA ACAIGTATGI ATAGGAGAT TITTITCICA ATITIGAAT AIGCIACTCA CCAATTTATA TTTTTAAAGC CAGTTGTTGC TTATCTTTTC CAAAAAGTGA AAAATGTTAA -2940 CCARTTATA TITTIARAGE CAGITGITGE THATCHTHE CARRAGEAR MARATCHIAN AACAGACAGE TEGTAARCT CAARCTCCAG CACTEGART AAGGTCICTA AAGCATCTGC TCTITTTTT TITTACEGAT AITTIAGTAA TAAATATGCT GGATAAATAT TAGTCCAACA ACTGRATTAN ATTANANATG TTGCRGCTCA TANAGRATTG GGACTCACCC CTACTGCACT ACCANATTCA TTTGACTTTG GAGGCARART GTGTTGRAGT GCCCTATGRA GTAGCARTTT TCTATAGGAA TATAGTTGGA AATAAATGTG TGTGTGTATA TTATTATTAA TCAATGCAAT ATTTANANTO AANTAGANC AANGAGGANA ATGGTRANAA CTTGANATGGGGGGGGTA TAGTTTOTCC TACAATAGAA AANGAGGANA GCTTCCTAGG CTGGGGCCT TAAATAGCTGC ATTATAACTG AGCCCTAGG GAAATAGTC CTGCCAATT TOTGTRAATT GTTTAAATT GTAMATAMAT TAMACTITTC TEGETTICTGT GEGANGGAMA TAGGGAMTCC MATEGRACEG TAGCETTIGCT TECAGTCTG TITCAMGATT TETCACTCCA CAMGTITAGTA GCAMACTEGG GAMTACTCG TECAGTCTGG GTTCCCTGCT TITTGGTAGC MAGGGTCCMG MATEGAGTG TTTTTTCGG GGAGCTAATA ACAAAAACAT TTTAAAACTT ACCTTTACTG AAGTTAAATC CTCTATTGCT GTTTCTATTC TCTCTTATAG TGACCAACAT CTTTTTAATT TAGATCCAAA TABOCATGTC CTCCTAGAGT TTAGAGGCTA GAGGGAGCTG AGGGGAGGAT CTTACTGAAA GCACCINGG GAGATIGATT GTCCTTAAAC CTAAGCCCA CHARCTIGAC ACCTGATCAG GTCTGGGAGC TACAAAATT GTCCTTATCC CTCACTGCC TTCTTCTGAG TGCCATTGGC CTGAATCAAG GAAAGCAGG CCTTGTGGGC CCCTTCTTT GGCGTTTCTG GTCAAATGAC ACCTCCAGCA GAGATTCCCT TAAGTGACTC CAGGTTTTCC ACCATCCTTC AGCGTGAATT AATITITAAT CAGTITGCIT TCTCCAGAGA AATITIAAA TAATAGAAGA AATAGAAATI TIGAATGTAT AAAAGAAAA GATCAAGTIG TCATITIAGA ACAGAGGGAA CITIGGGAGA TYGANTUTAT ARAGARARA GATCHAGTTG TCATTTIAGA ACAGGAGATG AGGCCTTCAA AGCAGCCCA ACATGATTAT TTGACAGTC AGGGCCTACA GGGCAAGAGA AGGCCACAG GANTATGGT GGGATTAAA GCAACATGT CTGCTTCATA CTTTTTCCTA GGCTTGGCA TGCCTTTCC TTTCCTAGGC CAATGGCACA TGCACTTCA GTCCGGTGAG GGATCAGCCA ACCTCTTCTC TATGGCTCAC CTTATTTGG GTGAGAAATC ARGGRACAG ACCIDATOR ATGATAGETC TORAGGCATT TOCAGGRATA GCCTUAACTG GTTGTICAGA ACAAACAAGG CATTCATGGA AATTGTTGTA TTCCTTCTCA GACCTCCTTCTTCTA GAAATCATGA TATCATTCAA AATTGTTGAT TOTATTCCTACA TITYCOSTIT TOTANTIGA COCTAMANT TATGGGTTTT AGACTRAGA TITTTATTGC CCCCCCCC TITTTTTTTA GAGCGAGGG TOGCTCVAG GACAGGGG GAGTGGATG GGTCCGATC CTGCTCAG AAAGCTCCGC CTCCCCGGGTC ASTCCATC TCCTGGCTCA GCCTCCTGAG TAGCTGGGAC TACAGGCGCC CACCACCACG CCCGGCTAAT TTTTTGTATT TTTAATAGAG ACGGGGTTTC ACTGTGTTAG CCAGGATGGT CTCGATCTCC TGACCTCGTG ATTEMPTAGE ACCOUNTIL ACTUATION CONSTRUCT CATALOGUE CONTINUES ATTEMPT ATTEMPT ATTEMPT ATTEMPT ATTEMPT ATTEMPT ATTEMPT ATTEMPT ACTUAL ACTUAL ATTEMPT ATT CTIGITITICO GITTARAGIC GICCICCITITI ANGUARCA TITTIGARCA GIGIGARAGI TGATCATACO ANTIGRATCA ATCITGARAT ACTCARCCA ANGUCAGIC AGANGCCAGO GGUARANAGA ACTCAGGGCA CARANTATIG GICCIAGRAT GGATATICTIC GIANGCCTAG E100 TTGCTGAAAT TTCCTGCTGT AACCAGAAGC CAGTTTTATC TAACGGCTAC TGAAACACCC ACTGTGTTTT GCTCACTCCC TCACTCACCG ATCAAAACCT GCTACCTCCC CAAGACTTTA CHARTICOGA TAAACTICC CAAAGAGCAA CCAGTACCAC TOCCTOFT ATAAACCTC TAACCATCT TITOTCTTT GAACATACTA AAACCAACT GGCTGCGAT TATGCCCGAT TITOTACTC TITTCTCTCA AATGAAAATT TAAATTAGA GATCATTC TATATTTCA CHARGEGE ATTATTATT COTTANANG GRAAGGTGA ATTATGGA TTTGAGTGTG CARGARANA TATTTTANA GCTTTCATT TTCCCCAGT GANGATTA GANTATTTA TGTANATATA CAGARGTTT TTCTTATT TTATAGGA GCAGTGCT ANANGCAG GOGGITTOTT TIGCALIGIT TIANCAGA TITTAGTATT GCTATTAAA GAAGTTACTT TGCTTTTAAA GAACTTGGC TGCTTAAAAT AAGCAAAAAT TGGATGCATA AAGTAAATATT TACAGATGTG GGGAGATGTA ATAAAACAAT ATTAACTTGG TTTCTTGTTT TTGCTGTATT TAGAGATTAA ATAATTCTAA GATGATCACT TTGCAAAATT ATGCTTATGG CTGGCATGGA AATAGAAATA CTCAATTATG TCTTTGTTGT ATTAATGGGG AATATTTTGG ACAATGTTTC ATTATCAAAT TOTOGACATC ATTAATATAT ATTGTAATGT TGGGAAGAGA TCACTATTTT GAAGCACAGC TITACAGATG AGTATCTATG ATACATATGT ATAATAAATT TIGATCGGGT ATTAAAAGTA TTAGAAGGTG GTTATAATTG CAGAGTATTC CATGAATAGT ACACTGACAC ATTAMARGTA TTAGARGGTG GITATARTIG CARRENTIC CRIGATIAN ACACANACA AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA GGCAATATTG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATGCCTGA ACTATAATA CAMGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG CARGATUATC CARCATARA GGIGCICIGI GETTACASI GARTETITICA ARGIGIGETEC CETACARACG TIANGACIGA TEATITCARA ARTETATATA CETATIATARA AGCETACAT TITHATATAG GITGAACCAR MATTICARIT CCAGTARCIT CIATIGIAAC CATTATTTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTA ATAGTAAAAT ACCOGNATACA TITCACGIGI CCITCAGIAI IGATITGGIT GAATATIGGG TCATAATGGI

TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC

TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTTCTCAT TAAAATCAAT 6720
GAACAATGCC AGGCTCATGG GGTTGTTGAA TGATTAAATT AGTTAATATA CCTAAAGTAC 6780

WO 02/086443 ATAGAACACT GCCTGCACAT AGTAAAAGAA TTATAAGTGT GAGGTAGTTG GTAAAATTAT 6840 GTAGTTGGAT ATACTACCGGA ACAATATCTA ATCTCTTTTT AGGGAAATAA AGTTTGTGCA 6900 TATATATATATA CCCGAAACATT CCCGAAACATT 6

5 Seq ID NO: 32 Protein sequence: Protein Accession #: NP_001932.1

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	1	1	1	1	1	1	
10		RGAVCLHLLL					60
	ADLIRSSDPD	PRVLNDGSVY	TARAVALSDK	KRSFTIWLSD	KRKQTQKEVT	VLLEHQKKVS	120
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	EPLNLFYIER	DTGNLFCTRP	VDREEYDVFD	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
	PVFTEATYNF	EVLESSRPGT	TVGVVCATDR	DEPOTMETRL	KYSILQQTPR	SPGLFSVHPS	300
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	EAFVEENAFN	VEILRIPIED	KDLINTANWR	VNFTILKGNE	NGHPKISTDK	ETNEGVLSVV	420
	KPLNYEENRO	VNLEIGVNNE	APFARDIPRV	TALNRALVTV	HVRDLDEGPE	CTPAAQYVRI	480
		NGYKAYDPEN					540
	KNRLYNITVL	AIDKDDRSCT	GTLAVNIEDV	NDNPPEILQE	YVVICKPKMG	YTDILAVDPD	600
20	EPVHGAPFYF	SLENTSPRIS	RLWSLTKVND	TAARLSYOKN	AGFQEYTIPI	TVKDRAGQAA	660
	TRILIBUNICE	CTHPTOCRAT	SRSTGVILGK	WAILAILLGI	ALLPSYLLTL	VCGVFGATKG	720
		NLIISNTEAP					780
	MMKCKINOTLR	SCRGAGHHHT	LDSCRGGHTE	VDNCRYTYSE	WHSFTOPRLG	EKLHRCNONE	840
		TYNYEGRGSP					
25	DIGIT DEDITIES	11111011001					

Seq ID NO: 33 DNA sequence Nucleic Acid Accsssion #: Eos sequence

Coding sequence: 64-2583

30	Coding sequ	ence: 64-25	83				
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~-	CCGATGGCCG	CCGCTGGGCC	CCGGCGCTCC	GTGCGCGGAG	COGTCTGCCT	GCATCTGCTG	120
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	CCTTCTAAAC	TAGAGGCAGA	CAAAATAATT	GGCAGAGTTA	ATTTGGAAGA	GTGCTTCAGG	240
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	TACACAGCCA	GGGCTGTTGC AACAGACACA	GCIGICIGAT	ANGOUGHT	CATTIACCAT	CARCARCOTA	420
40	GACAAAAGGA	GACACACTAG	BORRESONO	ACTOTOCTOC	CCNACAGGAG	ATCCCCACCT	480
40	TCGAAGACAA	CTATGCAAGA	CAATTCCTTT	CCCCCCTTTCC	CATTGTTTCT	TCAACAAGTT	540
	Charcecare	CAGCACAGAA	CTATACTOTC	TTCTACTCAA	TARGTGGACG	TGGAGTTGAT	600
	AAACAACCTT	TAAATTTGTT	TTATATAGAA	AGAGACACTG	GARATCTATT	TTGCACTCGG	660
	CCTCTCCATC	GTGAAGAATA	TGATGTTTTT	GATTTGATTG	CTTATGCGTC	AACTGCAGAT	720
45	GGATATTCAG	CAGATCTGCC	CCTCCCACTA	CCCATCAGGG	TAGAGGATGA	AAATGACAAC	780
	CACCOMMETT	TCACAGAAGC	AATTTATAAT	TTTGAAGTTT	TGGAAAGTAG	TAGACCTGGT	840
	ACTACAGTGG	GGGTGGTTTG	TGCCACAGAC	AGAGATGAAC	CGGACACAAT	GCATACGCGC	900
	CTGAAATACA	GCATTTTGCA	GCAGACACCA	AGGTCACCTG	GGCTCTTTTC	TGTGCATCCC	960
	AGCACAGGCG	TAATCACCAC	AGTCTCTCAT	TATTTGGACA	GAGAGGTTGT	AGACAAGTAC	1020
50	TCATTGATAA	TGAAAGTACA	AGACATGGAT	GGCCAGTTTT	TTGGATTGAT	AGGCACATCA	1080
	ACTTGTATCA	TAACAGTAAC	AGATTCAAAT	GATAATGCAC	CCACTTTCAG	ACAAAATGCT	1140
	TATGAAGCAT	TTGTAGAGGA	AAATGCATTC	AATGTGGAAA	TCTTACGAAT	ACCTATAGAA	1200
	GATAAGGATT	TAATTAACAC	TGCCAATTGG	AGAGTCAATT	TTACCATTTT	AAAGGGAAAT	1260
e e	GAAAATGGAC	ATTTCAAAAT	CAGCACAGAC	AAAGAAACTA	ATGAAGGTGT	TCTTTCTGTT	1320
55	GTAAAGCCAC	TGAATTATGA	AGAAAACCGT	CAAGTGAACC	TGGAAATTGG	AGTAAACAAT	1380
	GAAGCGCCAT	TTGCTAGAGA	TATTCCCAGA	GTGACAGCCT	TGAACAGAGC	CTTGGTTACA	1500
	GTTCATGTGA	GGGATCTGGA ACTTAGCAGT	TGAGAGGCCT	GAATGCACTC	CTGCAGCCCA	MANUGUCCO A	1560
	ATTAAAGAAA	GCAATGGTTT	GGGGTCAAAG	ATCHACGGCT	ATAMOGCATA	TOACCCCORN	1620
60	AATAGAAATG	TTTCAGGGTC	ANGGIACAAA	MARITOCATO	TOCATAGGA	COTTOBBACT	1680
00	CCCAAAAACC	AGTTGTATAA	TATTACACTC	CTCCCAATAG	ACABAGATGA	TAGATCATGT	1740
	ACTOGRACAC	TTGCTGTGAA	CATTGAAGAT	GTABATGATA	ATCCACCAGA	AATACTTCAA	1800
	CANTATCTAG	TCATTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAGTTTGC	CCAATACTTC	TCCAGAAATC	1920
65	AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGAATA	TACCATTCCT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	2100
	ACTTCAAGGA	GTACAGGAGT	AATACTTGGA	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCTTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTTTGG	TGCAACTAAA	2220
70	GGGAAACGTT	TTCCTGAAGA	TTTAGCACAG	CAAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTTATGA	CCCAAACTAC	CAACAACTCT	2340
	AGCCAAGGTT	TTTCTGGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAAACCATT	2400
	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
75	ACCCTGGACT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACTTACTCG	2520
13	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTGAAGAAT	CCATTAGAGG	ACMCACIGGI	2640
	TAAAAATTAA	ACATAAAAGA GTCCTCACTT	AATTGCATCG	ATGTAATCAG	AATGAAGACC	GEATGCCATC	2700
	CCAAGATTAT	GAAAAGCAGG	ATANCTATGA	COMPANIONS	TCICCMGCIG	TOGALOCCAL	2760
	CIGCIGCAGI	TTAGCAGAAG	AAUAAGATGU	CCTTGACTTT	Changeman	CO PARTY COLOR	2820
80	MITTATIACA	TINGCAGAAG	TTTTCCARAAA	TANTATTOTA	ADOTTOART	TCAACATGTA	2880
80	TTTGTCAGAC	GATTTTTTTC	TITICONOUN	AMERICAN	MCACCA ATTE	TCAMCATGIA	2940
	ACOCACTOCT	MCCTT-MCTT	TTCCAAAAAG	TEABARATET	TABABCAGAC	AACTGGTAAA	3000
	TOWCARACTO	CACCACTOCAL	ATTARCETCE	CTABAGCATC	TOCTOTTE	TTTTTTTACG	3060
	CATATOTAC	TARTARATAT	CONCERTAN	TATTAGTCCA	ACANTAGCTA	AGTTATGCTA	3120
85	ATATCACATA	ATTATOTATT	CACTTTAAGT	CATAGTTTAA	AAAATAAACA	AGAAATATTG	3180
-	AGTATCACTA	TOTOLOGIAL	GTTTTGGAAA	AGAAACAATG	AAGACTGAAT	TAAATTAAAA	3240
	ATCTTCCACC	TCATAAAGAA	TTGGGACTCA	CCCCTACTGC	ACTACCAAAT	TCATTTGACT	3300

	WO 02/	096443					
	TTGGAGGCAA	APPROPRIA	AGTGCCCTAT	GAAGTAGCAA	TTTTCTATAG	GAATATAGTT	3360
	GGAAATAAAT (GTGTGTGTGT	ATATTATTAT	TAATCAATGC	AAATTTTAAA	ATGAAATGAG	3420
	DDGDGGGGG	AATGGTAA	AAACTTGAAA	TGAGGCTGGG	GTATAGTTTG	TCCTACAATA	3480 3540
5	GAAAAAAGAG GAGGAAATAG	AGAGCTTCCT	AGGCCTGGGC	TOTTAAATGC	ATTGTAAATA	AATTAAACTT	3600
,	TTCTGGTTTC '	TGTGGGAAGG	AAATAGGGAA	TCCAATGGAA	CAGTACCTTT	GCTTTGCAGT	3660
	CTCTTTCAAC	TATEMENT	CACAAGTTA	GTAGCAAACT	GGGGAATACT	CGCTGCAGCT	3720
	GGGGTTCCCT	GCTTTTTGGT	AGCAAGGGTC	CAGAGATGAG	GTGTTTTTTT	COGGGGGGGCTA	3840
10	ATAACAAAAA TTCTCTCTTA	CATTITAAAA	CATCUTTTEA	ATTTAGATOC	ADATABCCAT	GTCCTCCTAG	3900
10	ACTITACACO	CTAGAGGGAG	CTGAGGGGAG	GATCTTACTG	AAAGCACCCT	GGGGAGATTG	3960
	ATTGTCCTTA	AACCTAAGCC	CCACAAACTT	GACACCTGAT	CAGGTCTGGG	AGCTACAAAA	4020
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15	AGGCCTTGTG CCTTAAGTGA	GGCCCCCTTC	TTTCGGCTTT	TTCAGCGTGA	AACACCICCA	AATCAGTTTG	4200
13	CTTTCTCCAG	AGAAATTTTA	AAATAATAGA	AGAAATAGAA	ATTTTGAATG	TATAAAAGAA	4260
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	TATTTGTACA	GTCAGAGGGC	AACAGGAAGA	TGCAGGCCTT	CAAGGGCAAG	GAGAGGCCAC	4380
20	AAGGAATATG CACTGCCTTT	GGTGGGAGTA	AAAGCAACAT	COTCTCCTTC	TORCTOCCCT	GAGGGATCAG	4500
20	CCAACCTCTT	CTCTATGGCT	CACCTTATTT	GGAGTGAGAA	ATCAAGGAGA	CAGAGCTGAC	4560
	TGCATGATGA	GTCTGAAGGC	ATTTGCAGGA	TGAGCCTGAA	CTGGTTGTGC	AGAACAAACA	4620
	ACCCATTCAT	GGGBATTGTT	GTATTCCTTC	TGCAGCCCTC	CTTCTGGGCA	CTAAGAAGGT	4680 4740
25	CTATGAATTA TGACCCTAAA	AATGCCTATC	TAAAATTCTG	ATTTATTCCT	ACATTTTCIG	CCCTTTTTT	4800
23	TTOAGACCA	CALCALCACALCAL	GACGCACAGG	CTGGAGTGCA	GTGGCTCCGA	TCTCTGCTCA	4860
	CONTRA DA COTTO	CCCCCCCCCCC	CTTCATCCCA	THETCHESTS	TCAGCCTCCT	GAGTAGCTGG	4920
	GACTACAGGC TTCACTGTGT	GCCCACCACC	ACCCCCGCCT	AATTTTTTGT	ATTTTTAATA	GAGACGGGGT	4980 5040
30	TTCACTGTGT	TAGCCAGGAT	GGTCTCGATC	TCCTGACCTC	GGCCTTGTTT	TCCCTTTAAA	5100
30	CTCCTCTTCT	AATSTA ATSTA A	TCATTTTGAA	CATGTGTGAA	AGTTGATCAT	ACGAATTGGA	5160
	THE REPORT OF THE PARTY OF THE	AATACTCAAC	CARARGACEG	TOGAGAAGOC	AGGGGGAGAA	AGAACTCAGG	5220
	GCACAAAATA	TTGGTCTGAG	AATGGAATTC	TCTGTAAGCC	TAGTTGCTGA	AATTTCCTGC	5280 5340
35	TGTAACCAGA	AGCCAGTTTT	ATCTAACGGC	CCAACACA	CCCACTGTGT	ATABACTTTC	5400
55	TCAAAGAGCA	ACCAGTATCA	CTTCCCTGTT	TATAAAACCT	ACTAGTGCCG CTAACCATCT	CTTTGTTCTT	5460
	TODACATOCT	GARAGCCACC	TGGTCTGCAT	GTATGCCCGA	ATTTGTAATT	CITITUTCIC	5520
	TAAADTAAA	TTAATTTTAG	GGATTCATTT	CTATATTTTC	ACATATGTAG	TATTATTATT	5580 5640
40	TCCTTATATG	TGTAAGGTGA	AATTTATGGT	ATTTGAGTGT	GCAAGAAAAT ATGTAAATAT	ACAGAATGTT	5700
70	TTTTTTACT	TTTATAAGGA	AGCAGCTGTC	TARARTGURG	TGGGGTTTGT	TTTGC/U/TGT	5760
	TTTABACACA	CTTTTAGTAT	TGCTATTAAA	AGAAGTTACT	TTGCTTTTAA	AGAAACTTGG	5820 5880
	CIGCITANAN	TAAGCAAAAA	TTGGATGCAT	AAAGTAATAT	TTACAGATGT ATTGGATGCA	TARACTARTA	5940
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							6060
	GAAATAGAAA	TACTCAATTA	TGTCTTTGTT	GTATTAATGG	GGAATATTT GTTGGGAAGA	GGACAATGTT	6120 6180
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							6540
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60	ATGAACAATG	CCAGCCTCAT	GGGGTTGTTG	AATGATTAAA	TTAGTTAATA	TACCTAAAGT	6900 6960
	ACATAGAACA	CTGCCTGCAC	ATAGTAAAAG	AATTATAAGT	GTGAGGTAGT	TACCTAAAGT TGGTAAAATT AAAGTTTGTG	7020
	CATATATATA	ATCCCGAAAC	ATG	IMMICICITI	1110000001	AMMILION	,,,,
65	Seq ID NO:	34 Protein	sequence:				
	Protein Ac	cession #:	NP_077741.1				
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70	1	1	1	1	1	1	60
70	MAAAGPRRSV	RGAVCLHLLL	TLVIFSRDGE	ACKKVILNVP	SKLEADKIIG	RVNLEECFRS VLLEHOKKVS	120
	PTDUTDUTUI.	DDAKDDWADY	DOSMOENST C	PPPLFLOOVE	SDAAONYTVE	YSISGRGVDK	180
	EPLNLFYTER	DIGNLECTRE	VDREEYDVFD	LIAYASTADG	YSADLPLPLP	IRVEDENDINH	240
75	DURTEATINE	EVIESSRPGT	TVGVVCATDE	DEPOTMETRA	KYSILOOTPR	SPGLFSVHPS	300
75						NAPTFRQNAY ETNEGVLSVV	360 420
	EAFVEENAFN	VNIETGVINE	APPARDIDOU	TALNEALUTY	HVRDLDEGPE	CTPAAQYVRI	460
	A DAIL WILLOWA	MCVKAVDDEN	PNONGLBYKK	LHDPKCWITI	DEISGSIITS	KILDREVETP	540
90	WAIDT VALTERIT.	ATDEDDDOCT	CTLAUNITEDU	NUNDERTION	YVVICKPKMG	YTDILAVDPD	600
80						TVKDRAGQAA VCGVFGATKG	660 720
							780
	MMKGGNQTLE	SCRGAGREHET	LDSCRGGHTE	VDNCRYTYSE	WHSFTQPRL	EESTRGHTG	

85 Seq ID No: 35 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 146-1273.

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5	GGGAGTGGGC	GTGGCGGTGC CCAGGTCTTT	TGCCCAGGTG	AGCCACCGCT	GCTTCTGCCC	AGACACGGTC	60 120
5	GGATAACTGT	GACTCCAGGC	CCGCAATGGA	TGCCCTGCAA	CTAGCAAATT	CGGCTTTTGC	180
	CGTTGATCTG	TTCAAACAAC	TATGTGAAAA	GGAGCCACTG	GGCAATGTCC	TCTTCTCTCC	240
	AATCTGTCTC	TOCACCTOTO	TGTCACTTGC	TCAAGTGGGT	GCTAAAGGTG	ACACTGCAAA	300 360
10	TGAAATTGGA	CAGGTTCTTC GATGTAAACA	ATTTTGAAAA	CTTTTTACTCA	CTGAAACTAA	TCAACCGGCT	420
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25	CTGTTCTCCT	TAAGTGGCAT	AGCCCATGTT	AAGTCCTCCC	TGACTTTTCT	GTGGATGCCG	1320
	A TOTO CONCERN A	ACTOTOGRATO	CAGAGATTCA	TOTTOTACET	BCBATAAATT	CCTAATCTTC	1380
	CTGGATCAGG	AAGCCGCCAG TCTATCTTTT	TACTTGTCAT	ATGTAGCCTT	CACACAGATA	GACCTTTTTT	1440
	TTTTTCCAAT	TCACGTTAGA	GTTTCCTTTT	TTCCCATAAG	ACAATGACAT	TOTOGGGGT	1500 1560
30	AGTTGGCAGA	AATACAGTCT	TCCACAAAGA	AAATTCCTAT	AAGGAAGATT	TGGAAGCTCT	1620
	TCTTCCCAGC	ACTATGCTTT TGAAGAAAGT	CCTTCTTTGG	GATAGAGAAT	GTTCCAGACA	TTCTCGCTTC	1680
	CCTGAAAGAC	TGAAGAAAGT	GTAGTGCATG	GGACCCACGA	AACTGCCCTG	GCTCCAGTGA	1740 1800
	GCAGGTGTTT	ATTARANTTC	TGAATTTTGG	GGATTTTCAA	AAGATAATAT	TTTACATACA	1860
35	CTGTATGTTA	TAGAACTTCA AACAAAATGT	TGGATCAGAT	CTGGGGCAGC	AACCTATAAA	TCAACACCTT	1920
	AATATGCTGC	AACAAAATGT	AGAATATTCA	GACAAAATGG	ATACATAAAG	ACTAAGTAGC	1980
	CCATAAGGGG	TCAAAATTTG	CTGCCAAATG	CGTATGCCAC	CAACTTACAA	CTACTACCTC	2040
	AAATGCAAGA	TTTTCAGATT CCCCAAGAGG	AAGTTCAGAT	CTTAATATAA	ATTCACTTTC	ATTTTTGATA	2160
40							2220
	GCACAGGGAT	TCTCACAATA TAGCGGGAAA	GCCGATATCA	GAATTTGTGT	TGAAGGAACT	TGTCTCTTCA	2280 2340
	CATTANAGEG	CTCACGTTAC	CTTGACACAT	ACTACTGCCT	TCTATGGGTT	TAGTTACTTT	2400
	AGATGGCAAG	CATGTAACTT	ATATTAATAG	TAATTTGTAA	AGTTGGGTGG	ATAAGCTATC	2460
45	CCTGTTGCCG	GTTCATGGAT TCTCCCATCT	TACTTCTCTA	TAAAAAATAT	ATATITACCA	AAAAATTTTG	2520
	TGACATTCCT	TTGAATTTCT	CTTCCTTGAC	ATGCATTGTA	AATAGGTTCT	TCTTGTTCTG	2580
	AGATTCAATA	TIGAATTICT	CCIAIGCIAI	TGACAATAAA	AIAIIAIIGA	ACTACC	
		36 Protein					
50	Protein Ac	cession #: 1	NP_002630.1				
	.1	11	21	31	41	51	
	1	1	1	Ī	1	1	
55	MDALQLANSA	FAVOLPKQLC	EKEPLGNVLP	SPICLSTSLS	LAQVGAKGDT	ANEIGOVLHF	60
33	ENVKDIPFGF	QTVTSDVNKL QINNSIKDLT	SSFYSLKLIK	RLYVDKSLNL NOWNDOTKIL	STEFISSTER	PYAKELETVD	120 180
	KECPPRINKT	DTKPVCMMNM	EATFCMGNID	SINCKLIELP	PONKHLSMFI	LLPKDVEDES	240
	TGLEKIEKOL	NSESLSQWIN	PSTMANAKVK	LSIPKPKVEK	MIDPKACLEN	LGLKHIFSED	300
60	TSDFSGMSET	KGVALSNVIH	KVCLEITEDG	GDSIEVPGAR	ILQHKDELNA	DHPFIYIIRH	360
00	NKTRNIIFFG	KFCSP					
	Seq ID NO:	37 DNA seq	uence				
65		id Accession		8583			
05	coaing seq	uence: 72-8	12				
	1	11	21	31	41	51	
	1	I	1	1	1	1	
70	GGAGTGGGGG	AGAGAGAGGA GATGTTTCAA	GACCAGGACA	GCTGCTGAGA	CCTCTAAGAA	TTACCCCAGA	60 120
,,,	CCATGGCCCA	GTTTGGAGGC	CTGCCCGTGC	CCCTGGACCA	GACCCTGCCC	TTGAATGTGA	180
							240
	ATGGCCTGCT	GTCTGGGGGC	CTGTTGGGCA	TTCTGGAAAA	CCTTCCGCTC	CTGGACATCC	300
75	TGAAGCCTGG	GTCTGGGGGC AGGAGGTACT TGGCCTGAAC	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGA	CAGCTGCTGG	360 420
, ,							480
	TAAAGCTCCA	AGTGAATACG TGCAGAAATC	CCCCTGGTCG	GTGCAAGTCT	GTTGAGGCTG	GCTGTGAAGC	540
	TGGACATCAC	TGCAGAAATC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGGTCC	600
80	GOOT GOOD AND	CACCCATTCC TCAAGGTCTT	COCCA CACCC	TCACAGGGAT	CTTVERATERA	GTCCTGCCTG	660 720
50	AGTTGGTTCA	GGGCAACCTC	TATAL CALL AND A SALE	TCAATGAGGT	TCTCAGAGGC	TTGGACATCA	780
	CCCTGGTGCA	TGACATTGTT	AACATGCTGA	TCCACGGACT	ACAGTTTGTC	ATCAAGGTCT	840
	AAGCCTTCCA	GGAAGGGGCT	GGCCTCTGCT	GAGCTGCTTC	CCAGTGCTCA	CAGATGGCTG	900
85	GCCCATGTGC	TGGAAGATGA CGTGTGTAAC	CACAGTTGCC	CCTCACCTAA	TABANTOCT	CTTCTTCTCC	960 1020
0.5		AAAAAAAAA		CCICACCIAA	IMMARIUGEI	C. ICIICIGC	1020
		nnnnnnnnn					

WO 02/086443 Seq ID No: 38 Protein sequence: Protein Accession #: NP_057667

	Procein Acc	:4 11014495	15_02,601				
_	1	11	21	31	41	51	
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	MFQTGGLIVF	YGLLAQTMAQ	FGGLPVPLDQ	TLPLNVNPAL	PLSPTGLAGS	LTNALSNGLL	60
	SCCLLGILEN	LPLLDILKPG	GGTSGGLLGG	LLGKVTSVIP	GLINNIIDIKV	TOPQLLELGL	120
	VOSPDGHRLY	VTIPLGIKLQ	VNTPLVGASL	LRLAVKLDIT	AEILAVRDKQ	ERIHLVIGDO	180 240
10	DIVMMLINGL	LLDGLGPLPI	OGPIDALLET	PNKATPETAG	GNACLTANEA	LKGLDIILVA	240
10	DIAMMTINGD	GLATKA					
	Seq ID NO:	39 DNA sequ	ence				
1.5	Nucleic Aci	id Accession	1 #: NM_0043	63.1			
15	Coding sequ	ence: 115-2	223				
		11	21	31	41	51	
	î	1	Ī.	1	1	Ĭ .	
	CTCAGGGCAG	AGGGAGGAAG	GACAGCAGAC	CAGACAGTCA	CAGCAGCCTT	GACAAAACGT	60
20	TOOTGGAACT	CARGCTCTTC	TCCACAGAGG	AGGACAGAGC	AGACAGCAGA	GACCATGGAG	120
	TOTOCTOGG	CCCCTCCCCA	CAGATGGTGC	ATCCCCTGGC	AGAGGCTCCT	GCTCACAGCC	180
	TCACTTCTAA	CCTTCTGGAA	CCCGCCCACC	ACTGCCAAGC	TCACTATTGA	ATCCACGCCG	240 300
	TTCAATGTCG	CAGAGGGGAA GCTGGTACAA	GGAGGTGCTT	CTACTTGTCC	ACCOUNTCIDEC	TATAGGATAT	360
25	CTAATACCAA	CTCAACAAGC	TACCCCAGGG	CCCGCATACA	GTGGTCGAGA	GATAATATAC	420
23	CCCAATGCAT	CCCTGCTGAT	CCAGAACATC	ATCCAGAATG	ACACAGGATT	CTACACCCTA	480
							540
	GAGCTGCCCA	AGCCCTCCAT CCTGTGAACC	CTCCAGCAAC	AACTCCAAAC	CCGTGGAGGA	CAAGGATGCT	600
30	GTGGCCTTCA	CCTGTGAACC	TGAGACTCAG	GACGCAACCT	ACCIGIGGIG	COTCARCTOTA	660 720
30	CAGAGCCTCC	CGGTCAGTCC	CAGGCTGCAG	TACABATTATA	AAACCCAGAA	CCCAGTGAGT	780
	CCCACCCCCA	CAAGAAATGA GTGATTCAGT	CATCCTGAAT	GTCCTCTATG	GCCCGGATGC	CCCCACCATT	840
	TCCCCTCTAA	ACACATCTTA	CAGATCAGGG	GAAAATCTGA	ACCTCTCCTG	CCACGCAGCC	900
	TOTALCOCAC	CTGCACAGTA	CTCTTGGTTT	GTCAATGGGA	CTTTCCAGCA	ATCCACCCAA	960
35	GAGCTCTTTA	TCCCCAACAT	CACTGTGAAT	AATAGTGGAT	CCTATACGTG	CCAAGCCCAT	1020
	AACTCAGACA	TCATCACCAG	TAGGACCACA	GTCACGACGA	TCACAGTCTA	TOCAGAGCCA	1080
	CCCAAACCCT	AACCTGAGAT	TCACAACTCC	ACCURACYTON	COTCOCTABA	TRATCAGAGC	1200
	CTCCCGGTCA	GTCCCAGGCT	GCAGCTGTCC	AATGACAACA	GGACCCTCAC	TCTACTCAGT	1260
40	GTCACAAGGA	GTCCCAGGCT ATGATGTAGG	ACCCTATGAG	TGTGGAATCC	AGAACGAATT	AAGTGTTGAC	1320
	CACAGCGACC	CAGTCATCCT	GAATGTCCTC	TATGGCCCAG	ACGACCCCAC	CATTTCCCCCC	1380
	TCATACACCT	ATTACCUTCC	AGGGGTGAAC	CTCAGCCTCT	CCTGCCATGC	AGCCTCTAAC	1440 1500
	TTTATCTCCA	ACATCACTOR	GRAGRACAGC	GGACTCTATA	CCTGCCAGGC	CAATAACTCA	1560
45	GCCAGTGGCC	ACAGCAGGAC	TACAGTCAAG	ACAATCACAG	TCTCTGCGGA	GCTGCCCAAG	1620
	CCCTCCATCT	CCAGCAACAA	CTCCAAACCC	GTGGAGGACA	AGGATGCTGT	GGCCTTCACC	1680
	TGTGAACCTG	AGGCTCAGAA	CACAACCTAC	CTGTGGTGGG	TARATGGTCA	GAGCCTCCCA	1740 1800
	BCARTCOCA	CARGAGCCTA	TOTA TOTGO	ATCCAGAACT	CAGTGAGTGC	CAATGTCACA AAACCGCAGT	1860
50							1920
	TCCTCTTACC	TTTCGGGAGC	GAACCTCAAC	CTCTCCTGCC	ACTCGGCCTC	TAACCCATCC	1980
	CCGCAGTATT	CTTGGCGTAT	CAATGGGATA	CCGCAGCAAC	ACACACAAGT	CERCOCTACE	2040
	GCCAAAATCA	ATTCCATACT	CAAGAGCATC	ACACTCTCTC	CATCTGGAAC	TTCTCCTGGT	2160
55	CTCTCAGCTG	GGGCCACTGT	CGGCATCATG	ATTGGAGTGC	TGGTTGGGGT	TGCTCTGATA	2220
	TAGCAGCCCT	GGTGTAGTTT	CTTCATTTCA	GGAAGACTGA	CAGTTGTTTT	TTCTCCTGGT TGCTCTGATA GCTTCTTCCT	2280
	TABARCATTT	CCAACAGCTA	CAGTCTAAAA	TIGCITCITI	ACCAAGGATA	TTTACAGAAA	2340 2400
	AGACTCTGAC	CAGAGATCGA	GACCATCCTA	GCCAACATCG	TGAAACCCCA	CTCCCCCCCCC	2460
60	TORGGCAGGA	CAATCCCTTC	AACCCGGGAG	GTGGAGATTG	CAGTGAGCCC	CTCGGGAGGC AGATCGCACC	2520
00	ACTUCACTO	AGTETTGGCAA	CAGAGCAAGA	CTCCATCTCA	AAAAGAAAAG	AAAAGAAGAC	2580
							2640
	AACTTTAATG	AACTAACTGA	CAGCTTCATG	AAACTGTCCA	CCAAGATCAA	GCAGAGAAAA AATGTCTTGT	2700
65	TAATTAATTT	CATGGGACTA	AATGAACTAA	TGAGGATTGC	TGATTCTTTA	CARTTTYCATT	2760 2820
03	TTCCCAGATT	TCAGGAAACT	TITITITITI	ATTENDED	TOTOGOTATO	TOGTOGCTCC	2880
	AGACTTCCCA	AACTATICAT	CARTATTAT	ATTGTATGGT	AATATAGTTA	TTGCACAAGT	2940
	TCAATAAAA	TCTGCTCTTT	GTATAACAGA	AAAA		TTGCACAAGT	
-							
70		40 Protein					
	Protein Ac	cession #:	NP_004354.1				
	1	11 .	21	31	41	51	
	ī	1	1	1	1	1	
75	MESPSAPPHR	WCIPWORLLL	TASLLTFWNP	PTTAKLTIES	TPPNVAEGKE	ALTEANTED	60
	HLFGYSWYKG	ERVDGNRQII	GYVIGTQQAT	PGPAYSGREI	IYPNASLLIC	MIIQNDTGFY	120
	TLHVIKSDLV	NEEATGOFRV	YPELPKPSIS	SNNSKPVEDK	DAVAPTCEPE	NIIQNDTGFY TQDATYLMWV LNVLYGPDAP	180 240
							300
80	ARNSDTGLNR	TTVTTITUVA	RPPKPPITSN	NSNPVEDEDA	VALTCEPEIC	NTTYLWWVNN	360
	QSLPVSPRLO	LENDNRTLTL	LSVTRNDVGP	YECGIQNELS	VDHSDPVILN	NTTYLWWVNN VLYGPDDPTI	420
	SPSYTYYRPG	VNLSLSCHAA	SNPPAOYSWL	IDGNIQQHTQ	RELIGIOUS	NSGLYTCOAN	480
	NSASGHSRTT	VKTITVSABL	PKPSISSNNS	KPVEDKDAVA	FTCEPEAQNT	TYLWWVNGQS	540
85	LPVSPRLQLS	NGNRTLTLFN	VTRNDARAYV	CUIQNSVSAN	KSDPVTLDVI	YGPDTPIISP GTYACFVSNL	660
03	PDSSYLSGAN	SITVSASGTS	POLSAGATVO	IMIGVLVGVA	LI	GI LACT YORL	-000
	ALCIANOITE						

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Seq ID NO: 41 DNA sequence Nucleic Acid Accession #: NM_006952.1 Coding sequence: 11-793

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-	1	11 -	21	31.	41	51	
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	ANTOCCIACA	ATGGCGAAAG	ACAACTCAAC	TGTTCGTTGC	TTCCAGGGCC	TGCTGATTTT	60
	TGGAAATGTG	ATTATTGGTT	GTTGCGGCAT	TGCCCTGACT	GCGGAGTGCA	TCTTCTTTGT	120
10	ATCTGACCAA	CACAGCCTCT	ACCCACTGCT	TGAAGCCACC	GACAACGATG	ACATCTATGG	180
	GGCTGCCTGG	ATCGGCATAT	TTGTGGGCAT	CTGCCTCTTC	TGCCTGTCTG	TTCTAGGCAT	240
	TGTAGGCATC	ATGAAGTCCA	GCAGGAAAAT	TCTTCTGGCG	TATTTCATTC	TGATGTTTAT	300
	AGTATATGCC	TTTGAAGTGG	CATCTTGTAT	CACAGCAGCA	ACACAACGAG	ACTTTTTCAC	360
	ACCCAACCTC	TTCCTGAAGC	AGATGCTAGA	GAGGTACCAA	AACAACAGCC	CTCCAAACAA	420
15	TYGATGACCAG	TGGAAAAACA	ATGGAGTCAC	CAAAACCTGG	GACAGGCTCA	TGCTCCAGGA	480
	CAATTGCTGT	GGCGTAAATG	GTCCATCAGA	CTGGCAAAAA	TACACATCTG	CCTTCCGGAC	540
	TGAGAATAAT	GATGCTGACT	ATCCCTGGCC	TCGTCAATGC	TGTGTTATGA	ACAATCTTAA	600
	AGAACCTCTC	AACCTGGAGG	CTTGTAAACT	AGGCGTGCCT	GGTTTTTATC	ACAATCAGGG	660
	CTGCTATGAA	CTGATCTCTG	GTCCAATGAA	CCGACACGCC	TGGGGGGTTG	CCTGGTTTGG	720
20	ATTTGCCATT	CTCTGCTGGA	CITTTTGGGT	TCTCCTGGGT	ACCATGTTCT	ACTGGAGCAG	780
	AATTGAATAT						

Seq ID NO: 42 Protein sequence: Protein Accession #: NP_008883.1

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30	IGIFVGICLP PLKQMLERYQ DADYPWPRQC	FQGLLIFGNV CLSVLGIVGI NNSPPNNDDQ CVMNNLKEPL	MKSSRKILLA WKNNGVTKTW	YFILMFIVYA DRLMLODNCC	FEVASCITAA GVNGPSDWQK	YTSAFRTENN	60 120 180 240

35 Seq ID NO: 43 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 83-2605

	11	21	31	41	51	
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0000000000	TCTGCGCGTA	TOTALARCO	GGCCCAGTTG	TGAACTAGGA	GAGCTTTGGG	60
GCCGGACAGA	CAAGCAAGAG	ACAMCAATCC	MORCTATAGA	GGCAGAGGAT	TTGGACGAGG	120
ACCICIOTOC	AGCTGGAAAA	COCCANGE	TOCTOGGAAC	TTCTCAGGAA	AATGGAGAGA	180
AAGATITCAA	AGACCTGATC	TOROTTOROG	CACAGGAAAA	CCTACTTCTG	AACAAACCCC	240
AAGAGAACAC	CTTTCAACAA	1GAGTAGACA	CHICAGOGOGO	TCAACATTGG	ATCGATTCAT	300
ACAGTTTTTG	GGCTGGAAGC	MUNICULACA	TONTOCHO	AGCGATAGCT	CTCCTTTGAT	360
ACCATATAAA	CAAGCATTTG	111MILITURE	CACAACCCAT	ATTYCKTTYCT	ATGACAAGGA	420
TGAGAAGATT	AGAAAGGGAA	AMAMATITITI	ACAMOGCA1	CAACTCACAG	AAGGTGGTGA	480
TGAAATAGAA	TTGATACCAG	DEPARTMENT	TCAACTAAGA	GATGCACCTG	AGAAAACCTT	540
AGTANCTAAC	GGTTTGGCAA	MINIMOCANC	CTITALCTARG	CACCTTGAAA	GGCATGCAGC	600
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TATTCATGCA	AAATACATTG	ACTATOROCC	Characacac	COTOTCAGTA	ATATAAAGCC	780
TTACTATGGA	AAGATGGCTT	CTCTAAGAGG	TOTAL TOTAL	COLOTOGO	CTTTCTCT	840
TCTTTGCACC	AAATACAGTC	TICTITIGIC	TOCKTOTOON	CONCRETE	GAGGCAGGTC	900
TCCAGATGGA	CTCCGCAGCT	TTCCCACAGA	GIGICCIGIG	CCIGIGIGIC	CAAMCAAAAT	960
ATTTACTGCT	ATGTCTGATG	CTCCTCTCAC	AGTTACGATG	SWC1GGCKG1	CANTAGAATG	1020
CCAGGAATTG	CATGATCTTG	ATCAGAGAGA	AGCAGGICGG	ATTCCACCAA	CHARTACTOC	1080
TGAGCTTGTT	CATGATCTTG	TGGATAGCTG	TGTCCCGGGA	GACACAGIGA	CIMITACIO	1140
AATTGTCAAA	GTCTCAAATG	CGGAAGAAGG	TTCTCGAAAT	AAGAATGACA	CARACTEC	1200
CCTTTTGTAT	ATTGAAGCAA	ATTCTATTAG	TAATAGCAAA	GGACAGADAAA	CAMMONGTIC	1260
TGAGGATGGG	TGTAAGCATG	GAATGTTGAT	GGAGTTCTCA	CTTAAAGACC	TTTATGCCAT	1320
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CATTTTTGGT	CATGAACTTG	TTAAAGCAGG	TTTGGCATTA	GCACTCTTTG	GAGGAAGCCA	1440
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COTTO CAMBOT	CCABATGAGC	ATCATCATCA	CTTACTCTCT	GAACATGTGA	TTGCAATAAG	1920
BOOMSON N NO	CACAGAGCA	TTACCACTCC	CACAGTAGCT	CGTATGAATA	GTCAAGATTC	1980
A A A TACTTO	CTACTTCAAC	ADTECTOR	GAAGCCATTA	TCAGAAAGAC	TAAAGGTGGT	2040
marmackan k	ACABERCATO	CONTROCO	CCAGCTATTC	BAGAAAGTACA	TTGGCTATGC	2100
TOCOCAGTAT	CTOTACCCA	CCCTATCCAC	: AGAAGCTGC7	CGAGTTCTTC	AAGATTTTTA	2160
COTTGAGCTC	CCCAAACACA	GCCAGAGGTI	* AAATAGCTC	L CCAATCACTA	CCAGGCAGCT	2220
CONTRACTOR	ATTYVETOTICS	CAGAGGCACG	AGCAAGGTTC	GAATTGAGAG	AGGAAGCAAC	2280
CARAGRAGAC	COTTONOCATE	TAGTGGAAAT	TATGAAATAT	AGCATGCTAG	GAACTTACTC	2340
WATER BATT	COCCARCOTAC	ATTTTGAGCG	AT CCCAGCA7	GGTTCTGGA	TGAGCAACAG	2400
CTICK TOTAL CO.	BARRORTTE	THE PROPERTY OF THE PROPERTY O	CARCARCGI	r gctgaaagaj	CTTATAATAA	2460
TO TO THE CAR	TTTCBTCBAC	TTYTHERAGAT	TGCCAAAGA	A CTAAACATTO	AGGITGCTGA	2520
TOTAL DESCRIPTION OF THE PARTY	PASSAMPATER 1	CACTABATGE	CCAGGGTTAG	CICITGAAA	AAGGCCCAAA	2580
NORMAL CONC	CONCABACTI	TYPENABRICE	CTTCACCAAC	TTAGGGCCTC	CTGGGTTTAT	2640
TOTAL BATTA	BOCCATCTC	CTCAACATAT	r GCGTGCACG	- ACAGACAGAG	AGACACACAC	2700
1010101010	T BCBCBCBCBC	* ACACACACAC	" ACACACAGT	- AAATACTGT	r CTCTGAAAAA	2760
MUNUACACAC	- ACACACACACA	. ASTROCALA	MAGCATTAN	TATAATAAA	TAATTTAAGA	282
TGATGTCCC	ANNOTATIA:	. WINGONGO	· Muchina			

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	AGTGATAAAG	TCTCCAGATG	CAGTAGCTCA	CACTGTAATC	ACAGTGACTC	AGGAGGCTGA	2880
	GGTGAGAGGA	TTCCTTGAGG	CCAGGGTTCG	AGACCAACCT	TGGGCAACAT	AGCAAGACCC	2940
	CATTTCTTAA	AAAAAAAAA	AAAAAATTTA	AACTTAGCTG	GGTATGGTGG	CACATGCCTA	3000
5	TREACTORGE	CACAATCACA	CCAATCACTC	CACTOCAGCC	TOGGCAATAA	AGTAACTCTT	3120
	GACTCAAAAA	AAAAAAAA	ATTGTAGTGG	TAGCCATGTG	TTAATTGTTA	AATAAATTCT	3180
	CCAAAGGGCT TTATATGTAT	AAAAGTAAAT	TACTTATAAA	TTTTTTTATAG	TIGTATITIT	GACCTGCCTT	3240
	AAACCAATGA	BARTATTICA	TAGTTTTGCA	TCCAATAAAA	CTTTATTTAT	GGACACTAAA	3360
10	ATTTGAATTT	CATAAAATTT	TCCCATGTCA	AGAATACAAA	ATACTTGAGT	TTTGTTTTTA	3420
	GCTATTTAAT	AATAGGTCTC	ATTTATTCCA	CAGGCTGTAG	TTTGTAGTCT	TGCTTGAAAC	3480 3540
	AATAGAAACA AATTATTAGA	AGGCAGGTGA	ACCAGGAGAAG ACCAGGAGAG	TANGCTTCCA	GCAGCAATTT	GTAAAACCAT	3600
	GCCTTAGAAT	TGGACTAAGG	AAGAAGCTGC	TGACACTCCA	CTGCCACACA	GGGCACTGGA	3660
15	AGAAAGTGCT	GCTGCCTCCC	TGCCCCACCT	TTGCCACTTC	TGCAGCAGGA	ATAGGTAGAA	3720
	GAATGCCCCC	ACCCGCACCG TCAAAAAAAGA	GAACAGCAAC	AAAAGGATTC	TGCATGAGAT	GCCTCCCTAA	3780 3840
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	AATAAGACCA	GAATTTCTCA	TATGTTGTGA	GAGGATTCAA	ATGTTACAGG	GTTGCCAGCC	3960
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25	GGAATCAAAA	GGGGCCAGGT	GCAGTGGCTC	ACATCTATAA	TCCCAGAGCT	TTGGGAGTTC	4260
25	GAGGCAGGAG	GATCACTTGA AAAAATAGAT	AGCCAGTTTT	GAGACCAGCC	TATGCAACAC	ATTGAGACCC	4320 4380
	GTGGAGGCTG	AAAAATAGAT	TCACTTGAGC	CCGAGAGTTT	GAGGTTACAG	TGAGCTATGA	4440
	TTATACCACT	GCACTCCAGC	CTGGGCAAGA	GAGCAAGACC	TIGICICIT		
30							
30	Seq ID NO:	44 Protein ession #: 0	sequence:				
	PIOCESIII ACC						
	1	11	21	31	41	51	
35	I DIOCENTO COCK	GRGRFQSWKR	CDCCCMPCCK	WOVEDWEEN.	SKTTCKPTSE	OTPOFLISTK	60
33	TROCMOSTI.D	RETDYKOWKT.	VESEVVSDSS	PLIERIOAPE	KFFTRHIDLY	DKDEIERKGS	120
	ILVDPRELTE	GGEVTNLIPD	IATELRDAPE	KTLACMGLAI	HOVLTKOLER	HARELQAQEG	180
	LSNDGETMVN	VPHIHARVYN PPLPDGKYSL	AEBLIOTKNA	RANYYGRYIA	LRGTVVRVSN	IKPLCTKMAP	240 300
40	OREAGRIPHT	IECELVHDLV	DSCVPGDTVT	ITGIVKVSNA	BEGSRNKNDK	CMFLLYIEAN	360
	SISNSKGOKT	KSSEDGCKHG	MLMEFSLKDL	YAIQBIQARE	NLPKLIVNSL	CPVIPGHELV	420
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	TTTTSGLTVT	LSKDSSSGDF PARTSIIAAA	ALEAGALVIG	DOGICGIDES.	SALLSD FOLV	PILLDTPNEK	600
45	HOHLLSEHVI	AIRAGKORTI	SSATVARMIS	ODSNTSVLEV	VSEKPLSERL	KVVPGETIDP	660
	IPHOLLRKYI	GYAROYVYPR	LSTEAARVLQ	DFYLELRKQS	QRLNSSPITT	ROLESLIRLT	720
	BARARLELRE	EATKEDAEDI YNNIFQFHQL	VEIMKYSMLG	TYSDEFGNLD	FERSOHGSGM	CDICUYOLOTM	780
	SALNNVAERT	INNIPOPHOL	ROTAKBENTO	ANDERNEIGS	шидатына	drice (Quegan	
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55	Nucleic Act Coding sequence ACCAGATECC	ld Accession nence: 149.	#: NM_0054	31 TTCTCTGCAC	AGCAGATGAT AGGAGCTTAG	CCCTGAGCAG AGGATTCTTC	120
	Nucleic Act Coding sequence ACCAGATCCC CTGAAGACCA AAAGACTGTG	Id Accession nence: 149. 11 	#: NM_0054	31 TTCTCTGCAC TGCTTAATTC GAGTTCTTAC	AGCAGATGAT AGGAGCTTAG CAGCAGAAGC	CCCTGAGCAG AGGATTCTTC AGACCTTTAC	120 180
55 60	Nucleic Act Coding sequence ACCAGATCCC CTGAAGACCA AAAGAGTGTG CCCACCACCT	Id Accession nence: 149. 11 AGAGGCTGAA GAAAAGCCAC TCCACGATCC CAGCTTCAAC	#: NM_0054 .658 21 CACCTCGACC TAAGACTTC TTTGAAGCAT AGCAGCAGGT	31 TTCTCTGCAC TGCTTAATTC GAGTTCTTAC GAAACAACCC	AGCAGATGAT AGGAGCTTAG CAGCAGAAGC AGCCAGCCTC	CCCTGAGCAG AGGATTCTTC AGACCTTTAC CACCTCAGGA	120
	Nucleic Act Coding sequ ACCAGATCCC CTGAAGACCA AAAGAGTGTG CCCACCACCT AATATTTGTT AAAGATTCCA	Id Accession nence: 149. 11 AGAGGCTGAA GAAAAGCCAC TCCACGATCC CAGCTTCAACC CACACACCA AGAGCTACGCT	#: NM_0054 .658 21 	31 TTCTCTGCAC TGCTTAATTC GAGTTCTTAC GAAACAACAC CCCTGAGCCA	AGCAGATGAT AGGAGCTTAG CAGCAGAGCCTC GTTCCACAAC GGCTGTACCA	CCCTGAGCAG AGGATTCTTC AGACCTTTAC CACCTCAGGA CTGGAAACAC AGGTCCCTGA	120 180 240 300 360
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60 65 70	Nucleic Aci Coding Beeg Coding Beeg CODING BEEG ANAGATOCC TOTANGACOA ANAGATOTO TOTANGACOA ANAGATOTO TOTANGACOA ANAGATOTO COMMATTOTO ANAGATOCO COMMATTOTO ANAGATOCO COMMATTOTO TOTANGACOA TOTTOCCACO TOTANGACO TOTANGACOA TOTOCOCCAC TOTANGACOA TOTOCOCCAC TOTANGACOA TOTOCOCCAC TOTANGACOA TOTOCOCCAC TOTANGACOA TOTOCOCCAC TOTANGACOA T	Id Accession Length 19. In Agricultural Landschaft 19. In Agricultural Landschaft 19. In Landschaft	a B. NW_0054 21 1 CACCTORACC THRAGACTTC THRAGACTTC THRAGACTTC THRAGACAT GHACAAGG GHACAAGG GHACAAGG CTCAAAGG CTCAAAGG CTCCAAGG CTCAAGG CTC	31 TECHTOGAC TOGTIANTIC GRANCANCC GRATTCTTAC GRANCANCC COCCENARA COCCENCANC	AGCAGATGAT AGGAGTTAG AGGAGTTAG AGGAGTTAG AGGAGTTAG AGCAGTTAGA GGCTTACAA GGCTTACAA GGCTTACAA GGCTTACAA GGCTTACAA GGCTTACAA AGACAAAC AGGATTATTATT TTCATGAGGTT TTCATGAGTTT TTCATGAGTT TTCATGAGT T	CCCTGAGCAG AGGATTCTTC AGACCTTTAC AGACCTTTAC CACCTCAGGA CTGGAAACA AGGTCCTGA AGGTCCTGA AGGTCCTGA AGGTCCTGA AGGTCCCTGA AGGTCCCTGA AGGTCCCTGA AGGTCCCTGA AGGTCCCTGA CAGGAGCAC TCTGAGACAC TCTGAGCTCC CCAAGCCAC TCTGGGTCTCC CTGGTCCTCC 51 TKIDEBGGCTTA TKIDEBGCTTA TCTTA TCTTCTA TCTTTCTA TCTTCTA TCTTCTA TCTTTCTA TCTTCTA TCTTTCTA TCTTCTA TCTTTCTA TCTTTTTA TCTTTCTA TCTTTTTA TCTTTTA TCTTTTA TCTTTTTA TCT	120 180 240 360 420 480 540 660 720 840 900 960

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5	AAGGCTCGTT TTGCAATTAA GAAAATGGAT TTTGGGGAAA	11 CAGGCGTCCC AGAATTCGCC GCTTAGGGAA TAGAGAAACT GTGCCCCGAC GGCGGCAGCG	CTAGAGCTGT CCAGCAACAA TCTTCCCCGA CGCAGAGGCG	ATCATGTATT AAGCAAACTT TTTAAGGGGA ACGACAGGGG	TTCTTTCAAA GGCCCGAGGT AAGATTCCTG AGCAGGAAGC	TTAACTTTGC CGTTCACCGC CGGCCAGCGC TGCTCACGGT	60 120 180 240 300 360
10	TARGGATARC	ATCCTGGAAA CCTGTGGAGT TGTGAGAATT	TYPACTTCTCT	ACCOTTTGAG	CCCAACTGCA	CACTCATGAC	420 480
15	Seq ID NO: Nucleic Aci	48 DNA sequ d Accession	nence: n #: CAT clu	ster	``		
	i.	11	21	31	41	51	
20	TTTTAGTAAA CTCCAAGTCA TCCTTACTCT COGACTACCG	TTTTTTTGT TGAGATTATG TGAGTGTGCA TCTCGGAGCC TGAGCAGCTT	TTCATGAATG GTTGGGCTCA CACATCGCCC CCTGCTCCCC	TGTTTGGTAA AACCGTACAG AGATGAGGAA TGTCGTCGCC	ACTGTAACTC AAGTCATTTC GGCCACCGCT TCTGCGGTCG	CACAGGCCAG CAGGATGTTA GCCGCCAACG GGGCACTTTC	60 120 180 240 300
25	ATTTTCGCGG	TGGCCGCAGG TGAACGACCT AGTTAATTTG AATGAGGGAA	CGGGCCAAGT	TIGCTTTTGT	TGCTGGTTCC	CTAAGCTTAA	420 480 540
30	Seq ID NO: Nucleic Ac:	49 DNA sequ Ld Accession	lence l #: CAT clu	ster			
35	CCTGCCGACC	11 GCTGCTCGTT TCTGTTGTCT CGAAACCATT GACCAGTTTT	CTTCTCTGAT	AGCCGGTCGC	GGGAGAAGCT	GACCGGTGAG GGGAGAACCC	60 120 180 240
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45	TGCTGGTATC GACGTGGGGA CCGGGTCTCT	GTGCACTCCA GTCCTGCAGC GAGCTGGTCT CCTGGCCCCG CATTTATGAG	CCCATCCTCG ATATATCCGG GGGACCTAGT	GTTCCATTGC GTGAAGCTCA ATTTTTGCCA	GCTGCCAGGC GCTGTGGCAC CGAGTGTACA	AGGGTGCTGG ACCTTGGATG CCAAACAAAG	600 660 720 780 840
50	Nucleic Ac:	50 DNA sequid Accession	a #: L05187				
55	1	11	21	31	41	51	
	TCAGAAAGGA CAGAAGAAGG	GCAGGTAGAA GGAAAAGGCC ATTAGCCCCT	AGGGCAGATG GAAAGTCCCT	TCTGGGTGGA GAAGTAGGAG	GTGAAGGGAA AAGGGTAAAG	AAAGTGATCC GTGTGGTTGG	60 120 180
60	AGAGTCATAA GGAAATGGAT ATTTCTAGCT	CAGGTTTTCC GTAAATTATT GGAAGGTCTT TCCACCTTCA TCCCACCTAT	CTGAATGTGT GGACTCTGAG CCAAGGCAGA	GTAGTTTAAT ACAAGGGGTC CAAGGAGGGC	GGAATTGGGA TATAATCAGT CCACCTCAGC	CCATTTCATT TCCTCTGCTC	240 300 360 420 480
65	ACAACCATCT CCAGGGTTAA CCCTGCACCT CAGCCAGCTA	CAATGACAAG CTCATGAAAC GGGTCTGAGG GTGCCAAAAA GTAGTGTGAG	GACAGCAGGT CCTCCATGAA ATGAGGGTGG ATATCAGGTG	GGCAAGGCTC GCCTGCTGCT CAGTGAAAAT GTGTTCATCA	AACAGGACTC CACCCCTCCC TAGGCCAGTG AATAAGCCGA	AGATGTCCCC TCAAGGCAAG ACATCATTTT GCCAACCGGT	540 600 660 720 780
70	AGCTTCTATT TCACACCAAA ATTGCAACAA ATATGTGTAA	TCCTTGAGGC CCCAAGGGAC ACTGGCAATT GCAGGTTAAT	AGGGCTCATT CACACAGCCC CTAGTGTACT CCAGGGTTTC	CATCTTATAA ATTCTGCTCC TTTTCATTAT AATGGGAGAT	AAGCCAGCTG GTATACCAGG TAGAAATTAG AGAGAATAGT	GCCATTGCCT TAAGTCTCTG CTAAAGGCAA GGAATATCTT	940 900 960 1020
75	CCTCAGTAGA AGTTCATAGC TGACAAGATA	AGAACTAGAA TTTATAGAAA GTATCCTAGG	ACTGGGAGTC CTCAGGCCAG TTTTAATTTA	CTGGAGAAGA AGCACTCTCA TTAGATGGAT AAATCAATGC	TTGTTCAAAT GTAACACTGC CTCTACTGAG CCTAACGTAC	GCCCATGGGA AATTTCCCCC CATTTATTCC TTACTTAACA	1080 1140 1200 1260 1320
80	AACATAAAAC AGTAATTGGC AGGAGACCTC AGATGGGAAG	CTAGCAGGAA ATGACGGAGA TAGGGTGTCA AAAAGCATTT	GGTAATACAT TGGGCAGAGA AGTGATGTGA GGAAGGGACT	ATATATAAT AGGGCTGTGC GCTATGATGG GTGTAAGCAC	AARTGAAATG ACTTTTGGGA AGGGGTATTT AGACCAGAAG	CAAAGTAGAT GACTTGCTCA GGACAAGCAG CAAAACCATA	1380 1440 1500 1560
85	GAGGCTTAGA GAGGAAAGTG GAGCCAGCT GAGCCAAGAA	TGAATATAAA GTCTGATGCC TTAGTAGGGC GAGAACTCCA CTGAAAATTA	GCCATCCTAT ATTTTCCAAA ATTTTTCCAG ATAAAATGGA	AAGTCACAGG AGACCTAATA AACAGATATA GCAGAAGAAA	TGCGGACCTC AGGTGCCTTG TTGCCTTTTA	GGTACTAGGA ATGTCCCTCA GGTAGGAAGG GCTCCTCCTC	1620 1680 1740 1800 1860

5	WO 02/ GGGAGATGAA TTGTATCCAT CATTTGAAGC GCAGCAGCAG CAAGGAGCCC CCAGCCCAAG CACTCCAGCA TTGAGGAGCT	AGGCTTTCTC CTTTCTTTAA ATGAATTCTC GTGAAACAAC TGCCAACCCA ATTCCAACCCA	TTGRATCACT AGCAGCAGAA CTTGCCAGCC AGGTGCCTGA	GTGTCAGCTT GCAGCCTTGC TCCACCCCAG GCCTGCCAC	TCTGTCTCTA ACCCCACCCC GAACCATGCA CCCAAAGTGC GAGCCCTGCC	GAAAAAACA CTCAGCCTCA TCCCCAAAAC CTGAGCCCTG CTTCAACGGT	1920 1980 2040 2100 2160 2220 2280
10	GCCTATTGAC CTAAAAAGAT GTCTCACTGA	GGCCACTGGA CCTGCAGTTA GTCCCTTACC CTGAGCTAGT ACCATCCCTA	CTCATTCTGG CTTCTTGTTG				2340 2400 2460 2520
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20	MNSQQQKQPC IPEPCQPKVP	TPPPQPQQQQ EPCPSTVTPA	AKÖLGÖLLEĞ AKÖNGÖLLEĞ İ	EPCIPKTKEP	COBKABBACH	PKVPEPCQPK	60
25	Nucleic Aci	52 DNA sequid Accession lence: 120-4	#: NM_0026	38.1			
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30	GCTGGACTGC TGAGGGCCAG AGGCAGCTGT	AAGGAATTAT ATAAAGATTG CAGGTTCTTG CACGGGAGTT AGATCCCGTT	GTATGGCCTT ATCGTGGTGG CCTGTTAAAG AAAGGACAAG	AGCTCTTAGC TGTTCCTCAT GTCAAGACAC TTTCAGTTAA	CAAACACCTT CGCTGGGACG TGTCAAAGGC AGGTCAAGAT	CCTGACACCA CTGGTTCTAG CGTGTTCCAT AAAGTCAAAG	60 120 180 240 300 360
35	TCCGGTGCGC TCAAGAAGTG CGGTCCTTGC TGCTGCCCTT	AGTCAAAGGT CATGTTGAAT CTGTGAAGGC TGCACCTGTG CCCCTTCCCA TCTCATCCAC	CCCCCTAACC TCTTGCGGGA CCGTCCCCAG CACTGTCCAT	GCTGCTTGAA TGGCCTGTTT AGCTACAGGC TCTTCCTCCC	AGATACTGAC CGTTCCCCAG	TGCCCAGGAA TGAAGGGAGC CCTAAGTCCC	420 480 540 600
40	Sea ID NO	53 Protein	sequence:				
	,	11	21	31	41	51	
45	1 MRASSPLIVV AQEPVKGPVS	11 VPLIAGTLVL TKPGSCPIIL	21 EAAVTGVPVK IRCAMLNPPN	31 GQDTVKGRVP RCLKDTDCPG	i	51 VSVKGQDKVK MACPVPQ	60
45 50	Seq ID NO: Nucleic Ac	1	EAAVTGVPVK IRCAMLNPPN uence h #: NM_0196	GODTVKGRVP RCLKDTDCPG	i	VSVKGQDKVK MACPVPQ	60
	Seq ID NO: Nucleic Ac	VPLIAGTLVL TKPGSCPIIL 54 DNA seq id Accession	EAAVTGVPVK IRCAMLNPPN uence h #: NM_0196	GODTVKGRVP RCLKDTDCPG	i	Ĭ-	60
	Seq ID NO: Mucleic Ac Coding seq 1 GGCACGAGCC GAGACAACCA ATCAATCAAT	VPLIAGTLVL TRPGSCPIIL 54 DNA sequid Accession uence: 75-5 11 ACGATTCAGT CACTATGAGA GTGTAAACCTT TCAGGACCTT TCAGGACCCTT TCAGGACCCTT	EAAVTGVPVK IRCAMINPPN LEGICE 1 #: NM_0190 84 21 CCCCTGGACT GGCACTCCAG ATTACTGGGA ATTACTGGGTA	GODTVKGRVP RCLKDTDCPG 518 31 GTAGATAAAG GAGACGCTGA CTATTAATGA	I PNGQDPVKGQ IKKCCEGSCG 41 I ACCOTTTCTT TGGTGGAGGA TTTTGAATCAG CAGTGTGACC	VSVKGQDKVK MACPVPQ 51 GCCAGGTGCT AGGGCCGTCT CAACTGTGGA	60 120 180 240
50	Seq ID NO: Nucleic Ac Coding seq 1 GGCACGAGCC GAGACACCA ATCAATCAAT CCCTTCAGG TTGCTGTAT ATTTGGGAT CCTTCTTTT CGGACTGGTTT	VPLIAGTLVL VPLIAGTLVL VPLIAGTLVL S4 DNA seq id Accessio uence: 75-5 11 acgattcagt Cacratgaga GTGTAACCTT CACATGCAGG CCAGAATCCA AAAAGACCAG CTACCGTGCC CATMCCTCC CATMCCTCC	EAAVTGVPVK IRCAMINPPN Lence n #: NM_0194 64 21 CCCCTGGACT CGGCACTCCAG ATTACTGGGA GTGGCAGTTC TATCCAGAGG AAGATCATGG AAGATCATGG AAGATCATGGTA TCCAGAGGGA TCCAGAGAGGA TCCAGAGAGGA TCCAGAGAGGA TCCAGAGAGGA TCCAGAGAGGA TCCAGAGAGGA	GODTVKGRVP RCLKDTDCPG 118 31 GTAGATANAG GAGACSCTGA CTATTANTGA CACGAGGTGA CTCTTGAGGA TGTATTGTGA ATCTGTATGG GGACCTCCAC ACCAGGCCTAT	PROGDPYKOO IKKCCEGSCG IKKCCEGSCG IKKCCEGSCG IKKCCEGSCG IKKCCEGSCG ACCCTTATT TGGTGGACCA AGCAGAGGG CAACCCGGG CCTTGATTGAC CATTTTGATCAC CTTTGATTCAC CTTTGATTTGA	51 GCCAGGTGCT AGGCCGTCT CAGTGTGGA GACCAGTTGGA GATCCGATTT GAACAGCCA CCGTGAAACTG GAACAGCCCA CTGAGACTTG CTAGAAGTG	60 120 180 240 300 420 480 540
50	Seq ID NO: Nucleic Ac Coding seq 1 GOCACUAGCC GAGACACCA ATCAATCAAT TATTTCAGGAT TATTTCAGGAT CATTTCAGGAT CATTTCAGGAT CATTCAGGT GGAGTTGATTA GAGACTAGT TGAAGTCATT TAATGAAGAA	VPLIAGTLVL TKPGSCPIIL S4 DNA sequitence: 75-5 11 ACGATTCAGT CACTATGAGA GTGTNAACCTT CACTATGAGA GTGTNAACCTT CACTATGAGA CTAGTNAACCTT CACTATGAGA CTAGTNAACCTT CACTATGAGA CTAGTNAACCTT CACTATGAGA CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC CATTGAGTNAC GAAGCANTAGAGT GAAGT GAAGCANTAGAT GAAGT GAAGCANTAGAGT GAAGT GAAGCANTAGAT GAAGT G	BAAVTGVPVK IRCAMINPPN uence a #: NM_0196 84 21 CCCCTGGACT GGCACTCCAG ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGGA ATTACTGGA ATTACTGGA ATTACTGGA ATTACTGGA ATTACTGGA ATTACTGGA ATTACTGGA ATTACTGCA ATTACTGCA ATTACTGCA ATTACTACTGCA ATTACTCATAGGA ATTACTCATAGGA ATTACTCATAGGA	GODTVKGRVP RCLKDTDCPG S18 31 1 STAGATANAG GAGACSCTGA CHOTTOMOGA CHOTTGAGGA ACCAGCCCAN ACCAGCCCAN ACCAGCCCAN ACCAGCCCAN ACCAGCCCAN ACCAGCCCAN ACCAGCCAN TATANATGA TACCAATGAGAG ACCAGGGCA ACCAGGCAGA ACCAGGA ACCAGGCAGA ACCAGGA ACCAGGA ACCAGGA ACCAGGA ACCAGGA ACCAGA ACCAGGA ACCAGGA ACCAGA ACCAGGA ACCAGGA ACCAGA ACCAGAGA ACCAGA ACCAGAGA ACCAGA ACCAG	PINGODPVIGO I KKCGEGSCG 1 KKCG	S1. GCAGGTGCT AGGGCGTCT CAAGTGTGGA CCAGGTGCT GATCCCATTT GATCAGCCCA CCGTGAAACT CCTAGAACTG CCTAGAAGGTG ACATTTCTA TCTCATTTTA CTCAGAAGGCA ACAGGGCA ACAGGCA AC	60 120 180 240 360 480 540 600 720 780
50 55 60	Seq ID NO: Nucleic Ac coding seq	VELIAGILVIL TRESEGIIL TRES	EAAVTOUPUK IRCAUGIPPN LIRCAUGIPPN LIRCAUGI	GODTYKRIVP RCLEDTICEG GODTYKRIVP RCLEDTICEG GODTYKRIVP GODTYCH JAMES GODTYC CHATTANTAG GOGAGGCTA CACCAGAGTAG CACCAGAGTAG ACCAGAGTAG	HINGOPPUKOG IKKCCEGSCO IKKCCEGSCO IKKCCEGSCO IKKCCEGSCO IKKCCEGSCO IKCCCEGSCO IKCCCCEGSCO IKCCCCCEGSCO IKCCCCEGSCO IKCCCCCEGSCO IKCCCCCEGSCO IKCCCCCCC IKCCCCCCC IKCCCCCCC IKCCCCCCC IKCCCCCCC IKCCCCCCCC	51 1 CCAGGGTGCT AGGGCGTGCT AGGGCGTGCT GATCCATT GATCCATT GATCCATT GATCCATT CCAGAGGTG CCAGAGGTG CCAGAGGTG CCAGAGGTG CCAGAGGTG CCATT CCAGAGGTG CCAGAGGTG CCAGAGGTG CCATT	60 120 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60 65	Seq ID No: Nucleic As Coding seq in Coding seq in Coding seq in Coding seq in Coding seq in Coding seq in Coding seq in Coding seq in Coding seq in Coding Seq in Coding C	VELIAGILVIL TRESCRITIL TRESCRITIL TRESCRITIL TRESCRITIL TRESCRITIC	ЕАЛУТОГРИК В САМИТОГРИК В На МИ ОЗРА В Н	GODTYKORYP RCLEDTICES (18 31 31 GTAGATANAG GAGAGCTGA CACCAMOTON ATTOTATTGGA ACCAGCCAT ATTOTATGGA ACCAGCCAT ATTOTATGGA CACCAGCCAT ATTOTATGGA CACCAGCCAT ACCAGCCAT ACCAGCCAT ACCAGCCAT ACCAGCCAT ATTOTATGGA CACCAGCCAT AND ATTOTATGGA CACCAGCCAT AND ATTOTATGGA CACCAGCCAT AND ATTOTATGGA CACCAGCAGCAGC CACCAGCAGCAGC CACCAGCAGCAGC CACCAGCAGCAGC CACCAGCAGC CACCAGCAGCAGC CACCAGCAGCAGC CACCAGCAGC CACCAGCAGCAGC CACCAGCAGCAGC CACCAGCAGCAGC CACCAGCAGCAGC CACCAGCAGCAGCAGC CACCAGCAGCAGCAGCAGCAGC CACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	PROGUPYKOG IRKCCESSCO IRKCCESSCO IRKCCESSCO IRKCCESSCO IRKCCESSCO IRCCCESSCO	S1 S1 GCAGGGGCTC AAGTGTGC AAGGCCCTC CAAGTGTGC GT GT GT GT GT GT GT GT GT GT GT GT GT	60 120 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60 65 70	See ID NO. NOLLIC & CONTINUE OF THE PROPERTY O	VPLIAGILVIL TRESCEDIL TRES	EAAVTOUPVK IRCMGMPPN IRCMGPPN IRCMGMPPN IRCMGM	GDDTVKGRVP RCLKOTDCSG 516 31 11 GTAGATARAG GAGACSCTGA CACCATAGAC C	HIVAVPRSDS	STANDARDA CONCACTOR CONCAC	600 1200 2400 3600 6500 6500 1020 1020 1020 1020 1020 1020 6600 660

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	1	11	21	31	41	51	
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10	AGCACCAGCC AGCCGGCCAC CAATTAGCAT	CAGCAGAAGA CAGATGCTGA TCTGTCTCCC TGAATGAAGC AGAGAGACTT	CCAAGCAGAA ATCCCCTATC CCAAAAAAGA	GTAATGTGGT CCATTCTGTG ATGTGCTATG AGTACCAGAG	CCACAGCCAT TATGAGTCCC AAGCTTTCIT CTAGTTTTCA	GCCCTTGAGG ATTTGCCTTG TCCTACACAC GCTGCTCAGA	360 420 480 540 600
15	AAATTCACTT	TCAATTCCA					
	Seq ID NO:	57 Protein	sequence:				
20	Plocein Acc	respion #. 1					
	1	11	21	31	41	51	
	ı	1	1	1	ammanana.	DIGUEDOODE	60
25	MSSQQQKQPC LPEPCHPKVP	IPPPQLQQQQ EPCPSIVTPA	PAQQKTKQK	EPCIPKTKEP	CHPKVPBPCH	PRVPEPCQPR	60
23	Nucleic Ac	58 DNA sequid Accession uence: 71-2	#: NM_0017	793.2			
30	1	11	21	31	41	51	
50	î	ī	Ĩ.	i	1	Ī	
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	TOCOGRAGACA	GTCCAGGAAA	GAAGGTCACT	GAAGGAAAGG	AATCCATTGA	AGATCTTCCC	360
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40	AGACACCAAG	ATTTTCTACA	CACCACCACCAC	CTTCTTGAAT	AAGCCACTGG	ACCGGGAGGA	600
	CITCGCIGIA	ATTTTCTACA GAGAAGGAGA TATGAGCTCT	TTGGCCACGC	TGTGTCAGAG	AATGGTGCCT	CAGTGGAGGA	660
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43							900
							960
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00	ACTGATTGAT	GTGCGCCAGG	TGCTGAACAT	CACGGACAAC	GACCTGTCTC	CCCACACCTC	1800
	OCCUPATION OF THE	COCCACCTCA	CAGATGACTC	AGACATCTAC	TGGACGGCAG	AGGTCAACGA	1860
	GGAAGGTGAC	ACAGTGGTCT	TGTCCCTGAA	GAAGTTCCTC	AAGCAĞGATA	CATATGACGT	1920
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03	CONTRACTO	GGGGCTGTCC	TOGATACCTO	GTTCCTCCTC	CTGGTGCTGC	TTTTGTTGGT	2100
	CACAAACAAC	COCKBOATCE	AGGAGCCCCT	CCTACTCCC	A GAAGATGACA	CCCGTGACAA	2160
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							2820
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80	TACAGTGGAG	TTTCTCTCTC	GAATGGAACC	CANAGETEE	T CANAGESCO	GCCCAGAGCT	3000
							3060
	maca mamama	- COMMONDATI	CTCACTOTO	CTAGGTTGC	C CCTTATTTT	TATTTTCCCT	3120
0.5	GTTGCGTTG	C TATAGATGA	GGGTGAGGA	AATCGTGTA	r atgractage	ACTITITAT	3180
85	TARAGARAC	TTTCCCAGA	AAAAA				

Seq ID NO: 59 Protein sequence:

	Protein Acc	ession #: 1	NP_001784.2				
	1	11	21	31	41	51	
5	MGLPRGPLAS	LLLLQVCWLQ DDFTVRNGET	CAASEPCRAV	 FREAEVILEA	 GGAEQEPGQA	LGKVFMGCPG	60 120
	KGPFPQRLNQ YELFGHAVSE	LKSNKDRDTK NGASVEDPMN	IFYSITGPGA ISIIVTDOND	DSP PEGVFAV HKPKPTQDTP	EKETGWLLLN RGSVLEGVLP	KPLDREEIAK	180 240
10	TDMDGDGSTT AWRATYLING PTSTATIVVH	GVVAYSIHSQ TAVAVVEILD GDDGDHFTIT VEDVNEAPVF	ANDNAPMFDP THPESNQGIL VPPSKVVRVO	QKYEAHVPEN TTRKGLDFEA EGIPTGEPVC	AVGHEVQRLT KNQHTLYVEV VYTAEDPDKE	VTDLDAPNSP TNEAPFVLKL NOKISYRILR	300 360 420 480 540
15	GAVLALLFLL GLEARPEVVL	DSGQVTAVGT RQITICMQSP KQDTYDVHLS LVLLLLVRKK RNDVAPTIIP SLSSLTSSAS	RKIKEPLLLP TPMYRPRPAN	TVIRATVCDC EDDTRONVFY PDEIGNFIIE	HGHVETCPGP YGEEGGGEED NLKAANTDPT	WTAEVNEEGD WKGGFILPVL QDYDITQLHR APPYDTLLVF	600 660 720 780
	DYEGSGSDAA	SUSSUISSAS	DODODIDIA	BWGSRPRRUA	DMIGGGEDD		
20	Nucleic Ac	60 DNA sequid Accession Lence: 162-	ı#: Eos se	equence			
0.5	1	11	21	31	41	51	
25		GGCGGCGGAT	mant t comma	l car amar am]	Chronnocom	60
	CATACGGACC	CCATTOTTT	CCCTCCCCA	GTGTCCCCGG	AGCTTGTGTG	CGATACAGAG	120
	AGCACCTCGG	AAGCTGAGGC	AGCTGGTACT	TGACAGAGAG	GATGGCGCTG	TCGACCATAG	180
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35							
	Seq ID NO: Protein Ace	61 Protein cession #: 1	Sos sequence				
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	NACASKCRVI	NKEHVLAAAK	VILKKSRG				
45	Nucleic Ac	62 DNA sequid Accession mence: 99-8	#: NM 000	94.2			
	1	11	21	31	41	51	
50	1	1	1	1	1		60
50	GAGGCTGGAGG	GGCGCTGGGC TCCTAGCTGA	CGGCTTTTAC	TGCCTAGGAT	GACGCTGCGG	CTTCTGGTGG	120
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	GAGTGACCTG	CACGCGCCTT	TACGCCGCTG	ACATTGTGTT	CTTACTGGAT	GGCTCCTCAT	240 300
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	CACGGACAGA	GTTCGGCCTG	GATGCACTTG	GCTCTGGGGG	TGATGTGATC	CGCGCCATCC	420
	ACCATGRET	CTACAAGGGG	CTGGCCGAC	CTGGTGTCCC	CAAGGTCTGC	ATCCTGATCA	480 540
	CACACCCCAA	GTOTTAGGAC	CTCCTCCACA	CAGCTGCCCA	DAGGCTYCAAG	GGGCAGGGGG	600
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	TOCCCCTCGT	TTCCCGGAGA	GTGTGCACGA	CTGCTGGTGG	CGTGCCTGTG	ACCCGACCTC	780
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	CONCTOTOCC	ACCTOCCACT	COUNTRACTOR	TOACATGGGG	GGTCCTCAGT	GGTGGGGCCCA	1200
70	CACAGCAGCA	GGAGCTGGGC TGAGGTGACC	CCTGGGCAGG	GTTCAGTGTT	GCTGCGTGAC	TTGGAGCCTG	1260
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	CTGCCACAGA	CATCACAGGG	CTGCAGCCTG	GAACCACCTA	CCAGGTGGCT	GTGTCGGTAC	2100
85	TGCGAGGCAG	CATCACAGGG AGAGGAGGGC	CCTGCTGCAG	TCATCGTGGC	TCGAACGGAC	CCACTGGGCC	2160
	CAGTGAGGAC	GGTCCATGTG CGCCACAGGA	ACTCAGGCCA	GCAGCTCATC	AGCCCACCATT	ACCTGGACCA CCAGAGAAAT	2220
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WO 02/086443 CCCAGTTGGT TTCTGGGGGAG GCCACGTTGG CTGAGCTGGA TGGACTGGA CCAGATACTG 2340 AGTATACGGT GCATATGAG GCCCATGTGG CTGGGGTTGGA TGGGCCCCCT GCCTCTGTGG 2400

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	201000000	moma occuran	roccord	COCTCACTOC	ACCCACACCC	TACACACTCC	2520
5	CCAGCGACGI	Chamathaga	ACCIOGOIAG	0001010100	ACTOCCALOCA	AACACACACT	2500
,	CCTGGGGCGG	GAGTGANGGC	GUCCCCATGA	GGCACCAGAI	ACTOCCAGGA	MICHCAGACT	2360
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10	AGTCCCGGGT	CCTGGGGCCC	GAGCTCAGCA	GCTATCACCT	GGACGGGCTG	GAGCCAGCGA *	2880
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	CACAGIACCG	COTOMOGCIO	MUIGICCING	0000000000	A CONTACTOR	TOTO COLOR	3000
	TGACTGCGCG	CACTGAGTCA GGTGACTTTG ACTCAGAGGC	CCTCGTGTTC	CAAGCATIGA	ACTACGIGIG	GIGGACACCI	
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	CCTTCACACC	TOACATATTC	ACCCCCATICC	CTCACCCCA	COCTTCTGGG	CTTAATGTGG	3660
	CCITGMGMGG	1000000000	AGCCCCCATCC	******************	mocommerco:	COCCCCTATCC	3720
25	TUATUTTUGG	ANTIGGETGGA	GCGGACCCAG	MGCMGC1GCG	reactioned	CCGGGTATGG	3780
23	ACTCTGTCCA	GACCTTCTTC	GCCGTGGATG	ATGGGCCAAG	CCTGGACCAG	GCAGTCAGTG	3780
	GTCTGGCCAC	AGCCCTGTGT	CAGGCATCCT	TCACTACTCA	GCCCCGGCCA	GAGCCCTGCC	3840
	CAGTGTATTG	TCCAAAGGGC	CAGAAGGGGG	AACCTGGAGA	GATGGGCCTG	AGAGGACAAG	3900
	TTGGGCCTCC	TGGCGACCCT	GGCCTCCCGG	GCAGGACCGG	TGCTCCCGGC	CCCCAGGGGC	3960
	CCCCTCCAAG	TOCCACTOCC	ADGCCCCAGA	agagetteec.	TOGAGCAGAT	GGGCGTCCAG	4020
30	CCCCIGGRAG	1000MC10CC	ANTOCOCCOCA	COCCUCATO	CCCCCCCCCTA	AAGGGCTCTC	4080
50	GCAGCCCIGG	CCGCGCCGGG	MAICCIGGGA	CCCCTGGMGC	LCCTOGCCTA	20000001010	4140
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	AGCCGGGGGC	TCCCGGACAA	GTCATCGGAG	GTGAAGGACC	TGGGCTTCCT	GGGCGGAAAG	4200
	GGGACCCTGG	ACCATCGGGC	CCCCCTGGAC	CTCCTGGACC	ACTGGGGGAC	CCAGGACCCC	4260
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	mmcccccan ac	COOMCOVCC	CAACCCCCCC	TTOGCCCCCC	TOGRADORA	COCCIONATION ANOTYPESCA. ANOTY	4440
	110000000	CCCTGGACCC	CONGCCCCG	TI GOCCCCCC	1000000000	COTTON CONCO	4500
	GIGACICIGA	GGATGGAGCT	CCAGGCCTCC	CAGGACAACC	1000101000	GGTGMGCMGG	4560
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	AACGIGGAGA	ACAGGGCAGA	GATGGCCCTC	CIGGACICCC	TOURNOCCCI	000000000	6400
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	ATGGAGACAG	AGGGAGCCCT	GGTGTGCCAC	GGTCACCAGG	TCTGCCTGGC	CCTGTCGGAC	6960
	A LOUNGACAG		- accordance	OUT CHUCKION	7010001000	CTCCCTCCCTC	7020
80	CTAAAGGAGA	ALCTGGCCCC	ACGGGGGCCC	CIGGACAGGC	101001000	ACTEGRANAG CCTGTCGGAC CTCCCTGGAG GAGCCGGGAG GGCCGTGCAG AAAGGTTCA CCAGGTGTGA TTCCCGGGTC GGTCTGGCAG	7020
οU	CAAAGGGAGA	GAAGGGAGCC	CCTGGAGGCC	TIGCIGGAGA	CCTGGTGGGT	GAGGGGAG	7080
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	*COCK CAPOO		OCCUPANCE.	Carcarage	TOTTOTO	TTCCCCCCCTC	7320
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		TCCCAGAGGC					8340
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Seq ID NO: 63 Protein sequence: Protein Accession #: NP_000085.1

MILLIUVAL CAGILABER VYAQUREEYI CITLIYAADTU FILDOSSIG RENPERVESP 60 ALIEMULPEGO AAAAQOVERA TVYSUSIDERI EUROLAGO QUITAAAGEN 120 AAAAQOVERA VARAAAGOVERA TVYSUSIDERI EUROLAGO QUITAAAGEN 120 SEPESQALA QUITAAAGENT GYACOUTELU GLOQUI-BERG QUANTENDES SERBEROM. 120 ATTOMOTYLLA HABIOLAGO GYALAGO TUATAAGEN GANTENDES SERBEROM. 120 ATTOMOTYLLA HABIOLAGO GYALAGO TUATAAGEN GANTENDES SERBEROM. 120 ATTOMOTYLLA HABIOLAGO GYALAGO TUATAAGEN TUATAAGEN GANTENDES SERBEROM. 120 ATTOMOTYLLA HABIOLAGO GYALAGO TUATAAGEN TUATAAGEN GANTENDES SERBEROM. 120 ATTOMOTYLLA HABIOLAGO TUATAAGEN TUATAAGEN TUATAAGEN GANTENDES SERBEROMYL AKTOMOTYLLA HABIOLAGO TUATAAGEN TU	35	1	11	21	31	41	51	
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SEPSESQUIN QUYTAASGOVT GYKOVTPUT GLOOPLESER GENVENDETS SVELEGLERE 100 TETCYTVIAL YANSIGENES GYRATTAASE SELTIQUITTA SELLVANSEV PACKTEVENT 100 TRUSCOPTIC GELEPOCASS LABBLERCTE TETCTATA SELLVANSEV PACKTEVENT 100 TRUSCOPTIC GELEPOCAS LABBLERCE GELEPOCAS LABBLERCE GELEPOCAS LABBLERCE GELEPOCAS LABBLERCE GELEPOCAS LABBLERCE GELEPOCAS LABBLERCE GELEPOCAS LABBLERCE GELEPO	40							
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50 RIGITIANSEN VIRITAWICHT GATAFILANG RESEGNERIN ILPONTESSAR INGLEGOTIVE #80 SVETALANDER REFERENCE VITTPERAPADA CHILOVORUS RESILLANDER PRAGESTERS SVETALANDER REFERENCE VITTPERAPADA CHILOVORUS RESILLANDER PRAGESTERS 55 STATEMENT VILOVISCOS RESILLANDER PRAGESTERS RESILLANDER PRAGESTERS RESILLANDER PRAGESTERS RESILLANDER PRAGESTERS RESILLANDER PRAGESTERS RESILLANDER PRAGESTERS RESILLANDER RESILLANDER RESILLANDER RESILLANDER PRAGESTERS RESILLANDER RE		SAHGDEKSOF	VSCEATVARI.	DGLEPDTRYT	VHVRAHVAGV	DGPPASVVVR	TAPEPVGRVS	
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ELROVOTS ID SYTLAMPING RASSYLLENIR PLERGOGRIVE GEFOTLANDES SIGNATURES 1020 OVERLEIGHT VILLOWINGER SYTCHTON GEROVOTHOL RECONSTRUCTION OF THE PROPERTY OF THE P		OPEGGOEOSR	VLGPELSSYH	LDGLEPATOY	RVRLSVLGPA	GEGPSAEVTA	RTESPRVPSI	960
55 LALGPIGEO VOCALESPES PROPERTIES SINCAPPURE ATCOMMENS ATTRAVERSUM 1000 ABETMILAPON VOCALESPES REPOLITIVE SINCAPPURE ATCOMMENS ATTRAVERSUM 1000 ABETMILAPON VOCALESPES REPOLITIVE SINCAPPURE SINCAPPU		ELRVVDTSID	SYTLAWTPUS	RASSYILSWR	PLRGPGOEVP	GSPOTLPGIS	SSORVIGLEP	1020
55 LALOPHIGPON VOYULLEYSE REPELPFEME SINDLETTERS INDESTRUCT SERVEYNDES GRELTAWYT 1140 ARWENLAND PORRIGHPON WILLVISSERS GROTISTERSEN GOSTLOWAGE GRANDFED. 1250 ARWENLAND PORRIGHPON WILLVISSERS GOTTSTERSEN GOSTLOWAGE GRANDFED. 1250 BERLEAGUVEP PORRICHART GRANDFED AND SERVEYNDES GRELTAWYT 1150 BERLEAGUVEP PORRICHART LANDFORM FOR FORRICHART LANDFORM FOR FOR FOR FOR FOR FOR FOR FOR FOR FOR		GVSYIFSLTP	VLDGVRGPEA	SVTOTPVCPR	GLADVVFLPH	ATODNAHRAE	ATRRVLERLV	1080
RELAPONOS (TYPAVIDOS SLODAVISIA. TALCASSTT (GREECTRY) CHROGOSCHO 1260 BELLAROUS PORTICIPATE (ALPOCATION SATALASSER) PARADERPSIS (INCREMENTER) 1260 ANGLICASSELI PORTICIPATE (ALPOCATION SATALASSER) PARADERPSIS (INCREMENTER) 1260 ANGLICASSELI PORTICIPATE (ALPOCATION SATALASSER) PARADERPSIS (INCREMENTER) 1260 PAGENCIACION SATALASSER (INCREMENTER) PARADERPSIS (INCREMENTER) 1260 PAGENCIACIO (SERVICIO) POSPOLOGICO PORTICIPATO MORTICIPATO MOR	55	LALGPLGPOA	VOVGLLSYSH	RPSPLFPLNG	SHDLGIILQR	IRDMPYMDPS	GNNLGTAVVT	1140
RELAPONOS (TYPAVIDOS SLODAVISIA. TALCASSTT (GREECTRY) CHROGOSCHO 1260 BELLAROUS PORTICIPATE (ALPOCATION SATALASSER) PARADERPSIS (INCREMENTER) 1260 ANGLICASSELI PORTICIPATE (ALPOCATION SATALASSER) PARADERPSIS (INCREMENTER) 1260 ANGLICASSELI PORTICIPATE (ALPOCATION SATALASSER) PARADERPSIS (INCREMENTER) 1260 PARAGEMENTS SATALASSER) PARADER PARADERS (PROPERTIES) PARADERS (INCREMENTS) PARADERS (IN		AHRYMLAPDA	PGRROHVPGV	MVLLVDEPLR	GDIFSPIREA	OASGLNVVML	GMAGADPEQL	1200
BMILROWUP FORDRUPPER GARPOGREG SATAKGEREF PAGGERERS GRARMITETER 1310 60 ANDLIAGSBEID PORTRUPPER GARPOGREGE ARCHITECTURE ARCHITECTURE GRARMITETER 1310 60 ANDLIAGSBEID PORTRUPPER GRARMITETER ARCHITECTURE ARCHITECTURE GRARMITETER 1310 FERRICATUR GERMENDER GRARMITETER GRARMITE		RRLAPGMDSV	OTFFAVDDGP	SLDOAVSGLA	TALCOASFTT	QPRPEPCPVY	CPKGQKGEPG	1260
APOLICISSPIL POPRICIPORES GEROPECERO A POQUI JOSCE POLICISCISCOP GEROPEOPER I 1980 PLODERISED PLOTECTURE DE CONTROLLE PORTOGRA DE COLICISCISCOP GEROPECTURE DE SECURITOR DE CONTROLLE PLANTA DE CONTROLLE PLANTA DE COLICISCISCO DE CONTROLLE PLANTA DE COLICISCISCO DE CONTROLLE PLANTA DE COLICISCISCO DE CONTROLLE PLANTA DE COLICISCO DE COLICISMO	EMGLRGOVGP	PGDPGLPGRT	GAPGPOGPPG	SATAKGERGF	PGADGRPGSP	GRAGNPGTPG	1320	
60 PLUDPERREP PELIPETARKE DEMORSHER POPUSOLAN GERELEKLES SPEGGFFUER 1444 PRICES PROCESSED BOARDANDO POSITIONERS GEVELOCITALES SPEGGFFUER 1444 PRICES PROCESSED BOARDANDO POSITIONERS GEVELOCITALES SPEGGFFUER 1444 PRICES PROCESSED PROCESSE		APGLEGSPGL	PGPRGDPGER	GPRGPKGEPG	APGQVIGGEG	PGLPGRKGDP	GPSGPPGPRG	1380
GRAGSBULPE VAGREPAKOP BUPPEPTORG GEKELEPRIND DRAVVORAVA GRKGEGOVO 1566 PAPPRAGUTO GERGEFORU I PURDOPEPTOR DEBONICITE GRAPPERGER PARENTOR GEKELEPRIN 1666 PAPPRAGUTO GEGETOR PAPPROCESCO DESPENDICE, PURASERERA GRAPPERGE PARENTOR 1660 ANGERCHIGHT REPRESENCE DESPENDICE, PURASERERA GRAPPERGE PERCENCIONES 1660 ANGERCHIGHT REPRESENCE PROPERTOR GRAPPERGER GRA	60	PLGDPGPRGP	PGLPGTAMKG	DKGDRGERGP	PGPGEGGIAP	GEPGLPGLPG	SPGPQGPVGP	1440
GRAGSBULPE VAGREPAKOP BUPPEPTORG GEKELEPRIND DRAVVORAVA GRKGEGOVO 1566 PAPPRAGUTO GERGEFORU I PURDOPEPTOR DEBONICITE GRAPPERGER PARENTOR GEKELEPRIN 1666 PAPPRAGUTO GEGETOR PAPPROCESCO DESPENDICE, PURASERERA GRAPPERGE PARENTOR 1660 ANGERCHIGHT REPRESENCE DESPENDICE, PURASERERA GRAPPERGE PERCENCIONES 1660 ANGERCHIGHT REPRESENCE PROPERTOR GRAPPERGER GRA		PCKKCEKCDS	RDGAPGLPGO	PGSPGEOGPR	GPPGAIGPKG	DRGFPGPLGE	AGEKGERGPP	1500
65 PAGERGATOV GORGOPPICU L'ROPOPPICO PEDRAPICAT GIAGAPEGAS PEGISCOPER 1420		GPAGSRGLPG	VAGRPGAKGP	EGPPGPTGRO	GEKGEPGRPG	DPAVVGPAVA	GPKGEKGDVG	1560
DERRIGEROSS DERREDRESS PROPRIERTO TOTALABERGE PECANOCERS GEREDRESS. 1746 ANGERICATE PROPRIERTO PROPRIERTO ENGINEERING DERPETAÇUR SILLICIANA ANGERICA PROPRIERTO PROPRIERTO DERREPAÇUR SILLICIANA ANGERICA PROPRIERTO PROPRIERTO DERREPAÇUR SILLICIANA ANGERICA PROPRIERTO PROPRIENTO	PAGPRGATGV	OGERGPPGLV	LPGDPGPKGD	PGDRGPIGLT	GRAGPPGDSG	PPGEKGDPGR	1620	
DERRIGEROSS DERREDRESS PROPRIERTO TOTALABERGE PECANOCERS GEREDRESS. 1746 ANGERICATE PROPRIERTO PROPRIERTO ENGINEERING DERPETAÇUR SILLICIANA ANGERICA PROPRIERTO PROPRIERTO DERREPAÇUR SILLICIANA ANGERICA PROPRIERTO PROPRIERTO DERREPAÇUR SILLICIANA ANGERICA PROPRIERTO PROPRIENTO	PGPPGPVGPR	GRDGEVGEKG	DEGPPGDPGL	PGKAGERGLR	GAPGVRGPVG	EKGDQGDPGE	1680	
KAGDPGBIGH. PGILAGRIĞQÜE GISSPPGLIDG KONGENGENGI KONGEGERGE GIBCARGERGE KAGDREGERGE GIBCARGERGE GIBCAR	65	DGRNGSPGSS	GPKGDRGRPG	PPGPPGRLVD	TGPGAREKGE	PGDRGQEGPR	GPKGDPGLPG	1740
KAGDPGBIGH. PGILAGRIĞQÜE GISSPPGLIDG KONGENGENGI KONGEGERGE GIBCARGERGE KAGDREGERGE GIBCARGERGE GIBCAR		APGERGIEGE	RGPPGPOGDP	GVRGPAGEKG	DRGPPGLDGR	SGLDGKPGAA	GPSGPNGAAG	1800
POSABSERER DEPRESENCA GILLOPGOPPE LEGEVEPPEQ GPPOVEROT PREDESERE 1920 REGIGIATE GREEFE VANDELETS INFABRICATE TERRESSESSE LEVERERRE 1920 REGIGIATE GREEFE VANDELETS INFABRICATE TERRESSESSE LEVERERRE 1920 REGIGIATE CONTROL TO THE PROPERTY OF THE PROPERTY		KAGDPGRDGL	PGLRGEOGLP	GPSGPPGLPG	KPGEDGKPGL	NGKNGEPGDP	GEDGRKGEKG	1860
TO KEDSEGOPP GKERPICPO EROKKEDRED POPOPOLA LEBROPPOES GLAGERKIRO 2010 INCLUDENCE OF CONTROL OF CONT		DSGASGREGR	DGPKGERGAP	GILGPOGPPG	LPGPVGPPGQ	GFPGVPGGTG	PKGDRGBTGS	1920
TICLICARIAGO VIDRAGIPICAR GREGISCIBRIO EQUIDAPICI, POTAPOPOPPO GINAVOUEDO DE CONTROLO POR CONTRO		KGEOGLPGER	GLEGEPGSVP	NVDRLLETAG	IKASALREIV	ETWDESSGSP	LPVPERRRGP	1980
1101_FORAGO VORGAMENDER GERGERGERG EGGENGERGE FORTFORFORF GENTSVERFE 2100 PEGGEOGREP GLIKANIEGE SKROUGHERE REVORTERE ERVERTSVERFE SKROUGHERE AVERTSVERFE SKROUGHERE REVORTERE AVERTSVERFE SKROUGHERE SKROUGHERE SKROUGHERE GENTSVERFE SKROUGHERE AVERTSVERFE	70	KGDSGEOGPP	GKEGPIGFPG	ERGLKGDRGD	PGPQGPPGLA	LGERGPPGPS	GLAGEPGKPG	2040
75 GPTAMULIA PROPRIETUR GROUPEPPRA GELAGRAPE GPTAMULIA PROPRIETUR GROUPEPPRA GELAGRAPE GROUPEPRA GELAGRAPE GROUPEPRA GELAGRAPE GROUPEPRA GELAGRAPE GROUPEPPR		IPGLPGRAGG	VGEAGRPGER	GERGEKGERG	EQGRDGPPGL	PGTPGPPGPP	GPKVSVDEPG	2100
75 GPTAMULIA PROPRIETUR GROUPEPPRA GELAGRAPE GPTAMULIA PROPRIETUR GROUPEPPRA GELAGRAPE GROUPEPRA GELAGRAPE GROUPEPRA GELAGRAPE GROUPEPRA GELAGRAPE GROUPEPPR		PGLSGEOGPP	GLKGAKGEPG	SNGDOGPKGD	RGVPGIKGDR	GEPGPRGQDG	NPGLPGERGM	2160
75 GPPGANGLIGH POPOSOLIVOP COSPUENÇOY GETKIRGADE ROGASSICLOB ROSENVIYOSP 2200 CAPPORTOR EROTTAGO AVVOLANGLIGH SERMANDILAD DUMERSKAM DELIGHTERE 2340 CAPPORTOR CAPPORTO		AGPECKPGLO	GPRGPPGPVG	GHGDPGPPGA	PGLAGPAGPQ	GPSGLKGEPG	ETGPPGRGLT	2220
75 CLPGPYORKE DEOPTCARGO ANVOLFORKE ENGAPGIAGO LIVOREGRAND DRELIPERSE 2340 KORAGRADE DODESCORO, ANDRESERVED PROVINCESCO PROPERVOYME LICENTERIA 2460 GYOUPPGOTO PROBEMORPE SCENDIARDP GREATIGHES PROPERVOYME LICENTERIA 2460 GORVULLEUR GREGHESTOR BECHARDES PROVINCESCORO RECERTIOR DESCRIPTOR 2460 GORVULLEUR GREGHESTOR BECHARDES PROVINCESCORO RECERTIOR DESCRIPTOR 2460 GORVULLEUR GREGHESTOR BECHARDES PROVINCESCORO RECERTIOR DESCRIPTOR DESCRIPTOR 2460 GORGED CONTROL PROPERTOR DESCRIPTOR D		GPTGAVGLPG	PPGPSGLVGP	OGSPGLPGOV	GETGKPGAPG	RDGASGKDGD	RGSPGVPGSP	2280
KORAGIAGEP GOPGEROGIC APORGEPROD POTUVOSCE PROPERVICIO LILICIARIA) 2400 GOVERNO RESIDUAÇÃO PROSIDUAÇÃO GERILIFICAÇÃO FROMENSICO LILICIARIA) 2400 GOVERNO RESIDUAÇÃO PROSIDUAÇÃO GERILIFICAÇÃO FROMENSICO LILICIARIA 2400 BONTLAPER PRANACINAS ROPROLUÇÃOS GERILIFICAÇÃO GERILIFICAÇÃO GERILIFICAÇÃO GERILIFICAÇÃO FROMENSICO PROSIDUAÇÃO GERILIFICAÇÃO GERILIFIC	75	GLPGPVGPKG	EPGPTGAPGO	AVVGLPGAKG	EKGAPGGLAG	DLVGEPGAKG	DRGLPGPRGE	2340
GOVERPOQTO PROSMOGORE SCIENCIACOPE GREATEGREA REGISTRATOR PROPERSORE PROSECUTION 2460 GOPPOULDER GREGARGORE REPROLICAÇÃOS REGISTRATOR SERENDIRANO SANCIALEROS 2350 BONTLIPPO PROMEDIOS PROGRAPIOS REGISTRATOR SERENDIRANO SANCIALORIA 2350 GLAPOQUIO AGRICADORE REPROLICAÇÃO GERCUNICOR CONSISTENCIA CONTROLICAÇÃO CON		KGRAGRAGEP	GDPGEDGOKG	APGPKGPKGD	PGVGVPGSPG	PPGPPGVKGD	LGLPGLPGAP	2400
GOPOVOLPUP ROSRGEFOTA GEOGRAPOGEO PROLITOPPOS ROSROSEROW GRANLEGOMO 2520 80 DSAVILLEPPO PROLITORES ROPROLIDODOS (PROMODEOS DAGRACEGOMO 2530) GLIJOPOGOPO ANOTODOSE PORTOGOPOTA GENGOVOPRO PROLITORES WIGAGEORE 1550 GENCTFOTOCO PROPROSEROS ADPROPAÇÃO (PRORIDOS PRORROPROS PROTROCOSE 2750 ANCINCADORES ROPROPAGOS ADPROPAÇÃO (PRORROPROS PORTOGOSE EVICANOSVICO 2750 ANCINCADORES (PROJAROSE GENALIZATION GRAPFOREOS) (PROCAQOPIA SOSPELEPSYA 1220) 85 DESCRITATION REVIENDAS TRACESPORAD CONSINERO PEREZUREZO PROVINGONO 2540 BESCRITATION REVIENDAS TRACESPORAD GONOMINERO FRAZZORECO PROVINGONO 2540		GVVGPPGQTG	PRGEMGOPGP	SGERGLAGPP	GREGIPGPLG	PPGPPGSVGP	PGASGLKGDK	2460
80 DEAVILEPEC PROMOCINE ROPRINLODIK GPROMODOD DIKSKREEDEN KOSAMINTIAN 5550 OLDOPOODO AAACTERIOS PROMOTODIS GEROMOTODIS CHRININGERVI KASALLOZIKK 2670 DIKELAGIPO ROLLAGRIKE MERIOVYOGS GAPKIKELIS PROMOTODIS CIPELICICKIK 2700 DIKELAGIPO ROLLAGRIKE MERIOVYOGS GAPKIKELIS PROMOTODIS CIPELICICKIK 2700 ANTICKINGERO PROMOTODIS CIPELICICKIK 2700 ANTICKINGERO PROMOTODIS GAPKIKELIS CHRININGEROS CHRININGERO PROMOTODIS CONTINENT CHRININGER PROMOTODIS CONTINENT CHRININGER PROMOTODIS CONTINENT CHRININGER PROMOTODIS TRACIENTORY GOVERNOR DISCONNINES TRACERPOR PROMOTOGORY 2880 BESCHATTLE RITHERATIOS TRACEIPPORT GOVERNOR PREADERCH PROMOTOGORY 2880		GDPGVGLPGP	RGERGEPGIR	GEDGRPGCEG	PRGLTGPPGS	RGERGEKGDV	GSAGLKGDKG	
SU GLIJPĢOQPO AAOTPODOSE PRINCOVPOTA GEKODVOPAM PRILIVORISVY KAACIJOJOKE 2640 GKRENDEGOP REGLARISKO MEDEPVOPOS GAPKKRIGITO PRIRIZORDEM 2700 GEROTROJOS PROPERSONOS AOPPOPPOSY GPROPESIÇO OKURROPPOS RVVAASVYNC. 2760 ANDERGOPRO PROJAGROKE GRAALITEOU REVFORENSY GARCAGOPTA SASPLEPSYN. 2820 ANTAROSQUIAN VYVLAVUBIAS ERSKYPPEND EYSKYSKYS ERKODPRAM DEDDPCSLIP. 2880 DEGSCTATATI RHYTHRANING TRACHEPPYNG GOXOMANER TRACHEZORDEV PRIVOSQORTO 2940		DSAVILGPPG	PRGAKGDMGE	RGPRGLDGDK	GPRGDNGDPG	DKGSKGEPGD	KGSAGLPGLR	2580
GENOTICIO: PROPENDAS AMPROPACIS (PROPENDA ONGEROPPES RIVIANAVIPO: 2750 APCERGEGOR REPROPECES GENALITEDED ROFFUNGASO (ACCOQUITA SUSPELPÈRA 2820 ADTAGSQUIAN VPULNUSIANE EBENVPPEDD EYSEVESTEV ESTOPPEARM DESDOCSILI. 2880 DESSCRITATI RHYMANYOS TRACEPPEND GOOGNANRES TERALESENCE PROVESCOTO	80	GLLGPQGQPG	AAGIPGDPGS	PGKDGVPGIR	GEKGDVGFMG	PRGLKGERGV	KGACGLDGEK	2640
GENOTICIO: PROPENDAS AMPROPACIS (PROPENDA ONGEROPPES RIVIANAVIPO: 2750 APCERGEGOR REPROPECES GENALITEDED ROFFUNGASO (ACCOQUITA SUSPELPÈRA 2820 ADTAGSQUIAN VPULNUSIANE EBENVPPEDD EYSEVESTEV ESTOPPEARM DESDOCSILI. 2880 DESSCRITATI RHYMANYOS TRACEPPEND GOOGNANRES TERALESENCE PROVESCOTO		GDKGEAGPPG	RPGLAGHKGE	MGEPGVPGOS	GAPGKEGLIG	PKGDRGFDGQ	PGPKGDQGEK	
APCERCEGOR PORACPROEK GRALITEDI ROFVRORMOG HCACQOQFIA SOSRPLPSYA 2820 ADTAGOQLIA VPVLRVGHAE EERRVPPEDD EYSEYSEYSV EEYQDPEARW DSDDPCSLPL 2880 DEGISCTATIL RWYHRAVTGS TEACHPFVVG GCGMANRRG TREACERRCP PRVVQSQGTG 2940		GERGTPGIGG	PPGPSGNDGS	AGPPGPPGSV	GPRGPEGLQG	OKCEROPPCE	RVVGAPGVPG	2760
ADTAGSQLHA VPVLRVSHAE EBERVPPEDD EYSEYSEYSV EBYQDPEAPW DSDDPCSLPL 2880 DEGSCTAYTL RWYHRAVTGS TEACHPFVYG GCGGNANRFG TREACERRCP PRVVQSQGTG 2940		APGERGEOGR	PGPAGPRGEK	GEAALTEDDI	RGFVRQEMSQ	HCACQGQFIA	SGSRPLPSYA	2820
85 DEGSCTAYTL RWYHRAVTGS TEACHPFVYG GCGGNANRFG TREACERRCP PRVVQSQGTG 2940		ADTAGSOLHA	VPVLRVSHAE	EEERVPPEDD	EYSEYSEYSV	EBYQDPEAPW	DSDDPCSLPL	2880
	85	DEGSCTAYTL	RWYHRAVTGS	TEACHPFVYG	GCGGNANRFG	TREACERRCP	PRVVQSQGTG	2940
		TAQD						

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Seq ID NO: 64 DNA sequence Nucleic Acid Accession #: NM_006945 Coding sequence: 1-219

5	1	11	21	31	41	51	
10	CCAAAGTGCC	CAGAGCCATG	GTGCAAGCAG TCCACCCCG TCAGCAGTGC TCCACCGAAG	AAGTGCCCTG CAGCAGAAAT	AGCCCTGCCC	ACCACCAAAG	60 120 180

Seq ID NO: 65 Protein sequence: Protein Accession #: NP_008876

- 20 Seq ID NO: 66 DNA sequence
 Nucleic Acid Accession #: NM_005629.1
 Coding sequence: 639-2546

	couring sequ	ience. 039-2					
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25	ī	1	ī	1	1	1	
	TAGTCGGAGC	GAGGTGGCGA	GTCGCTGAGC	CCGCCGCGGC	CCCGAGAGCG	GCTGCAGCCG	60
	CCGCCGCCGG	GAAGGAGAGG	GCGAGGCGCG	CCCGAGCCGC	ccccccccc	GCCACCGCCG	120
	CCGCCGCCAC	CACCGCCACC	GGAGTCGCGG	GCCAGCCGGG	CACCCTCCCC	GGGCCCCGGC	180
	CGGGGCGGGG	GGCGCGGGCC	ACAGGCCCCT	GCTCCGGCCG	TOGTTTGCAG	ACCGCGGGGCG	240
30	CCGATGTCGC	CCGCGCCCCG	TTAGGATGAG	TCTCGGGTCG	GGCGAGGAGC	CGCCGCAGCC	300
	GCCGCCGCCC	GAGCCGCGGG	CAGGAGCCTC	GGGAGCCGCC	GCCGCCGCCG	ccccccccc	360 420
	GCCGGGCCCC	GACGCCGCCC	GCGCGCCCC	GGGCCCCCGA	CACACATGAG	ATTUTUMGG	480
	CTCACTTTCA	AGTGCTTCGT	GGACTGCTTC	TUACTUCGCC	GCCCGCGCCC	COCACCCCCC	540
35	CGTCCGCCCG	CCGCCCCGTC	CCGCCGGTGC	OCCUPANT OF THE PROPERTY OF TH	*COCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCCTCAGCC	600
33	CCTCGGGGCC	CICCCCGGTG	GIGCGGCCCG	CCCCCCCCTG	GCCGCCGCCC	AGCCCCCAGA	660
	A COCCAMONA	TRACCITCTCC	CCCCACCAGA	AGAAGGGCCC	CCTCATCGCG	CCCGGGCCCG	720
	*COCCALCIA	GGCCAAGGGC	GACGGCCCCG	TGGGCCTGGG	GACACCCGGC	GGCCGCCTGG	780
	CCGTGCCGCC	GOGGGAGACC	TGGACGCGCC	AGATGGACTT	CATCATGTCG	TGCGTGGGCT	840
40	TOTOTTOGG	CTTGGGCAAC	GTGTGGCGCT	TCCCCTACCT	GTGCTACAAG	AACGGCGGAG	900
	GUYZUYZUTUCUT	TATTCCCTAC	GTCCTGATCG	CCCTGGTTGG	AGGAATCCCC	ATTTTCTTCT	960
	TAGAGATOTO	GCTGGGCCAG	TTCATGAAGG	CCGGCAGCAT	CAATGTCTGG	AACATCTGTC	1020
	CCCTGTTCAA	AGGCCTGGGC	TACGCCTCCA	TGGTGATCGT	CTTCTACTGC	AACACCTACT	1080
	ACATCATGGT	GCTGGCCTGG	GGCTTCTATT	ACCTGGTCAA	GTCCTTTACC	ACCACGCTGC	1140
45	CCTGGGCCAC	ATGTGGCCAC	ACCTGGAACA	CTCCCGACTG	CGTGGAGATC	TTCCGCCATG	1200
	AAGACTGTGC	CAATGCCAGC	CTGGCCAACC	TCACCTGTGA	CCAGCTTGCT	GACCGCCGGT	1260
	CCCCTGTCAT	CGAGTTCTGG	GAGAACAAAG	TCTTGAGGCT	GTCTGGGGGA	CTGGAGGTGC	1320
	CAGGGGCCCT	CAACTGGGAG	GTGACCCTTT	GTCTGCTGGC	CTGCTGGGTG	CIGGICIACI	1380
	TCTGTGTCTG	GAAGGGGGTC	AAATCCACGG	GAAAGATCGT	GTACTTCACT	GCTACATTCC	1440 1500
50	CCTACGTGGT	CCTGGTCGTG	CTGCTGGTGC	GTGGAGTGCT	GCTGCCTGGC	GCCCTGGATG	1560
	GCATCATTTA	CTATCTCAAG	CCTGACTGGT	CAAAGCTGGG	GICCCCTCAG	ACAGCCCTGG	1620
	ATGCGGGGAC	CCAGATTTTC	AACAACTGCT	*CATIGGCCI	CATCATCCTC	COTCTCATCA	1680
	GCAGCTACAA	CLUCTICALIC	GCTGGCTTCG	TOTAL	CATCCTGGGC	TTCATGGCTG	1740
55	ACAGTOGGAC	CAGCITCITI	TCCAAGGTGG	CAGAGTCAGG	COCCOCCTG	GCCTTCATCG	1800
55	CCTACCCCC	GCCTCTCACC	CTGATGCCAG	TGGCCCCACT	CTGGGCTGCC	CTGTTCTTCT	1860
	TCATGCTGTT	CONCETTAGE	CTCGACAGCC	AGTTTGTAGG	TGTGGAGGGC	TTCATCACCG	1920
	CONTONION	CCTCCTCCCC	GCCTCCTACT	ACTTCCGTTT	CCAAAGGGAG	ATCTCTGTGG	1980
	CCCTCTGTTG	TGCCCTCTGC	TTTGTCATCG	ATCTCTCCAT	GGTGACTGAT	GGCGGGATGT	2040
60	ACCITCTTCCA	CCTGTTTGAC	TACTACTCGG	CCAGCGGCAC	CACCCTGCTC	TGGCAGGCCT	2100
	TTTGGGAGTG	CGTGGTGGTG	GCCTGGGTGT	ACGGAGCTGA	CCGCTTCATG	GACGACATTG	2160
	CCTGTATGAT	CGGGTACCGA	CCTTGCCCCT	GGATGAAATG	GTGCTGGTCC	TTCTTCACCC	2220
	CGCTGGTCTG	CATGGGCATC	TTCATCTTCA	ACGTTGTGTA	CTACGAGCCG	CTGGTCTACA	2280
	ACAACACCTA	CGTGTACCCG	TGGTGGGGTG	AGGCCATGGG	CTGGGCCTTC	GCCCTGTCCT	2340
65	CCATGCTGTG	CCTCCCCCTC	CACCTCCTGG	GCTGCCTCCT	CAGGGCCAAG	GGCACCATGG	2460
	CTGAGCGCTG	GCAGCACCTG	ACCCAGCCCA	TCTGGGGCCT	CCACCACTIG	GAGTACCGAG	2520
	CTCAGGACGC	AGATGTCAGG	GGCCTGACCA	ECCTGACCCC	TCACCACCAC	AGCAGCAAGG ACCTCTGGTA	2580
	TCGTCGTGGI	GGAGAGTGTC	ATGTGACAAC	OT COCCOCCOCC	accentrac	CTTTCCCTGA	2640
70	GCCATAGCAG	CCCCTGCTTC	COCACCO	CACCCCCCCC	CATCACTCC	CACTAAAACA	2700
70	CACTTTTGGG	GICIGCCIOG	BACCCCA BAA	ATATCACAAC	CCACCAAAAA	TAGATGCCTC	2760
	TOTOGETOCE	CCCTACCC	AGCTGGTCCT	AGGCCCCCGCC	TAGTGCCCCA	CCCCCACCCA	2820
	CAGTGCTGCA	CTCCTCCTGC	CCCTGCCACG	CCCACCCCCT	GCCCACCTCT	CCAGGCTCTG	2880
	CTCTGCAGCE	CACCCGTGGG	TGACCCCTCA	CCCCAGAAGC	AGCAGTGGCA	GCTTGGGAAA	2940
75	TGTGAGGAAG	GGAAGGAGGG	AGAGACGGGA	GGGAGGAGAG	AGAGGAGAAG	GGAGGCAGGG	3000
	GAGGGGCAGG	AGAACCAAGG	CAAATATTTC	AGCTGGGCTA	TACCCCTCTC	CCCATCCCTG	3060
	TTATAGAAGG	TTAGAGAGCC	AGCCAGCAAT	GGAACCTTCI	GGTTCCTGCG	CCAATCGCCA	3120
	CCAGTATCA	TTGTGTGAGG	TTGGGTGOG	. GTGCACGCG1	GCGTGAGTAC	GGAGAGTATA	3180
	TATAGATCTO	TATCTTAC	CARAGGTGA	TGCCAGATGT	* AAATGGCGCC	TCTGGGCAAA	3240
80	GGAGGCTTGT	ATTTTGCACE	TTTTATAAAA	ACTTGAGAGA	ATGAGATTTC	TGCTTGTATA	3300
	TTTCTAAAA	CAGGAAGGAC	CCCAAACCA7	CCTCTCCTTA	CCACTCCCAT	CCCTGTGAGC	3360
	CCTACCTTAC	CCCTCTGCCC	CTAGCCAAGG	AGTGTGAATT	TATAGATCTA	ACTITCATAG	3420
	GCAAAACAAJ	AGCTTCGAGG	TGTTGCGTGT	GTGAGTCTGT	TGTGTGGATG	TGCGTGTGTG	3480
85	GTCCCCAGC	CCAGACTGG	TTGGAAAAG	GCATGGTGG	ATAMES CONTROL	CTGTCCCCAC	3540 3600
83	GCTGTCCCT	TGCCACAAG	CTGTGGGGC	MUNGGCTGC	COCCOCAC	CTGGGTGTCT CCCAGGAAGG	3660
	GGGCTGCTA	CCIGGCCTG	TCAGGCTTCC	. CALCUTTOTO	CONCERCO	CACCTCCAGT	3720
	GACCUTGGA	- ACGGCTCCC	COTCLAGGC		·		3.20

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CTTCTGTGTA	GCAGCTTTAA	CCCACGTTTG	TCTGTCACGT	CCAGTCCCGA	GACGGCTGAG	3780
TGACCCCAAG	AAAGGCTTCC	CCGACACCCA	GACAGAGGCT	GCAGGGCTGG	GGCTGGGTGA	3840
GGGTGGCGGG	CCTGCGGGGA	CATTCTACTG	TGCTAAAAAG	CCACTGCAGA	CATAGCAATA	3900
AAAACATGTC	ATTTTCC					

5 AAAACATGTC ATTTTCC

Seq ID NO: 67 Protein sequence: Protein Accession #: NP_005620.1

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		GLGNVWRFPY					120
	INVWNICPLF	KGLGYASMVI	VFYCNTYYIM	VLAWGPYYLV	KSFTTTLPWA	TCGHTWNTPD	180
	CVRIFRHEDC	ANASLANLTC	DOLADRRSPV	IEFWENKVLR	LSGGLEVPGA	LNWEVILCLL	240
15	ACWVLVYFCV	WKGVKSTGKI	VYFTATFPYV	VLVVLLVRGV	LLPGALDGII	YYLKPDWSKL	300
	GSPOVWIDAG	TOIFFSYAIG	LGALTALGSY	NRFNNNCYKD	AIILALINSG	TSFFAGFVVF	360
	SILGEMAARO	GVHISKVABS	GPGLAFIAYP	RAVTLMPVAP	LWAALFFFML	LLLGLDSQFV	420
	GVEGFITGLL	DLLPASYYFR	FOREISVALC	CALCEVIDLS	MVTDGGMYVF	QLPDYYSASG	480
	TTLLWOAPWE	CVVVAWVYGA	DRFMDDIACM	IGYRPCPWMK	WCWSPFTPLV	CMGIFIFNVV	540
20	YYEPLVYNNT	YVYPWWGEAM	GWAPALSSML	CVPLHLLGCL	LRAKOTMAER	WOHLTOPING	600
	LHHILEYRAGO	ADVRGUTTLT	PVSESSKVVV	VESVM			

25 Seq ID NO: 68 DNA sequence
Nucleic Acid Accession #: NM_021953.1
Coding sequence: 178-2469

	Coding sequ	lence: 178-2	469				
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	CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAAACGCAG	ATTCATAATG	180
	AAAGCTAGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCCT	TCCTGTTCAA	240
	AATGCCCCAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCCTGCCCA	ACAGGAGTCT	300
35	AATCAAGCAG	AGGCCTCCAA	GGAAGTGGCG	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATTA	TTAACCACCC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAAT	420
	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAAGAGAG	TGGCAGTAGT	480
		AATTCATCCT					540
4.0		CCCARACCAG					600
40		CTGCAGCTAG					660
	CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CARTAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
		AGGAAAAGGA					840
	CCTTCGAGAC	CATCAGCGTC	CTGGCAGAAC	TCTGTGTCTG	AGCGGCCACC	CTACTCTTAC	900
45	ATGGCCATGA	TACAATTCGC	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAAGAC	960
	ATCTATACGT	GGATTGAGGA	CCACTTTCCC	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
		TCCGCCACAA					1080
	AATGGCAAGG	TCTCCTTCTG	GACCATTCAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
	CAGGTGTTTA	AGCCACTGGA	CCCAGGGTCT	CCACAATTGC	CCGAGCACTT	GGAATCACAG	1200
50	CAGAAACGAC	CGAATCCAGA	GCTCCGCCGG	AACATGACCA	TCAAAACCGA	ACTCCCCCTG	1260
	GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
	CAGTTCCCGG	TGAACCAGTC	ACTGGTGTTG	CAGCCCTCGG	TGAAGGTGCC	ATTGCCCCTG	1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCCC	1440
	AAGGTGCTGC	TAGCTGAGGA	GGGGATAGCT	CCTCTTTCTT	CTGCAGGACC	AGGGAAAGAG	1500
55	GAGAAACTCC	TGTTTGGAGA	AGGGTTTTCT	CCTTTGCTTC	CAGTTCAGAC	TATCAAGGAG	1560
	GAAGAAATCC	AGCCTGGGGA	GGAAATGCCA	CACTTAGCGA	GACCCATCAA	AGTGGAGAGC	1620
	CCTCCCTTGG	AAGAGTGGCC	CTCCCCGGCC	CCATCTTTCA	AAGAGGAATC	ATCTCACTCC	1680
	TGGGAGGATT	CGTCCCAATC	TCCCACCCCA	AGACCCAAGA	AGTCCTACAG	TGGGCTTAGG	1740
60		GGTGTGTCTC					1860
60	AGCCGGTCTC	GGAGGAAACA	GCATCTACTG	CCTCCCTGTG	TGGATGAGCC	GGAGCIGCIC	
	TTCTCAGAGG	GGCCCAGTA C	TTCCCGCTGG	GCCGCAGAGC	TCCCGTTCCC	AGCAGACTCC	1920
	TCTGACCCTG	CCTCCCAGCT	CAGCTACTCC	CAGGAAGTGG	GAGGACCTTT	TAAGACACCC	1980
	ATTAAGGAAA	CGCTGCCCAT	CTCCTCCACC	CCGAGCAAAT	CrGrccrccc	CAGAACCCCT	2040
CE	GAATCCTGGA	GGCTCACGCC	CCCAGCCAAA	GTAGGGGGAC	TGGATTTCAG	CCCAGTACAA	2100
65		GTGCCTCTGA					2160
	ACTCCCTTGC	AAAGTGCTCC	CCCCCTTGAA	TCACCGCAAA	GGCTCCTCAG	TTCAGAACCC	2220 2280
	TTAGACCTCA	TCTCCGTCCC	CTTTGGCAAC	TCTTCTCCCT	CAGATATAGA	CGTCCCCAAG	
	CCAGGCTCCC	CGGAGCCACA	GGTTTCTGGC	CTTGCAGCCA	ATOGTTCTCT	GACAGAAGGC	2340
70	CIGGICCIGG	ACACAATGAA	TGACAGCCTC	AGCAAGATCC	TGCTGGACAT	CAGCTTTCCT	2400
70	GGCCTGGACG	AGGACCCACT	GGGCCCTGAC	AACATCAACT	GGTCCCAGTT	TATTCCTGAG	2460
	CTACAGTAGA	GCCCTGCCCT	TGCCCCTGTG	CTCAAGCTGT	CCACCATCCC	GGGCACTCCA	2520
	AGGCTCAGTG	CACCCCAAGC	CTCTGAGTGA	GGACAGCAGG	CAGGGACTGT	Tergereere	2580
	ATAGCTCCCT	GCTGCCTGAT	TATGCAAAAG	TAGCAGTCAC	ACCCTAGCCA	CTGCTGGGAC	2640
75	CTTGTGTTCC	CCAAGAGTAT	CTGATTCCTC	TGCTGTCCCT	GCCAGGAGCT	GAAGGGTGGG	2700 2760
13	AACAACAAAG	GCAATGGTGA	AAAGAGATTA	GGAACCCCCC	AGCCTGTTTC	CATTCTCTGC	2820
	CCAGCAGTCT	CTTACCTTCC	CIGATCIFIG	CAGGGTGGTC	CGTGTAAATA	GTATAAATTC	2880
	TCCAAATTAT	CCTCTAATTA	TAAATGTAAG	CTTATTTCCT	TAGATCATTA	TCCAGAGACT	2940
	GCCAGAAGGT	GGGTAGGATG	ACCTGGGGTT	TCAATTGACT	CONGRECATION	GCTTTTAGTT	
80	TIGATAGAAG	GGAAGACCTG	CAGIGCACGG	TITUITCUAG	CCLGAGGTAC	CIGGATCTIG	3000 3060
οu	GUTTCTTCAC	TCCCCGTGTT	CAGACAAGTG	GATCIGCITG	CAUAGTCCT	ATTIGUCUCT	3120
	CCCTGCCACC	TCCCCGTGTT	TCCAAGTCAG	CITICCIGCA	AGARGRAATC	CIGGITAAAA	3120
	AAGTCTTTTG	TATTGGGTCA	GGAGTTGAAT	1100001000	MOUNTOGATO	CARCIGRAGO	3240
	AGAGTGTGGG	TGCCCAGATG	TGCGCTATTA	GATGITTCTC	CRAINATGTC	PARCOCCOCC	3300
85	CCAGGGAGAC	TGGCATTGAC GGCTTCCTTA	GAGAACTCAG	CLOCKECT	A B C B C C C C C C C	AMMOGGCCCC	3360
ره	TUACCIGCCT	GGCTTCCTTA	GCTTGCCCCT	CAGCITIGCA	ANUAUCUACC	AGCGAAGGTG	
				MUNCINACT	MATCHATAAA	ADCUMBUTU	3420
	GACCINAAAAA	АААААААА	MANA				

WO 02/086443 PCT/US02/12476

Seq ID NO: 69 Protein sequence: Protein Accession #: NP_068772.1

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	MKASPRRPLI	LKRRRLPLPV	ONAPSETSEE	EPKRSPAQOE	SNOABASKEV	ABSNSCKFPA	60		
	GIKIINHPTM	PNTQVVAIPN	NANIHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTQPPG	120		
	LRPOTOTSYD	AKRTEVTLET	LGPKPAARDV	NLPRPPGALC	EOKRETCADG	EAAGCTINNS	180		
10	LSNIOWLREM	SSDGLGSRSI	KOEMEEKENC	HLEQRQVKVE	EPSRPSASWQ	NSVSERPPYS	240		
	YMAMIOFAIN	STERKRMTLK	DIYTWIEDHP	PYFKHIAKPG	WKNSIRHNLS	LHDMFVRETS	300		
		HPSANRYLTL					360		
	LGARRKMKPL	LPRVSSYLVP	IOPPVNQSLV	LOPSVKVPLP	LAASLMSSEL	ARHSKRVRIA	420		
	PKVLLAEEGI	APLSSAGPGK	EEKLLFGEGF	SPLLPVOTIK	REBLODGEEN	PHLARPIKVE	480		
15	SPPLEEWPSP	APSFKEESSH	SWEDSSOSPT	PRPKKSYSGL	RSPTRCVSEM	LVIQHRERRE	540		
	RSRSRRKOHL	LPPCVDEPEL	LPSEGPSTSR	WAAELPFPAD	SSDPASQLSY	SQEVGGPFKT	600		
		TPSKSVLPRT					660		
	TTPLOSAPPL	ESPORLLSSE	PLDLISVPFG	NSSPSDIDVP	KPGSPEPQVS	GLAANRSLTE	720		
	GLYLDTMNDS	LSKILLDISF	PGLDEDPLGP	DNINWSOFIP	BLO				
20									
	Sea In NO.	70 DNA seco	nence						
	Nucleic Acid Accession #: BC006529.1								

	are to vo. 20 pm. company									
	Seq ID NO: 70 DNA sequence Nucleic Acid Accession #: BC006529.1									
	Nucleic Acid Accession #: BC006529.1 Coding sequence: 178-2424									
25	coarng sequ	lence: 1/6-2	424							
23		11	21	31	41	51				
	t	†*	î	11	i	ĩ-				
	GGCACGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCCCT	COGGGGGCCCT	GGCTCGGCCC	60			
	CCAGGTTGGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120			
30	CAGTOTTOGAG	GGTCCACACT	TOTALTACTO	TOADADATAA	GAAAACCCAG	ATTCATAATG	180			
50		CCCGTCGGCC					240			
		GTGAAACATC					300			
	AATCAAGCAG	AGGCCTCCAA	GGAAGTGGCA	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360			
	ATCAAGATTA	TTAACCACCC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAAT	420			
35	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAAGAGAG	TGGCAGTAGT	480			
	GGGCCCAACA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540			
	CGGCCTCAAA	CCCAAACCAG	CTATGATGCC	AAAAGGACAG	AAGTGACCCT	GGAGACCTTG	600			
	GGACCAAAAC	CTGCAGCTAG	GGATGTGAAT	CTTCCTAGAC	CACCTGGAGC	CCTTTGCGAG	660			
40	CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCTA	720			
40	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780			
	CAAGAGATGG	AGGAAAAGGA	GAATTGTCAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840			
	CCTTCGAGAC	CATCAGCGTC	CTGGCAGAAC	TCTGTGTCTG	AGCGGCCACC	CTACTCTTAC	900			
	ATGGCCATGA	TACAATTCGC	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAAGAC	960			
40	ATCTATACGT	GGATTGAGGA	CCACTTTCCC	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020			
45	AAGAACTCCA	TCCGCCACAA	CCTTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGICIGCC	1080			
	AATGGCAAGG	TCTCCTTCTG	GACCATTCAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140			
	CAGGTGTTTA	AGCAGCAGAA	ACGACCGAAT	CCAGAGCTCC	GCCGGAACAT	GACCATCAAA	1200			
	ACCGAACTCC	CCCTGGGCGC	ACGGCGGAAG	ATGAAGCCAC	TGCTACCACG	GGTCAGCTCA	1260			
50	TACCTGGTAC	CTATCCAGTT	CCCGGTGAAC	CAGTCACTGG	TGTTGCAGCC	CTCGGTGAAG	1320			
50	GTGCCATTGC	CCCTGGCGGC	TTCCCTCATG	AGCTCAGAGC	TIGCCCGCCA	TAGCAAGCGA	1380			
	GTCCGCATTG	CCCCCAAGGT	GCTGCTAGCT	GAGGAGGGGA	TAGCTCCTCT	TTCTTCTGCA	1440			
	GGACCAGGGA	AAGAGGAGAA	ACTCCTGTTT	GGAGAAGGGT	TTTCTCCTTT	GCTTCCAGTT	1500			
	CAGACTATCA	AGGAGGAAGA	AATCCAGCCT	GGGGAGGAAA	TGCCACACTT	AGCGAGACCC	1560 1620			
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"		ACTCCTGGGA					1740			
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	GAGAGGAGGG	TGCTCTTCTC	GTCTCGGAGG	ADMICAGEATE	COTTOCCTCC	AGAGGTGGGAT	1860			
		ACTCCTCTGA					1920			
60	COMMENT	CACCCATTAA	CCCIGCCICC	CCCATCTCCT	CCACCCCCAG	CAAATCTGTC	1980			
00	CCTTTTAAGA	CCCCTGAATC	COMMICCICIO	POCCOCCOCA	CCARCCCCONG	CCCACTCCAT	2040			
	CICCCCAGAA	TACAAACCCC	CIGGREGACIC	TOTALOCCE	TECCTGACCC	CCTGGGGGCTG	2100			
	PACCIA POTOTA	GCACCACTCC	CTTGCAAAGT	actrococci	TTGAATCACC	GCAAAGGCTC	2160			
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65	ATAGACGTCC	CCAAGCCAGG	CTCCCCGGAG	CCACAGGTTT	CTGGCCTTGC	AGCCAATCGT	2280			
		AAGGCCTGGT					2340			
		TTCCTGGCCT					2400			
	CAGTTTATTC	CTGAGCTACA	GTAGAGCCCT	GCCCTTGCCC	CTGTGCTCAA	GCTGTCCACC	2460			
	ATCCCCGGGCA	CTCCAAGGCT	CAGTGCACCC	CAAGCCTCTG	AGTGAGGACA	GCAGGCAGGG	2520			
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	AGCCACTGCT	GGGACCTTGT	GTTCCCCAAG	AGTATCTGAT	TCCTCTGCTG	TCCCTGCCAG	2640			
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	TCCTTGCTTT	TAGTTTTGAT	AGAAGGGAAG	ACCTGCAGTG	CACGGTTTCT	TCCAGGCTGA	2940			
	GGTACCTGGA	TCTTGGGTTC	TTCACTGCAG	GGACCCAGAC	AAGTGGATCT	GCTTGCCAGA	3000			
	GTCCTTTTTG	CCCCTCCCTG	CCACCTCCCC	GTGTTTCCAA	GTCAGCTTTC	CTGCAAGAAG	3060			
	AAATCCTGGT	TAAAAAAGTC	TTTTGTATTG	GGTCAGGAGT	TGAATTTGGG	GTGGGAGGAT	3120			
80	GGATGCAACT	GAAGCAGAGT	GTGGGTGCCC	AGATGTGCGC	TATTAGATGT	TTCTCTGATA	3180			
	ATGTCCCCAA	TCATACCAGG	GAGACTGGCA	TTGACGAGAA	CTCAGGTGGA	GGCTTGAGAA	3240			
	GGCCGAAAGG	GCCCCTGACC	TGCCTGGCTT	CCTTAGCTTG	CCCCTCAGCT	TTGCAAAGAG	3300			
		CCCCAGCTGA			TTGAGAACAC	TAACTACTCA	3360			
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85										

Seq ID NO: 71 Protein sequence: Protein Accession #: AAH06529.1

85

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_	MKTSPRRPLI	LKRRRLPLPV	ONAPSETSEE	EPKRSPAQQE	SNQABASKEV	AESNSCKFPA	60
5	GIKIINHPTM	PNTQVVAIPN	NANIHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTQPPG	120
		AKRTEVTLET					180
		SSDGLGSRSI					240
		STERKRMTLK					300
• •		HPSANRYLTL					360
10		NQSLVLQPSV					420
		PGEGFSPLLP					480
		SOSPTPRPKK					540
		PSTSRWAAEL					600
	VLPRTPESWR	LTPPAKVGGL	DESPVQTPQG	ASDPLPDPLG	LMDLSTTPLQ	SAPPLESPOR	660
15		SVPFGNSSPS		EPQVSGLAAN	RSLITEGLVLD	TMNDSLSKIL	720
	LDISFPGLDE	DPLGPDNINW	SQFIPELQ				

20 Seq ID NO: 72 DNA sequence
Nucleic Acid Accession #: U74612.1
Coding sequence: 178-2583

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25	GGCACGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCCT	GGCTCGGCCC	60
	CCAGGTTGGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
	CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAAACGCAG	ATTCATAATG	180
	AAAACTAGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCCT	TCCTGTTCAA '	240
	AATGCCCCAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCCTGCCCA	ACAGGAGTCT	300
30	AATCAAGCAG	AGGCCTCCAA	GGAAGTGGCA	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATTA	TTAACCACCC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAAT	420
	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAAGAGAG	TGGCAGTAGT	480
	GGGCCCAACA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
	CCCCCCAAA	CCCAAACCAG	CTATGATGCC	AAAAGGACAG	AAGTGACCCT	GGAGACCTTG	600
35	GGACCAAAAC	CTGCAGCTAG	CGATGTGAAT	CTTCCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
	CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAAGAGATGG	AGGAAAAGGA	GAATTGTCAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
40		CATCAGCGTC					900
40	ATGGCCATGA	TACAATTCCC	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAAGAC	960
	ATCTATACGT	GGATTGAGGA	CCACTTTCCC	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
		TCCGCCACAA					1080
	AATGGCAAGG	TCTCCTTCTG	GACCATTCAC	CCCAGTGCCA	ACCUCTACTT	GACATTGGAC	1140
	CAGGTGTTTA	AGCCACTGGA	CCCAGGGTCT	CCACAATTGC	CCGAGCACTT	GGAATCACAG	1200
45	CAGAAACGAC	CGAATCCAGA	GCTCCGCCGG	AACATGACCA	TCAAAACCGA	ACTCCCCCTG	1260
	GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
						ATTGCCCCTG	1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCCC	1440
	AAGGTTTTTG	GGGAACAGGT	GGTGTTTGGT	TACATGAGTA	AGTTCTTTAG	TGGCGATCTG	1500
50						TTTATCAGTG	1560
	CTGCTAGCTG	AGGAGGGGAT	AGCTCCTCTT	TCTTCTGCAG	GACCAGGGAA	AGAGGAGAAA	1620
		GAGAAGGGTT					1680
	ATCCAGCCTG	GGGAGGAAAT	GCCACACTTA	GOGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
e e	TTGGAAGAGT	GGCCCTCCCC	GGCCCCATCT	TTCAAAGAGG	AATCATCTCA	CTCCTGGGAG	1800
55						TAGGTCCCCA	1860
						GAGGAGCCGG	
	TCTCGGAGGA	AACAGCATCT	ACTGCCTCCC	TGTGTGGATG	AGCCGGAGCT	GCTCTTCTCA	1980
	GAGGGGCCCA	GTACTTCCCG	CTGGGCCGCA	GAGCTCCCGT	TCCCAGCAGA	CTCCTCTGAC	2040
60	CCTGCCTCCC	AGCTCAGCTA	CTCCCAGGAA	GTGGGAGGAC	CTTTTAAGAC	ACCCATTAAG	2100
00	GAAACGCTGC	CCATCTCCTC	CACCCCGAGC	AAATCTGTCC	TCCCCAGAAC	CCCTGAATCC	2160
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	TTGCAAAGTG	CTCCCCCCCT	TGAATCACCG	CAAAGGCTCC	TCAGTTCAGA	ACCUTTAGAC	2400
65	CTCATCTCCG	TCCCCTTTGG	CAACTCTTCT	CCCTCAGATA	TAGACGICCC	CHIGCCHIGGC	2460
03	TCCCCGGAGC	CACAGGTTTC	TGGCCTTGCA	GCCAATCGTT	CICIGACAGA	AGGCCTGGTC	
	CTGGACACAA	TGAATGACAG	CCTCAGCAAG	ATCCTGCTGG	ACATCAGCTT	TCCTGGCCTG	2520
						TGAGCTACAG	
	TAGAGCCCTG	CCCTTGCCCC	TGTGCTCAAG	CTGTCCACCA	TCCCGGGCAC	TCCAAGGCTC	2640
70	AGTGCACCCC	AAGCCTCTGA	GTGAGGACAG	CAGGCAGGGA	CIGITCIGCT	CCTCATAGCT	2700
70	CCCTGCTGCC	TGATTATGCA	AAAGTAGCAG	TCACACCCCTA	GCCACTGCTG	GGACCTTGTG	2760 2820
						TGGGAACAAC	
						CTGCCCAGCA	
	GTCTCTTACC	TTCCCTGATC	TTTGCAGGGT	GGTCCGTGTA	AATAGTATAA	ATTCTCCAAA	
76	TTATCCTCTA	ATTATAAATG	TAAGCTTATT	TCCTTAGATC	ATTATCCAGA	GACTGCCAGA	3000
75	AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTTCTGTT	CCFTGCTTTT	AGTTTTGATA	3060
	GAAGGGAAGA	CCTGCAGTGC	ACGGTTTCTT	CCAGGCTGAG	GTACCIGGAT	CFIGGGTTCT	3120
	TCACTGCAGG	GACCCAGACA	AGTGGATCTG	CTTGCCAGAG	TCCTTTTTGC	CCCTCCCTGC	3180
	CACCTCCCCG	TGTTTCCAAG	TCAGCTTTCC	TGCAAGAAGA	AATCCTGGTT	AAAAAGTCT	3240
٥0	TTTGTATTGG	GTCAGGAGTT	GAATTTGGGG	TGGGAGGATG	GATGCAACTG	AAGCAGAGTG	
80	TGGGTGCCCA	GATGTGCGCT	ATTAGATGTT	TUTCTGATAA	IGTCCCCAAT	CATACCAGGG	3360
	AGACTGGCAT	TGACGAGAAC	TCAGGTGGAG	GCTTGAGAAG	GCCGAAAGGG	CCCCTGACCT	3420
		CTTAGCTTGC					3480
			TURUAACACT	AACTACTCAA	IMAAAGCGAA	GGTGGACAAA	3540
85	лалалалал	AAAAA					
03							

Seq ID NO: 73 Protein sequence: Protein Accession #: AAC51128.1

	W O 02/	000443					
	1	11	21	31	41	51	
5	 MKTSPRRPLI GIKIINHPTM LRPQTQTSYD LSNIQWLRKM YMAMIOPAIN	PNTQVVAIPN AKRTEVTLET SSDGLGSRSI	NANIHSIITA LGPKPAARDV KOEMREKENC	LTAKGKESGS NLPRPPGALC HLEOROVKVE	SGPNKFILIS EQKRETCADG EPSRPSASWO	CCGAPTOPPG EAAGCTINNS NSVSERPPYS	60 120 180 240 300
10	YMAMIQPAIN ANGKVSPWTI LGARROWKPL PKVPGEQVVP KLLPGEGPSP EDSSOSPTPR	LPRVSSYLVP GYMSKFFSGD LLPVQTIKEB	IQFPVNQSLV LRDFGTPITS EIQPGEEMPR	LQPSVKVPLP LFNF1FLCLS LARP1KVESP	Laaslmssel Vllaeegiap Pleewpspap	ARHSKRVRIA LSSAGPGKEE SFKEESSHSW	360 420 480 540 600
15	SEGPSTSRWA	AELPFPADSS GGLDFSPVQT SPSDIDVPKP	DPASQLSYSQ SQGASDPLPD GSPBPQVSGL	EVGGPFKTPI PLGLMDLSTT	KETLPISSTP PLQSAPPLES	SKSVLPRTPE PQRLLSSEPL	660 720 780
20	Nucleic Aci	74 DNA sequid Accession mence: 111-4	ı#: Eos sec	quence			
	1	11	21	31	41	51	
25	TCATCCTTCT CTCAAGCTGA ATGACAAGAT	AGGCTGAGCC ACTCGTGACG GAGGTCCATA TGAGAAGCCA	CTTCCCAGCT ATAGGCATGA AGCCTGCTGA	CTGGCTTTTT TCGACATGTT CGATGATGAA	GAAAGCAAAG TCACAAATAC GGAGAACTTC	ATGAGCAACA ACCAGACGTG CCCAACTTCC	60 120 180 240
30	TTAGTGCCTG AGAATGAGGA CAGACTACCA	TGACAAAAG TAAGAAGATT CAAGCAGAGC TGGGCCTCCA	GGCACAAATT GATTTTCTG CATGGAGCAG	ACCTCGCCGA AGTTTCTGTC CGCCCTGTTC	TGTCTTTGAG CTTGCTGGGA CGGGGGGCAGC	GACATAGCCA CAGTGACCCA	300 360 420
35	Seq ID NO: Protein Acc	75 Protein cession #: 1	Bos sequence				
	1	11	21	31	41	51	
40	MSNTQAERSI KKDKNEDKKI	IGMIDMPHKY DPSEFLSLLG	TRRDDKIEKP DIATDYHKQS	SLLTMMKENF HGAAPCSGGS	PNFLSACDKK Q	GINYLADVFE	60
45	Nucleic Ac	76 DNA sequid Accession	n 🛊: Bos se	quence		-	
	1	11	21	31	41	51	
50	TCATCCTTCT CTCAAGCTGA ATGGCAAGAT	ACTOGTGACA GAGGTCCATA TGAGAAGCCA	CTTCCCAGTT ATAGGCATGA AGCCTGCTGA	CTGGCTTTTT TCGACATGTT CGATGATGAA	GAAAGCAAAG TCACAAATAC GGAGAACTTC TGTCTTTGAG	CACATCTCAC ATGAGCAACA ACCGGACGTG CCCAATTTCC AAAAAGGACA	60 120 180 240 300
55	AGAATGAGGA CAGACTACCA	TAAGAAGATT CAAGCAGAGC GGGGCCTCCA	GATTTTTCTG	AGTTTCTGTC	TGGGGGAAGC	CAGTGATCCA	360 420
60	Seq ID NO: Protein Ac	77 Protein cession #: :	eequence: XP_048124.1	31	41	51	
	MSNTQAERSI KKOKNEDKKI	ī	TGRDGKIERP	SLLTMMKENF	PNFLSACDKK Q	GIHYLATVFE	60
65	Seq ID NO:	78 DNA seq id Accessio	uence	,			
	Coding sec	uence: 253-	#: 2/36/8 2433	••			
70							
	1	11	21 	31 	41	51	
	GGGGTGGTGC	AGGGCAGGGG	TGGTATATCC	TGTCTGACGG	AGGGCGGGCC	TOGCCAGTGC	60
75	CCTCGCACTC CGCTGCACCG CCTCCCGCCA	TATGGCCGTA CACCTCGCCT CCATGAACCA	GGGAGCCGCT CGCCTCTCTG CTCGCCGCTC	GAGAGCGAGA CTCTCCTAGG AAGACCGCCT TCGGACCAAA	AGAGCACGCT CCCCGGCCGC TGGCGTACGA AGATGAAAAC	CTCACGCGGA CCTGCCCGCC GCGCCACCCG ATGCTTCCAG AGGCACGTCT	120 180 240 300 360
80	AATTACAACT	ATGGGACCAC	CAGCAGGAGG	ACCUTCARGO	CCAAGTTCCA	GTCCAAGTCT CTTGGCTGAC GGCAGGGAAT CAACAGGGC	420 480 540 600 660
85	ACCACCGGCG CCCGACCTCT CAGAAGACCA	ACTOTGACCO CCCAGAACCO	CATCTGCTTC ACGGGGCACC CTACAGCTTT	TACAGCACCT TACAGCACCT	TCAAGGCGAG GCACGCTGGG GCAGTGGTCA	CAGCTGTAAC CCGCAGTGAG CAGCAAGGGC GAAGGCCATA GTATATCCCG	720 780 840 900

	CCCATCTCCT	GCAACAAGGA	CCTGTCCTTT	GGCCACTCTA	GGGCCAGCTC	CAAGATCTGC	960
							1020
	CAGGATGAGA	AGTACCAGGC	CATTGGGGCC	INTIACATCC	MUCAINCEIG	CTTCCAGGAT GGACCTCCTC CCTGGTGTTC	1000
_	GAATCTGCCA	AGCAACAGGT	CTATCAGCTG	GGAGGCATCT	GCAAGCTGGT	GGACCTCCTC	1140
5	CCCACCCCA	ACCAGAACGT	CCAGCAGGCC	GCGGCAGGGG	CCCTGCGCAA	CCTGGTGTTC	1200
	20001000001	-01100	CONTRACTOR CONTRACTOR	BCCCBCA AMC	COMMONGO	GGCAGTCAGC	1260
	AGGAGGAGGA	COMONGCI	GGAGACCCCGG	MOOCHGIATIG	GGMICCGCGM	GOCKETCHEC	
	CTCCTGAGGA	GAACCGGGAA	CGCCGAGATC	CAGAAGCAGC	TGACTGGGCT	GCTCTGGAAC	1320
	CTCTCTTCCA	CTGACGAGCT	GAAGGAGGAA	CTCATTGCCG	ACGCCCTGCC	TGTTCTGGCC	1380
	Character	management of the same	CTCTCCCTCC	TOTAL	ATACCARCAT	GTCCCGGGAA	1440
10	GACCGCGTCA	TCATTCCCTT	CICIOGCIOG	100001	TOTAL COM	0100000000	1500
10	GTGGTGGACC	CTGAGGTCTT	CTTCAATGCC	ACAGGCTGCT	TGAGGAACCT	GAGCTCGGCC	1500
	GATGCAGGCC	GCCAGACCAT	COGTAACTAC	TCAGGGCTCA	TTGATTCCCT	CATGGCCTAT	1560
	CONCOUNTS & CON	CTCTTACCCCC	Checcecter	GACCACAAGT	CTICTICGAAAA	CTGCATGTGT	1620
	GTCCAGAACT	GIGINGCOGC	CHRCCRCTOT	UNCONCUNGI	CIGIGGAAAA	CIOCHIGIGI	1600
	GTTCTGCACA	ACCTCTCCTA	CCGCCTGGAC	GCCGAGGTGC	CCACCCGCTA	COGCCAGCTG	1080
	GAGTATAACG	CCCGCAACGC	CTACACCGAG	AAGTCCTCCA	CTGGCTGCTT	CAGCAACAAG	1740
15	ACCORDED ACT	mentennennen	CAACTATGAC	TOCCOCTOC	CTURGURAGA	GACCAACCCC	1800
13	AGCGACAMGA	TONTONICHY	CARCIAIOAC	100000000	0701000101	oomer #GGGG	1860
	AAGGGCAGCG	GCTGUTTGTA	CCATTCAGAT	GCCATCCGCA	CCTACCTGAA	CCTCATGGGC	
	AAGAGCAAGA	AAGATGCTAC	CCTGGAGGCC	TGTGCTGGTG	CCCTGCAGAA	CCTGACAGCC	1920
	NOON NOCCCC	TO A TOTO CONC.	TOCCATGAGC	CACTTCATTC	CCCTCLARGGA	ARAGGGCCTG	1980
	MOCAMOGGGC	IGNIGICONG	TOUCHTONOC		magazaana	OCCUPATION OF THE PROPERTY OF	2040
••	CCACAAATTG	CCCGCCTCCT	GCAATCTGGC	AACTCTGATG	TGGTGCGGTC	CCCACCCTCC	2040
20	CTCCTGAGCA	ACATGTCCCG	CCACCCTCTG	CTGCACAGAG	TGATGGGGAA	CCAGGTGTTC	2100
	CCGGMGGIGM	COMMUNICAL	CACCAGCCAC	70100001177	CONTRACTOR OF	ACTGGCCAAG	2220
	TTGTCCTCGG	CCTGCTACAC	TGTGAGGAAC	CIGATGGCCT	COCHOCCACA	ACTOGCCAAG	2220
	CACTACTTCT	CCAGCAGCAT	GCTCAACAAC	ATCATCAACC	TGTGCCGAAG	CAGTGCCTCA CAAGGAACTG	2280
	COCKACCCC	CACAACCTCC	COCCOMMENT	CHCTCTCACA	TOTOGTCCAG	CAAGGAACTG	2340
25	CCCMIGGCCG	CHUMMUCIUC	CCGGCTTCTC	CIGICIGACA	TO10010010	AGCTGGGGCC AAGTTAGGCT GTTTTCTGTC	2400
25	CAGGGTGTCC	TCAGACAGCA	AGGTTTCGAT	AGGAACATGC	TGGGAACCTT	MICHGGGGCC	2400
	AACAGCCTCA	GGAACTTCAC	CTCCCGATTC	TAAGAAGAGA	CTGTCCAAGC	AAGTTAGGCT	2460
	MCCACCA ACA	TRACE COCK	CTCACAAGCC	CTCACCCCTC	COTTOGATGGG	GTTTTCTGTC	2520
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30	N.CCCNCCTTC	anaranaga	COCHMICTIO	ACTTABAGGG	CCTTATATGT	GATGTCAATA	2700
50							
	TTTCTTCCTC	TGAGAAATGG	TATATATATG	TGTCTANTGT	William	AIGCAIGIGC	2,00
	GCGTGCATGT	CICICICICI	GAGTGTCTTA	AAGCATAACC	ACAAACTGCA	AAAAGCTAGG	2820
	TA ACCULATED	TOTTOCOLCO	CATABGGTGG	TGBARAGGAC	TCTCCTGTGT	TTCTTACTCA	2880
	IMMOUNTLE	1011000001		acmacman ma	********	ARAGCTAGG TTCTTACTCA TGTGTGGTGC GCTTCCTACC TTACAAGGCT TCTGTAGTGTC AGAGGACAGC	2940
~ ~	TAGGCAAGGA	CAACATGTGC	TTTTTGGTGA	GCIGCICAIA	ATTCCTGRAM	Idididdidc	
35	CAGGGCAAGG	GGGCCATCAC	TGCAGTCAGG	CCCTCAGAGG	AGTCCTGCAG	GCTTCCTACC	3000
	ACTOCATORCO	ARCCCTCCAC	GAGTAACTGG	GGCTGGGCCA	GCCTCCCCCC	TTACAAGGCT	3060
	AGIGGICACO		maramam man	OMMOCON CAN	moreovoronon	CHATRACTATC	2120
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40	00000000000	> occupanto	COMO TO COMO CO	CATCACACCA	COCTCACCCT	GCBABGGCCC	3300
40	GGTGCCTTCC	ACCCICITIO	actatatacc	CATCAGAGCA	GGCICHOCCI	AATGATTTT	22.50
	TGCATTCAGA	GGTCTTGTAA	TCTACTTGTT	GCAGGAGAAA	GNAGGIANNA	MIGMITTI	3360
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	max-x mmaaa	NCMCCR CRCC	COLLONDO	CCCCTCCCC	TATACCTATT	CCGGCTTCTA	3480
	TCATALICCC	MOTOGROMO	GOWICHOTO	GOOCIGOCA	THIRDOUTHIA.		2540
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45	ACTYCAATTGA	CCCACTCTTT	GGGTCCCAGG	AGACTTGGAC	GGGGGGAGTT	TGGGTAGACT	3600
		* CMCCCC****	Character COO	CONTROL D	GOTTON CATOT	CAGCCAGGGG	3660
	AUGUANAGGAA	MGIGCCATAL	CHOCOTACCO	GIACCOGCAA	OCIONOMICI		3700
	CCATGCCCCA	CTTCCCCTGA	CCCCAGCTGT	CTTGTCTCCA	CICIGIGAAA	CCCACAGGGG	3 / 20
	ATGTGATAAA	CAGGGCTATT	ACCCCTATCA	GCCACGTCGA	GCCCCCAGAC	TCTGTGCACT	3780
	mananacana	ACCACCACCA	CCCCTCCCCA	CCCCCTTATY	BOARBACCTO	TGTGGACATC CCTTCCAGCT TCTGTGCCCT TCCCAAGTCT	3840
50	CHUNCONGC	MUNICIOUN	GGGCICCCOM		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		3000
30	CCTTGGTGTA	CACTAAGACA	GAGCAGAGCC	CAGCIGCTCCC	AAGCCTTCCT	CCTTCCAGCT	3900
	TCTACCTCCA	TGCTAGCATT	GCTGGTGTTA	GAGAGGAATT	AACITCCIGG	TCTGTGCCCT	3960
	TOTOTACANO	BRITATARGAT	CONCORDO	CTCACCCCTT	CTCAGCCTCC	TCCCAAGTCT	4020
	ICICINGHNO	Minimum	0010010010	ant comment	OCCUPATION TO	CAGGCTGGAA	4000
	TCCTCTTCTG	CACCACCCCC	GAGTCCAAAC	CCACCTCTTG	CCCCMBCHIL	CHOCCIGGAA	4080
	AACACTGATG	TGGACTCAGT	ATGACAACTG	AGATGGGGGA	AGCCAGACAT	GTGAGGACGC	4140
55	TOTAL	CAGGTGTCCC	COCCUTATION	CCAGCTGTGC	TCTCGTGCTG	TGGGTCTGTC	4200
-	IG1CCTCCO.		may an amaga	1000000 CTC	CONCECTOR CO.	TOTOCOTOTO	4260
	ATACCCTCCC	TIGCTICIGI	TCACACTGGG	MUGCCCACIC	CIGGCICACC	GTGAGGACGC TGGGTCTGTC TCTCCCTCTC	1200
	COMPRESENTATION	ATCAGE ACCC	BORGODATTO	TTCTCTTAAA	AAATACCTAT	GGCATACCAA	4380
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	GCATCCCCTC	GCCTCATGTT	CCTCCCACCT	TCAAAGAATG	AAGAGCCCCA	TGGGCCCAGC	4680
	CONTRACTOR OF THE PARTY OF THE	GGBACCAGGC	ACCUTTOCAG	ACCTCAGGGG	CTGAGGCAGA	CTATTAGGGC	4740
65	CCCIGCOGIG		macconsumacc	CHOTTON CCCC	ACCREAGER	ACCCGGGCCT	4800
U.S	AGGGCTGACT	TIGGIGACAC	TUCCCATTCC	CICIOROGCE	. MOCICHOUIC		-800
	CTGACCCAGG	CCTGTCACTT	TGAGAGGGGC	AAAACTGAGA	GGGGCTTTTC	CTAGAGAAAG	4860
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	home candon		GGGGS ANCOC	Chananasco	ACTOCICATOR	TOTOTOTOTO A A	4900
	ATTGGCCTCA	CACTAGCCTA	OGCCAATGCC	CAMMITARGO	WILL	TTAAGTCCAC TGGGGCCAAA	
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70	GTCATTGGG	ACCAGCCAC	TOTGCAGTOG	GGACCACACT	AGCAGCCCTC	ACTCCACACT	5100
, ,	- TONI TOUCK		Chamara 100	- STORES	CONCOPPOS	ATCTGGCTGA	5160
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	- GIONGGAI	000000011	Ca Campano	COCCOCAMA	CTAATCTATE	Maintaintaine	5340
76	AACCTIGIGO	. WGCCAGGCC	CAGTTTCCTT	GIGIGATACA	CIMMIGIATI		2340
75	GGANATAGAG	AAAATCAATA	AATTGCTAGT	GTTTCTTTG	AAAAAAAA	TTTGTAGAGG	
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Seq ID NO: 79 Protein sequence: Protein Accession #: CAA98022.1

80	1	11	21	31	41	51	
	ī	Ĩ.	1	1	1	1	
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	TLSHSNRGSM	YDGLADNYNY	GTTSRSSYYS	REPORCEIGSING	YPIYNGTLKR	EPDNRRFSSY	120
	SOMERWSRHY	PRGSCNTTGA	GSDICFMQKI	KASRSEPDLY	CDPRGTLRKG	TLGSKGQKTT	180
85	ONRYSFYSTC	SGOKATEKCP	VRPPSCASKO	DPVYIPPISC	NKOLSPGESR	ASSKICSEDI	240
	ECSGLTIPKA	VOYLSSODEK	YOAIGAYYIQ	HTCFODESAK	QQVYQLGGIC	KLVDLLRSPN	30
	OVERSOON N N CON	I DATE STEED COMM	WALL DEED DOOR	TOPAUCT.I.PP	TONARTOKOL.	TOLLANDASST	3.6

w	o	02/	08ϵ	44.

		ALPVLADRVI					420
	QTMRNYSGLI	DSLMAYVONC	VAASRCDDKS	VENCMCVLHN	LSYRLDAEVP	TRYROLEYNA	480
		GCPSNKSDKM					540
_	DATLEACAGA	LONLTASKGL	MSSGMSQLIG	LKEKGLPQIA	RLLQSGNSDV	VRSGASLLSN	600
5		MGNQVFPEVT					660
	SSMLNNIINL	CRSSASPKAA	EAARLLLSDM	WSSKELQGVL	ROOGFDRNML	GTLAGANSLR	720
	NFTSRF						

10 Seq ID NO: 80 DNA sequence
Nucleic Acid Accession #: NM_006516.1
Coding sequence: 180-1658

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		CAGTGGGAGT					120
	CGCACGCCCG	TCGCCACCCG	CGTACCCGGC	GCAGCCAGAG	CCACCAGCGC	AGCGCTGCCA	180
	TGGAGCCCAG	CAGCAAGAAG	CTGACGGGTC	GCCTCATGCT	GGCTGTGGGA	GGAGCAGTGC	240
20	TTGGCTCCCT	GCAGTTTGGC	TACAACACTG	GAGTCATCAA	TGCCCCCCAG	AAGGTGATCG	300
	AGGACTTCTA	CAACCAGACA	TOGGTCCACC	GCTATGGGGA	GAGCATCCTG	CCCACCACGC	360
	TCACCACGCT	CTGGTCCCTC	TCAGTGGCCA	TCTTTTCTGT	TGGGGGCATG	ATTGGCTCCT	420
	TCTCTGTGGG	CCTTTTCGTT	AACCGCTTTG	GCCGGCGGAA	TTCAATGCTG	ATGATGAACC	480
	TGCTGGCCTT	CGTGTCCGCC	GTGCTCATGG	GCTTCTCGAA	ACTGGGCAAG	TCCTTTGAGA	540
25		GGGCCGCTTC					600
		GGGTGAAGTG					660
	AGCTGGGCAT	CGTCGTCGGC	ATCCTCATCG	CCCAGGTGTT	CGGCCTGGAC	TCCATCATGG	720
	GCAACAAGGA	CCTGTGGCCC	CTGCTGCTGA	GCATCATCTT	CATCCCGGCC	CTGCTGCAGT	780
	GCATCGTGCT	GCCCTTCTGC	CCCGAGAGTC	CCCGCTTCCT	GCTCATCAAC	CGCAACGAGG	840
30		CAAGAGTGTG					900
		GAAGGAAGAG					960
		CTCCCCCCCCC					1020
		GTCTGGCATC					1080
	COCCCCCCA	GCAGCCTGTG	TATGCCACCA	TTGGCTCCGG	TATCGTCAAC	ACCCCCTTCA	1140
35		GCTGTTTGTG					1200
		GGCGGGTTGT					1260
		GTCCTATCTG					1320
		CCCCATCCCA					1380
	CAGCTGCCAT	TGCCGTTGCA	GGCTTCTCCA	ACTGGACCTC	AAATTTCATT	GTGGGCATGT	1440
40		TGTGGAGCAA					1500
	TOGTTCTGTT	CTTCATCTTC	ACCTACTTCA	AAGTTCCTGA	GACTAAAGGC	CGGACCTTCG	1560
	ATGAGATOGC	TTCCGGCTTC	CGGCAGGGGG	GAGCCAGCCA	AAGTGATAAG	ACACCCGAGG	1620
	AGCTGTTCCA	TCCCCTGGGG	GCTGATTCCC	AAGTGTGAGT	CGCCCCAGAT	CACCAGCCCG	1680
		AGCAGCCCTA					1740
45	AACCTGACAG	ATGTCAGCCG	AGCCGGGCCT	GGGGCTCCTT	TCTCCAGCCA	GCAATGATGT	1800
	CCAGAAGAAT	ATTCAGGACT	TAACGGCTCC	AGGATTTTAA	CAAAAGCAAG	ACTGTTGCTC	1860
	AAATCTATTC	AGACAAGCAA	CAGGTTTTAT	AATTTTTTTA	TTACTGATTT	TGTTATTTTT	1920
	ATATCAGCCT	GAGTCTCCTG	TGCCCACATC	CCAGGCTTCA	CCCTGAATGG	TTCCATGCCT	1980
		ACTAAGCCCT					2040
50	CTGGACCTAT	GTCCTAAGGA	CACACTAATC	GAACTATGAA	CTACAAAGCT	TCTATCCCAG	2100
	GAGGTGGCTA	TGGCCACCCG	TTCTGCTGGC	CTGGATCTCC	CCACTCTAGG	GGTCAGGCTC	2160
		TGCCCCTTCC					2220
	CCTGAGACCA	GTTGGGAGCA	CTGGAGTGCA	GGGAGGAGAG	GGGAAGGGCC	AGTCTGGGCT	2280
	GCCGGGTTCT	AGTCTCCTTT	GCACTGAGGG	CCACACTATT	ACCATGAGAA	GAGGGCCTGT	2340
55	GGGAGCCTGC	AAACTCACTG	CTCAAGAAGA	CATGGAGACT	CCTGCCCTGT	TGTGTATAGA	2400
	TGCAAGATAT	TTATATATAT	TITIGGTIGT	CAATATTAAA	TACAGACACT	AAGTTATAGT	2460
	ATATCTGGAC	AAGCCAACTT	GTAAATACAC	CACCTCACTC	CTGTTACTTA	CCTAAACAGA	2520
		TGGTTTTTAG					2580
	TTTGGATGGG	AGTGAGACAG	AAGTAAGTGG	GGTTGCAACC	ACTGCAACGG	CTTAGACTTC	2640
60	GACTCAGGAT	CCAGTCCCTT	ACACGTACCT	CTCATCAGTG	TCCTCTTGCT	CAAAAATCTG	2700
		GTTACCCAGA					2760
	ATCACATATT	TGATAGTTGG	TGTTCAAAAA	AACACTAGTT	TTGTGCCAGC	CCTGATGCTC	2820
	AGGCTTGAAA	TCGCATTATT	TTGAATGTGA	AGGGAA			

65 Seq ID NO: 81 Protein sequence: Protein Accession #: NP_006507.1

٠.	1	11	21	31	41	51	
70		RLMLAVGGAV					60
		IFSVGGMIGS					120
		VYCGLTTGFV					180
	GNKDLWPLLL	SIIPIPALLQ	CIVLPFCPES	PRFLLINRNE	ENRAKSVLKK	LRGTADVTHD	240
		MMRRKKVTIL					300
75		IGSGIVNTAF					360
		AIPGFVAPPE					420
	CPQYVEQLCG	PYVPIIFTVL	LVLFFIFTYP	KVPETKGRTF	DELASGFROG	GASQSDKTPE	480
	ELPHPLGADS	QV					

Seq ID NO: 82 DNA sequence Nucleic Acid Accession #: BC001291 Coding sequence: 44-541

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	AGATCCAGAG	GACTCCCAGC	GAACGGACGA	GGGTGACAAT	AGAGTGTGGT	GTCATGTTTG	180
	TGAGAGAGAA	AACACTTTCG	AGTGCCAGAA	CCCAAGGAGG	TGCAAATGGA	CAGAGCCATA	240 300
	CTGCGTTATA	GCGGCCGTGA GCAGCGATGG	AAATATTTCC	ACGITTTTTC	ATGGTTGCGA	AGCAGTGCTC TCCTGGAAGA	300 360
5	GCCCATGCCC	TTCTTTTACC	TCAAGTGTTG	TAAAATTCGC	TACTGCAATT		420
	ACCTATCARC	TCATCAGTGT	TCAAAGAATA	TGCTGGGAGC	ATGGGTGAGA	GCTGTGGTGG	480
	GCTGTGGCTG	GCCATCCTCC	TGCTGCTGGC	CTCCATTGCA	GCCGGCCTCA	GCCTGTCTTG	540 600
	AGCCACGGGA	CTGCCACAGA TTAAACTTGT	CTGAGCCTTC	TTACCTCTTG	CTTTCACTTC	CCAGGGTCTT	660
10	CCCATCCCAC	ACTYCCGGATC	AGGTGCAGTT	GCCTCTTAAC	CCTCAAGGGT	TCTTTAACTC	720
	ACATTCAGAG	GAAGTCCAGA	TCTCCTGAGT	AGTGATTTTG	GTGACAAGTT	TTTCTCTTTG	780
	AAATCAAACC	TTGTAACTCA	TTTATTGCTG	ATGGCCACTC	TTTTCCTTGA	CTCCCCTCTG	840 900
	CCTCTGAGGG	CTTCAGTATT	TTCACCTCAC	GCAGGAACAC	TEGGGGGAGTC	TGAATGATTG	960
15	CGCTGAAGAC	ATCCCTGGAG	TGAAGGACTC	CTCAGCATGG	GGGGCAGTGG	GGCACACGTT	1020
	AGGGCTGCCC	CCATTCCAGT	GGTGGAGGCG	CTGTGGATGG	CTGCTTTTCC	TCAACCTTTC	1080
	CTACCAGATT	CCAGGAGGCA ACAGGTGCAC	GAAGATAACT	AATTGTGTTG	AAGAAACTTA	BACATCACCC	1140 1200
	ACCRGCIGGC	AGTAGAGAGC	ATCAGGGTAA	ATGGCGTTCA	TTTCTCTGTT	AAGATGCAGC	1260
20	CATCCATGGG	GAGCTGAGAA	ATCAGACTCA	AAGTTCCACC	AAAAACAAAT	ACAAGGGGAC	1320
	TTCAAAAGTT	CACGAAAAA	AAAAAAAAA	AAAAAAAAA	лалаалааа	AAA	
	Sea ID NO:	83 Protein	sequence:				
	Protein Acc	ession #: /	AH01291				
25			21	31	41	51	
	1	11	21	11	11	1	
	MALLALLLVV	ALPRVWTDAN	LTARQRDPED	SORTDEGDNR	VWCHVCEREN	TFECOMPRRC	60
	KWTEPYCVIA	AVKIPPRPPM	VAKQCSAGCA	AMERPKPEEK	RPLLEEPMPP	FYLKCCKIRY	120
30	CNLEGPPINS	SVFKEYAGSM	GESCGGLWLA	AAIRALLLII	GLSLS		
	Seg ID NO:	84 DNA sequ	uence				
	Nucleic Ac	id Accession	n #: NM_022	893.1			
35	Coding seq	uence: 229-2	2726				
33	1	11	21	31	41	51	
	1	1	1	1	L	1	60
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40	TTTTCTCTGG	AGTCTCCTTC	TTTCTAACCC	GGCTCTCCCG	ATGTGAACCG	AGCCGTCGTC	180
	CGCCCGCCGC	CGCCGCCGCC	GCCGCCGCCG	CCCGCCCCGC	AGCCCACCAT	GTCTCGCCGC	240
	AAGCAAGGCA	AACCCCAGCA ATGATGAACC	CTTAAGCAAA	CGGGAATTCT	CGCCCGAGCC	TCTTGAAGCC	300 360
	CTCCTCACCT	GTGGGCAGTG	CCAGATGAAC	TTCCCATTGG	GGGACATTCT	TATTTTTATC	420
45	GAGCACAAAC	GGRAACAATG	CAATGGCAGC	CTCTGCTTAG	AAAAAGCTGT	GGATAAGCCA	480
	CCTTCCCCCTT	CACCAATCGA	GATGAAAAAA	GCATCCAATC	CCGTGGAGGT	TGGCATCCAG	540
	GTCACGCCAG	AAGATGACGA CAGATAAACT	TTGTTTATCA	ACGTCATCTA	GAAGAATTIG	TTCTGCACAT	600 660
	GGAGCTCTAA	TCCCCACGCC	TGGGATGAGT	GCAGAATATG	CCCCGCAGGG	TATTTGTAAA	720
50	GATGAGCCCA	GCAGCTACAC	ATGTACAACT	TGCAAACAGC	CATTCACCAG	TGCATGGTTT	780
	CTCTTGCAAC	ACGCACAGAA	CACTCATGGA	TTAAGAATCT	ACTTAGAAAG	CGAACACGGA	840 900
	CCACCTCTCC	CCCCGCGGGT ATGGGATTCA	TATTGCAGAC	AATAACCCCT	GTGCAGAATG	AAGAATACCA	960
	GGATCAGTAT	CGAGAGAGGC	TTCCGGCCTG	GCAGAAGGGC	GCTTTCCACC	CACTCCCCCC	1020
55	CTGTTTAGTC	CACCACCGAG	ACATCACTTG	GACCCCCACC	GCATAGAGCG	CCTGGGGGCG	1080
	GAAGAAATGG	CCCTGGCCAC	CCATCACCCG	TTCTCTAGGA	GACTTAGAGA	GCTGGCAGGG	1140
	AACACGTCTA	GCCCACCGCT	GTCCCCAGGC	CGGCCCAGCC	CTATGCAAAG	GTTACTGCAA	1260
	CCATTCCAGC	CAGGTAGCAA	GCCGCCCTTC	CTGGCGACGC	CCCCCCTCCC	TCCTCTGCAA	1320
60	TCOGCCCCTC	TTCAGAGCAA	GCCCCCGGTC	AAGTCCAAGT	CATGCGAGTT	CTGCGGCAAG	1380 1440
	TACAACTCCA	ACCTGTGCGA	CCACGCGTGC	ACCCAGGCCA	GCAAGCTGAA	GCGCCACATG	1500
	AAGACGCACA	TGCACAAATC	GTCCCCCATG	ACGGTCAAGT	CCGACGACGG	TCTCTCCACC	1560
65	GCCAGCTCCC	CGGAACCCGG	CACCAGCGAC	TTGGTGGGCA	GCGCCAGCAG	CGCGCTCAAG	1620 1680
05	CACCACCAAC	CCAAGTTCAA AGGAGGACGA	CGAGGAAGAAC	GACCCCCACC	AGGAAGAGA	GGAGGAGGAG	1740
	CTGACGGAGA	GCGAGAGGGT	GGACTACGGC	TTCGGGCTGA	GCCTGGAGGC	GGCGCGCCAC	1800
	CACGAGAACA	GCTCGCGGGG	CGCCGTCGTG	GGCGTGGGCG	ACGAGAGCCG	CGCCCTGCCC	1860
70	GACGTCATGC	AGGGCATGGT	GCTCAGCTCC	ATGCAGCACT	TCAGCGAGGC	CATTCCACCAG	1920 1980
70	TGCGACGAAG	ACTOGGTGGC	CGGCGAGTCG	GACCGCATAG	ACGATGGCAC	TGTTAATGGC	2040
	COCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCA	GTCGGCCTCG	GGGGGCCTGT	CCAAAAAGCT	GCTGCTGGGC	2100
	AGCCCCAGCT	CGCTGAGCCC	CTTCTCTAAG	CGCATCAAGC	TCGAGAAGGA	GTTCGACCTG	2160
75	CCCCCGGCCA	AGCTCAAAGA	TOCCTTOCTT	AGCTTCGGAG	ACTCCAGACA	CGGCTACGCG	2280
	CCCTCCTCGT	CGGAGCACTC	CTCGGAGAAC	GGGAGCTTGC	GCTTCTCCAC	ACCGCCCGGG	2340
	CACCTCCACC	CACCGATCTC	GGGGGGGCAGC	GGCACGGGAA	GTGGAGGGAG	CACGCCCCAT	2400
	ATTAGTGGTC	CGGGCACGGG	CAGGCCCAGC	TCAAAAGAGG	CTCTCCACAC	GAGAAGCCAC	2460 2520
80	ACCIGICGAAA	GCCTTATAA	ATGCGAGCTG	TGCAACTATG	CCTGTGCCCA	GAGTAGCAAG	2580
	CTCACCAGGC	ACATGAAAAC	GCATGGCCAG	GTGGGGAAGG	ACGTTTACAA	ATGTGAAATT	2640
	TOTALGATOO	CTTTTAGCCT	GTACAGTACC	CTGGAGAAAC	: ACATGAAAA	ATGGCACAGT	2700 2760
	GATCGAGTGT	TGAATAATGA	TATARARACT	CCCTTTCCCC	ATOGCOCTO	AGCCCCACTC	2820
85							2880
	ACGAAGCTAA	GAATATGAGA	GTGCTTGTCA	CCAGCACACO	TGTTTTTTT	CTTTTCTTT	2940 3000
	TICTTTTTTC	TITTTCCTTT	TITITITITI	LCCITTATG	LUCICACCUTT	LONNIGCATE	2000

		/000443					
	ATCTGTATGG	GGCAATACTA	TTGCATTTTA	CGCAAACTTT	GAGCCTTTCT	CTTGTGCAAT	3060
	AATTTACATG	TTGTGTATGT	TTTTTTTTAA	ACTTAGACAG	CATGTATGGT	ATGTTATGGC	3120
	TATTTTAAAT	TGTCCCTAAT	TTTTTTTTAA TCGTTGCTGA	GCAAACATGT	TGCTGTTTCC	AGTTCCGTTC	3180
-							3240
5	CATGTACAGT	TTTATTTTAT	AACGTGAGGA AAAAAAAATC	GGAAAAACAG	TCTTTGGATT	AACCCTCTAT	3300
	AGACAGAATA	GATAGCACTG	AAAAAAAATC	TCTATGAGCT	AAATGTCTGT	CTCTAAAGGG	3360
	TTABATGTAT	CAATTYGGAAA	GGAAGAAAA	AGGCCTTGAA	TTGACAAATT	AACAGAAAAA	3420
	CAGAACAAGT	TTATTCTATC	ATTTGGTTTT CTTGTTATAA CATATAATTC	AAAATATGAG	TGCCTTGGAT	CTATTAAAAC	3480
	CACATCGATG	GTTCTTTCTA	CTTGTTATAA	ACTTGTAGCT	TAATTCAGCA	TTGGGTGAGG	3540
10	TARTARACCT	TAGGAACTAG	CATATAATTC	TATATTOTAT	TTCTCACAAC	AATGGCTACC	3600
	TANANAGATG	ACCCATTATO	TCCTAGTTAA	TCATCATTTT	TOTAL	TAATTTTATA	3660
	BACABACTC	ACCUMITATE	TATABARCCE	ACTITION	TOOTCAGAGC	TTABARARA	3720
	MOGGGGGGGGGG	MCCCCCA	TATAAAAGCT TTTATTTTTT	MCT T T T T T T T T T T T T T T T T T T	A TOTAL A TOTAL	A TOTAL A TOC	3780
	TOGGCIGITI	TOCCCOMMOI	ATTAAATACA	TIMUMCANIO	WIINNITION	MIGIGIAMIG	3840
15	TGCMMMGCC	CIGGAACGCA	ATTAMATACA	CINGIANGGA	GIICAIIIIA	TGAAGATATT	3900
13	TGCTTTAATA	ATGICITIT	AAAAATACTG AATGATAAAC	GCACCAAAAG	AAATAGATCC	AGATCTACTT	3960
	GGTTGTCAAG	TGGACAATCA	AATGATAAAC	TITAAGACCT	TGTATACCAT	ATTGAAAGGA	
	AGAGGCTGAC	AATAAGGTTT	GACAGAGGGG	AACAGAAGAA	AATAATATGA	TTTATTAGCA	4020
	CAACGTGGTA	CTATTTGCCA	TTTAAAACTA TTAAGACTTG	GAACAGGTAT	ATAAGCTAAT	ATTGATACAA	4080
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20	GAGAAAGAAT	TTTAAGAGTA	GCAGTATATA	TGTCTGTGCT	CCCTAAAAGT	TGTACTTCAT	4200
	TTCTTTTCCA	TACACTGTGT	GCTATTTGTG	TTAACATGGA	AGAGGATTCA	TTGTTTTTAT	4260
	TTTTATTTT	TTAATTTTTT	CTTTTTTATT	AAGCTAGCAT	CTGCCCCAGT	TGGTGTTCAA	4320
	ATAGCACTTG	ACTOTGCCTG	GCTATTTGTG CTTTTTTATT TGATATCTGT	ATCTTTTCTC	TAATCAGAGA	TACAGAGGTT	4380
	GAGTATAAAA	TARACCTGCT	CAGATAGGAC	AATTAAGTGC	ACTGTACAAT	TITCCCAGIT	4440
25	TACAGGTCTA	TACTTAAGGG	AAAAGTTGCA	AGAATGCTGA	AAAAAAATTG	AACACAATCT	4500
	CATTGAGGAG	CATTTTTTAA	AAACTAAAAA	AAAAAAAACT	TTGCCAGCCA	TTTACTTGAC	4560
	TATTGAGCTT	ACTTACTTGG	ACGCAACATT	GCAAGCGCTG	TGAATGGAAA	CAGAATACAC	4620
	TTAACATAGA	AATGAATGAT	TECTTTCECT	TCTACAGTGC	AAGGATTTTT	TTGTACAAAA	4680
	CTTTTTTAAA	TATABATCTT	TGCTTTCGCT AAGAAAAATT	TTTTTTTAAAA	AACACTTCAT	TATGTTTAGG	4740
30	GCCGAACTCC	ATTITACOUT	TCCATTGTCT	TOOTOOTOTT	ACANGACTTG	TTATCCATTT	4800
50	DALL DECOME	CINCULATION	TATCCCCTTCC	ATTACACACOC	CTCTTCACCT	TOTTARABARA	4860
	ARABACATAC	DIGGOOGAAA	TATGCCTTGG GGTTTAAGAT	TATATACTAC	TTO SATATAGE	CARAGGGGG	4920
	AAAAACATAC	ATTOGGGAAA	TARABATA CAT	TATATAGIAC	TIMMINIAG	THOTACAC	4980
	ACTUATOTTO	ATTCCTATGC	TAAAATACAT TCTAGTGTTA TCTTAAAAGG	CCCLCCT	TITICIOINI TAMENTO TAME	Chacommons	5040
35	GIATTIGANI	TAAATGTTCA	TCTAGTGTTA	GGCACIAIAG	INTIMIATI	GAAGCIIGIA	5100
33	TTTTTTAACTG	TIGCITGITC	GTATATTTTT	TATCAATGTA	CCTTTTTGG	TAGTGGAAAA	
							5160
	ATTTGTATGC	TTCAAAAAA	AAAAAAAGAG	AGAAACAAAA	AAGTGTGACA	TTACAGATGA	5220
	GAAGCCATAT	AATGGCGGTT	TGGGGGAGCC TTGTTCCTTT	TOCTAGAATO	TCACATGGAT	GGCTGTCATA	5280
40	GGGGTTGTAC	ATATCCTTTT	TTGTTCCTTT	TTCCTGCTGC	CATACTGTAT	GCAGTACTGC	5340
40	AAGCTAATAA	COTTGGTTTG	TTATGTAGTG	TGCTTTTTGT	CCCTTTCCTT	CTATCACCCT	5400
	ACATTCCAGC	ATCTTACCTT	CATATGCAGT CAGTTTTTT	AAAAGAAAGA	AAGAAAAAA	AAGGAAAAA	5460
	AAAAAAAAAC	CARTCTTTC	CAGTTTTTTT	CATTGCCAAA	AACTAAATGG	TGCTTTATAT	5520
	TTAGATTGGA	AAGAATTTCA	TATGCAAAGC	ATATTAAAGA	GAAAGCCCCCC	TTTAGTCAAT	5580
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45	ACTITITIGE ADAGCTGTTT	AAGAATTTCA AAATGGCAAT GTCGTAACTT	TATGCAAAGC GCAGAATATT GAAATTTTAT	ATATTAAAGA TTGTTATTGG CTTTTACTAT	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT	TTTAGTCAAT TCCTGTAATG ATTTATTATT	
45	ACTITITICS AAAGCTGTTT GCTTATGTGC	AAGAATTTCA AAATGGCAAT GTCGTAACTT	TATGCAAAGC GCAGAATATT GAAATTTTAT ACAGAGGCAC	ATATTAAAGA TTGTTATTGG CTTTTACTAT TTAATTTGAT	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTTT	5640 5700
45	ACTITITICS AAAGCTGTTT GCTTATGTGC	AAGAATTTCA AAATGGCAAT GTCGTAACTT	TATGCAAAGC GCAGAATATT GAAATTTTAT ACAGAGGCAC	ATATTAAAGA TTGTTATTGG CTTTTACTAT TTAATTTGAT	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTTT	5640 5700 5760
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	TTAGATTGGA ACTITITIGI AAAGCTGTTT GCTTATGTGC TATTTTTTT TTTCTGGTCT	AAGAATTICA AAATGGCAAT GTCGTAACTT CCTGTTCAAA TTTATTTAGA TTGTTAAGTT	TÄTGCAAAGC GCAGAATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA	ATATTAAAGA TTGTTATTGG CTTTTACTAT TTAATTTGAT TCATTACAAC AACCACTGTC	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT CTGGCTTTTT TGTGTTTTTT	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTTT ATTGTATTTG TGGCAGTTGT	5640 5700 5760 5820 5880
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45 50	TTAGATTGGA ACTITITIGI AAAGCTGTTT GCTTATGTGC TATTTTTTT TTTCTGGTCT	AAGAATTICA AAATGGCAAT GTCGTAACTT CCTGTTCAAA TTTATTTAGA TTGTTAAGTT	TÄTGCAAAGC GCAGAATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA	ATATTAAAGA TTGTTATTGG CTTTTACTAT TTAATTTGAT TCATTACAAC AACCACTGTC	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT CTGGCTTTTT TGTGTTTTTT	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTTT ATTGTATTTG TGGCAGTTGT	5640 5700 5760 5820 5880
	TTAGATTGGA ACTITITITGT AAAGCTGTTT GCTTATTGTGC TATTTTTTTT TTTCTGGTCT CTGCATTAAC A	AAGAATTTCA AAATGGCAAT GTCGTAACTT CCTGTTCAAA TTTATTTAGA TTGTTAAGTT CTGTTCATAC	TATGCAAAGC GCAGAATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA ACCCATTTTG	ATATTAAAGA TTGTTATTGG CTTTTACTAT TTAATTTGAT TCATTACAAC AACCACTGTC	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT CTGGCTTTTT TGTGTTTTTT	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTTT ATTGTATTTG TGGCAGTTGT	5640 5700 5760 5820 5880
	TTAGATTGA ACTITITIGA AAAGCTGTTT GCTTATGTGC TATTTTTTT TTTCTGGTCT CTGCATTAAC A Seq ID NO:	AAGAATTTCA AAATGGCAAT GTCGTAACTT CCTGTTCAAA TTTATTTAGA TTGTTAAGTT CTGTTCATAC	TATICANAGE GCAGAATATT GAAATTTAT ACAGAGGCAC TGACCANAGG CTATTGGANA ACCCATTTTG BEQUENCE:	ATATTAAAGA TTGTTATTGG CTTTTACTAT TTAATTTGAT TCATTACAAC AACCACTGTC	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT CTGGCTTTTT TGTGTTTTTT	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTTT ATTGTATTTG TGGCAGTTGT	5640 5700 5760 5820 5880
	TTAGATTGA ACTITITIGA AAAGCTGTTT GCTTATGTGC TATTTTTTT TTTCTGGTCT CTGCATTAAC A Seq ID NO:	AAGAATTTCA AAATGGCAAT GTCGTAACTT CCTGTTCAAA TTTATTTAGA TTGTTAAGTT CTGTTCATAC	TATICANAGE GCAGAATATT GAAATTTAT ACAGAGGCAC TGACCANAGG CTATTGGANA ACCCATTTTG BEQUENCE:	ATATTAAAGA TTGTTATTGG CTTTTACTAT TTAATTTGAT TCATTACAAC AACCACTGTC	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT CTGGCTTTTT TGTGTTTTTT	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTTT ATTGTATTTG TGGCAGTTGT	5640 5700 5760 5820 5880
50	ACTITITION AAAGCTGTIT GCTTATGTGC TATTTTTTT TTTCTGGTCT CTGCATTAAC A Seq ID NO: Protein Ac	AAGARTTTCA AAATGGCAAT GTCGTAACTT CCTGTTCAAA TTTATTTAGA TTGTTAAGTT CTGTTCATAC 85 Protein cession #: I	TATSCAAAGC GCAGAATATT GAAATTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA ACCCATTTTG BEQUENCE: NP_075044.1	ATATTAAAGA TTGTTATTGG CTITTACTAT TTAATTTGAT TCATTACAAC AACCACTGTC TCCCTTTATT	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT CTGGCTTTTT TGTGTTTTTT GAAAAAATAA	TITAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTTT ATTGTATTTG TGGCAGTTGT AAAAAATTAA	5640 5700 5760 5820 5880
	TTAGATTGA ACTITITIGA AAAGCTGTTT GCTTATGTGC TATTTTTTT TTTCTGGTCT CTGCATTAAC A Seq ID NO:	AAGAATTTCA AAATGGCAAT GTCGTAACTT CCTGTTCAAA TTTATTTAGA TTGTTAAGTT CTGTTCATAC	TATICANAGE GCAGAATATT GAAATTTAT ACAGAGGCAC TGACCANAGG CTATTGGANA ACCCATTTTG BEQUENCE:	ATATTAAAGA TTGTTATTGG CTTTTACTAT TTAATTTGAT TCATTACAAC AACCACTGTC	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT CTGGCTTTTT TGTGTTTTTT	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTTT ATTGTATTTG TGGCAGTTGT	5640 5700 5760 5820 5880
50	TTAGATTGGA ACTITITGT AAAGCTGTTT GCTTATGTGC TATTTTTT TTTCTGGTCT CTGCATTAAC A Seq ID NO: Protein Ac	AAGATTTCA AAATGGCAAT GTCGTAACTT CCTGTTCAAA TTTATTTAGA TTGTTAAGTT CTGTTCATAC 85 Protein cession #: I	TATSCARAGE GCAGAATATT GCAATTTTAT ACAGAGGCAC TCACCAAAGG CTATTGGAAA ACCCATTTTG Bequence: NP_075044.1	ATATTAAAGA TTGTTATTGG CTTTTACTAT TTAATTTGAT TCATTACAAC AACCACTGTC TCCCTTTATT	GAAAGCCCGC CCITTICTAT GGGAGTCACT CTITTATITIT CTGGCTTTTT TGTGTTTTTT GAAAAAATAA	TITAGTCAATC TCCTGTAATC ATTIATTATT TCTTTGTTTT ATTIGTATTG TCGCAGTTGT AAAAAATTAA	5640 5700 5760 5820 5880 5940
50	TTAGATTGGA ACTITITGT AAAGCTGTTT GCTTATGTGC TATTTTTT TTTCTNGTCT CTGCATTAAC A Seq ID NO: Protein Ac. 1 MSRRKQGKPQ	AAGANTTCA AAATGGCAAT GTCGTAACTT CCTGTTCAAA TTTATTTAGA 85 Protein ccession #: 1 11	TATSCAAAGC GCASAATATT GAAATTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA ACCCATTTG Bequence: NP_075044.1 21 PLEAILTDDE	ATATTAAGA TTGTTATTGG CTITTACTAT TTAATTTGAT TCATTACAAC AACCACTGTC TCCCTTTATT 31 PDHGPLGAPE	GAAAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT CTGGCTTTTT GAAAAAATAA 41 	TITAGTCAATG ATTATTATT TCTTTGTTTT TCTTTGTTTT TTGGCAGTTGT AAAAAATTAA	5640 5700 5760 5820 5880 5940
50	TTAGATTGGA ACTITITOT AAAGCTGTTT GCTTATGTGC TATTTTTT TTTCTGGTCT CTGCATTAAC A Seq ID NO: Protein Ac. 1 MGRRRQGRPQ MERREGGRPQ	AAGAATTCA AAATGCAAA GTCGTAACTT CCTGTTCAAA TTGTTAGA TTGTTAGA 85 Protein cession #. I	TATECARAGE GCAGAATATT GAAATTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA ACCCATTTG sequence: WP_075044.1 21 PLEAILTDDE PLEAILTDDE	ATATTAAAG CTITTACTAT TGTAATTGAT TCAATTACAA AACCACTGTC TCCCTTTATT 31 PDHGPLGAPE	GARAGECCGE CCTTTTCTAT GGGAGTCACT CTTTATTTT TGTGTTTTT TGTGTTTTT GARARATAA 41 GDHDLLTCGQ GDHDLLTCGQ	TTTAGTCART TCCTGTAATG ATTTATTATT TCTTTGTTTT ATTGTATTG TGCAGTTGT AAAAAATTAA 51 CQMMPPLGDI DCLSTSSRRI	5640 5700 5760 5820 5880 5940
50 55	TTAGATTGGA ACTITITOT AAAGCTGTTT GCTTATGTGC TATTTTTT TTTCTGGTCT CTGCATTAAC A Seq ID NO: Protein Ac. 1 MGRRRQGRPQ MERREGGRPQ	AAGAATTCA AAATGCAAA GTCGTAACTT CCTGTTCAAA TTGTTAGA TTGTTAGA 85 Protein cession #. I	TATECARAGE GCAGAATATT GAAATTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA ACCCATTTG sequence: WP_075044.1 21 PLEAILTDDE PLEAILTDDE	ATATTAAAG CTITTACTAT TGTAATTGAT TCAATTACAA AACCACTGTC TCCCTTTATT 31 PDHGPLGAPE	GARAGECCGE CCTTTTCTAT GGGAGTCACT CTTTATTTT TGTGTTTTT TGTGTTTTT GARARATAA 41 GDHDLLTCGQ GDHDLLTCGQ	TTTAGTCART TCCTGTAATG ATTTATTATT TCTTTGTTTT ATTGTATTG TGCAGTTGT AAAAAATTAA 51 CQMMPPLGDI DCLSTSSRRI	5640 5700 5760 5880 5880 5940
50	TTAGATTGGA ACTITITIVI AAAGCTGTIT GOTTATGTGC TATTITTIT TTCRGGTCT TGCATTACC A Seq ID NO: Protein Ac- MGRREGGEPQ MGRREGGEPQ LIFIERRERQ CPKQEHIADE SAMFILIGIEN	AAGAATTCA AAATGCATA GTCGTAACTT GTCGTACATA TTTATTTAGA TTTATTAGAT CTGTTCATAC 85 Protein cession #: 1 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TATECARAGE GCAGAATATT GAAATTTTAT ACAGAGGCATTTG TACCAATTTG ACCCATTTG ACCCATTTG ACCCATTTG PLOTE 1 PLEAILTDDE VDKPPSPSPI RSAKGALPT RSEKGSPLTPR	ATATTAAAG CTITTACTAT TTAATTGAT TTAATTGAAC AACCACTOTC TCCCTTTATT 31 pohgplgape emkkasnpve pgmsaevapo ggiesglgae	GARAGCCCGC CCTTTTCTAT GGGAGTCACT CTGTTTTTT TGTGTTTTT TGTGTTTTT GAAAAATAA 41 GDHDLLTCGQ VGIQVTPEDD GICKDEPSSY VGSQCPSQPBHGI	TTTAGTCAAT TCCTGTAATG ATTATTATT TCTTTGTTT ATTGTATTG TGGCAGTTGT AAAAAATTAA 51 CQMPPLGDI CCLSTSSRRI TCTTCKQPFT TCTTCKQPFT	5640 5700 5760 5820 5880 5940
50 55	TTAGATTGGA ACTITITION AAAGCTGTTI GCTTATGTGC TATTTTTTT TTCTNGTCT CTGCATTAAC A Seq ID NO: Protein Ac 1 MSRRKQGKPQ LIFIENERKRQ LIFIENERKRQ CPKQENIADK SAMPLLGHAQ ENDEGGED	AAGAATITCA AAATGGCATACT GCCGTAACT CCTGTTCAAA TTGATTAGAT TCGTTCATAC 85 Protein cession #: 1 11 HLSKREFSPE CNGSLCLEKA LHHRGLSSP HTHGLRIYLE ACGLAPTOPP	TATECARAGE GCAGGATTTG GAAATTTTAT ACAGAGGCAC TGACCARAGG CTATTGGAAA ACCCATTTG sequence: NP_075044.1 21 PLEAILTDDE VDKPPSFSPI ESAGGALIPT SEHGSPLTPR TSHAGGALIPT SEHGSPLTPR TDDI.FSDPD	ATATTAAAG TIGTTATTGG CTITTACTAT TIGTTATTGAT TTAATTGAT TCATTACAAC AACCACTOT TCCCTTTATT 31	GARAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT GGTGTTTTT GAAAAAATAA 41 GDHDLLTCGQ WGIQVTFBEID GICKDEPSSY CPSQPPLHGI	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTT ATTGTATTG TGGCAGFTGT AAAAAATTAA 51 [CQMMPPLGDI DCLSTSSRRI TCTTCKQPFT HIANNEPNL TCTTCKQPFT HIANNEPNL THHESA BTDV	5640 5700 5760 5820 5880 5940
50 55	TTAGATTGGA ACTITITION AAAGCTGTTI GCTTATGTGC TATTTTTTT TTCTNGTCT CTGCATTAAC A Seq ID NO: Protein Ac 1 MSRRKQGKPQ LIFIENERKRQ LIFIENERKRQ CPKQENIADK SAMPLLGHAQ ENDEGGED	AAGAATITCA AAATGGCATACT GCCGTAACT CCTGTTCAAA TTGATTAGAT TCGTTCATAC 85 Protein cession #: 1 11 HLSKREFSPE CNGSLCLEKA LHHRGLSSP HTHGLRIYLE ACGLAPTOPP	TATECARAGE GCAGGATTTG GAAATTTTAT ACAGAGGCAC TGACCARAGG CTATTGGAAA ACCCATTTG sequence: NP_075044.1 21 PLEAILTDDE VDKPPSFSPI ESAGGALIPT SEHGSPLTPR TSHAGGALIPT SEHGSPLTPR TDDI.FSDPD	ATATTAAAG TIGTTATTGG CTITTACTAT TIGTTATTGAT TTAATTGAT TCATTACAAC AACCACTOT TCCCTTTATT 31	GARAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT GGTGTTTTT GAAAAAATAA 41 GDHDLLTCGQ WGIQVTFBEID GICKDEPSSY CPSQPPLHGI	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTT ATTGTATTG TGGCAGFTGT AAAAAATTAA 51 [CQMMPPLGDI DCLSTSSRRI TCTTCKQPFT HIANNEPNL TCTTCKQPFT HIANNEPNL THHESA BTDV	5640 5700 5760 5880 5880 5940
50 55	TTAGATTGGA ACTITITION AAAGCTGTTI GCTTATGTGC TATTTTTTT TTCTNGTCT CTGCATTAAC A Seq ID NO: Protein Ac 1 MSRRKQGKPQ LIFIENERKRQ LIFIENERKRQ CPKQENIADK SAMPLLGHAQ ENDEGGED	AAGAATITCA AAATGGCATACT GCCGTAACT CCTGTTCAAA TTGATTAGAT TCGTTCATAC 85 Protein cession #: 1 11 HLSKREFSPE CNGSLCLEKA LHHRGLSSP HTHGLRIYLE ACGLAPTOPP	TATECARAGE GCAGGATTTG GAAATTTTAT ACAGAGGCAC TGACCARAGG CTATTGGAAA ACCCATTTG sequence: NP_075044.1 21 PLEAILTDDE VDKPPSFSPI ESAGGALIPT SEHGSPLTPR TSHAGGALIPT SEHGSPLTPR TDDI.FSDPD	ATATTAAAG TIGTTATTGG CTITTACTAT TIGTTATTGAT TTAATTGAT TCATTACAAC AACCACTOT TCCCTTTATT 31	GARAGCCCGC CCTTTTCTAT GGGAGTCACT CTTTTATTTT GGTGTTTTT GAAAAAATAA 41 GDHDLLTCGQ WGIQVTPEND GICKDEPSSY CPSQPPLHGI	TTTAGTCAAT TCCTGTAATG ATTTATTATT TCTTTGTTT ATTGTATTG TGGCAGFTGT AAAAAATTAA 51 [CQMMPPLGDI DCLSTSSRRI TCTTCKQPFT HIANNEPNL TCTTCKQPFT HIANNEPNL THHESA BTDV	5640 5700 5760 5820 5820 5880 5940
50 55	TTAGATTGGA ACTITITATI ANAGCTGTIT GCTTATGTGC TATTTTTTT TTCTNGTCT CTGCATTAAC A Seq ID NO. Protein Ac I MGRRKQGKPQ LIFIERKEKQ CPKQBEHJADK SAWPLLGHAG LRIFGSVSRE LRILDMAMED PPLOSAPPPS	AAGAATTCA AAATGCATAAT GTCGTAACT CTGTTCAAA TTTATTAGA TTGTTAAGT TTGTTAAGT CTGTTCATAC 85 Protein cession #. 1 11 HISKREFSPE CNGSICLEKA LIMHKGLESP NTHGLRIVLE ASGLACERP PAMDFSRELR PAMDFSRELR	TATECARAGE GCAGATATT GAAATTTAT ACAGAGGC TGACCAAAGE CTATTGGAA ACCCATTTG sequence: PP_075044.1 21 PLEAILTDDE VDKPPSPSPI SEHGSPLTPR ESAGGALIFT SEHGSPLTPP LAGNTSSPP ELANTSSPP ELANTSSPP FOGKTFRPOS	ATATTAAGA TIGITATTGG CTITACTAT TTAATTTGAT TCATTACAAT TCATTACAAT AACCACTOTC TCCCTTTATT 31 POHGPLGAPE EMKRASNEVE PGMSAEVAPQ VGIPSGLGAE RHHLDPHEIE LSPGRPSIMG	GARAGCCCGC CCTTTTCTAT GGGGTCAT CTTTTATTT CTGGCTTTTT CTGGCTTTTT GAAAAAATAA 41 GDHDLLTCGQ VGIQVTFEDD GICKDEPSSY CPSQPPLHGIA RLLQPFQPGS RLGAEERGIA RLLQPFQPGS GEKPYKCNLC	TTTAGTCAST TCCTGTAATG ATTATTATT TCTTTGTTT ATTGTATTG TGGCAGTTG TAGACAGTTG AAAAAATTAA 51 CQMMPPLGDI CCIMTSTSSRRI TCTTCKQPF HIADNMPFNL TCTTCKQPF HIADNMPFNL KPPLATPPL LDHACTOASKL	5640 5700 5760 5820 5820 5880 5940 60 120 180 240 300 360 420
50 55 60	TTAGATTGGA AAGTTITITTT AAAGCTGTTT GCTTATGTGC TATTTTTTT TTCTGGCT CTGCATTAAC A Seq ID NO: Protein Ac I MSRRKQGKPQ LIFIBHKRKQ CPKQBHLADK SAMFILIGHAQ LRIFGSVSRB LRLNDWAMED PPLQSAPPPS RRHMSTHPBEK RRHMSTHPBEK RRHMSTHPBEK	AAGAATTICA AAATGCGAA GTGTAACTT CCTGTTCAAA TTTATTTAGA TTGTTAAGTT CCGSTCATAC 85 Protein	TATEGARAGE GCAGAATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA ACCCATTTG sequence: NP_075044.1 21 PLEAILTDDE VDKPPSPSPI RSAKGALIPT TEHGSPLTPR PTPPLFSPPP ELAGNTSSPP FCGGTFKPGS GLSTASSPEP	ATATTAAAGA TIGITATTAG CITTACTAT TTAATTTAGAT TAATTTAGAT TAACACATGTC TCCCTTATT 31	GARAGCCCGC CCTTTTCTAT GGGGTCACT CTTTTATTCTCAGGCTTTTT CTGGCTTTTT CTGGCTTTTT GARAAAATAA 41 GDHDLLTCGQ WGIQWTPEDD GICKDEPSSY GICKDEPSSY RLGGEGRALA RLLQFFQPGG GEKPYKCNLC SALKSYWAKF	TTTAGTCAST TCCTGTAATG AITIATTATT TCTTGTTT ATTGTATTG TGGCAGTTG TAGCAGTTG AAAAAATTAA 51 CQMMFPLGDI CQMSPLGDI CCTCKQPFT HADNNEFNL THIBOSAPDRV CHPPLATPPL DHACTQASKL	5640 5700 5760 5820 5880 5940 120 180 360 480
50 55	TTAGATTGGA AAGTITITATI AAAGCGGTTI GCTATAGTAC TATTTTTTT TTTCTNGTCT CTGCATTAAC A Seq ID NO: Protein Ac I MGRRKQGKPQ LIFIBENGRQ CPKQBHIADK SAMPILGHAQ LRIFGSVGRE LELINDAMEPS RCHWKTHMEK ENGDEEGEBD	AAGAATTICA AAATGCGAA GTCGTAACTT CTGTTCAAA TTTATTTAGA TTTATTTAGA TTTATTAGA 11 ILSKREFSPE CNGGLCLEKA LIHNGLESP NTHGLRIYLE ANGLAEGREP PAMDFSRELR QPPVKSKCE SSPMTVKSDG DEBEEEBEEBE	TATEGARAGE GCAGAATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA ACCCATTTG SEQUENCE: P_075044.1 PLEAILTDDE VDKPPSSPPI ELAGNTSSPP ELAGNTSSPP ELAGNTSSPP ELAGNTSSPP ELAGNTSSPP GGETFRSPQ GLSTASSPEF EREELITESER	ATATTAAAGA TIGITATTIGG CTITTACTAT TTAATTIGAT TCATTACAAC AACCACTOTC TCCCTTTATT 31 POHGPLGAPE EMKRASNEVE EMKRAS	GARAGCCCGC CCTTTTCTAT GGGGTCATT CTGGGTTTTT CTGGGTTTTT GARARATAA 41 GDHDLLTCQQ VGTQVTFEDD GICKDEPSSY CPSQFPLHGI RLIGPFQPGS GEKPYKCNLC SALKSVVARF GEKPYKCNLC SALKSVVARF	TTTAGTCART TCCTGTAATG ATTATATAT TCTTTGTTT ATTGTATTG TGGCAGTTG TAGCAGTTG AAAAAATTAA 51 CQMMFPLGDI CQMMFPLGDI CCTTCKQPF HIADNMFFNL THEBSAFDRV KPPLATPFL HACTGASKL KSENDFNLIP GAVVGVGUS	5640 5760 5760 5820 5880 5940 60 120 120 120 240 360 420 480 540
50 55 60	TTAGATTGGA AAGTTITITTAT AAAGCTGTTT GCTTATGTGC TATTTTTTT TTCTGGCT CTGCATTAAC A Seq ID NO: Protein Ac I MSRRKQGKPQ LIFIENKRKQ CPKQBHLADK SAMFILIGHAQ LRIFGSVSRE LRINDMAMED PPLQSAPPPS REMMITHPSK ENGDEEEEED RALPDVMGGM	AAGAATTICA AAATGCATAAATGCATAAATGCATAAATGCATAAATGCATAAATGCATAAATGTAATTIAGA TITATITAGA TIT	TATEGARAGE GCAGAATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG CTATTGGAAA ACCCATTTG sequence: NP_075044.1 21 PLEAILTDDE VDKPPSPSPI RSAKGALIPT TEPLIFSPPP TEPLIFSPPP ELAGNITSSPF FCGKTFKPGS GLSTASSPEE EEELITESER APHOVILGERA	ATATTAAGA TIGITATTGG CTITACTAT TTAATTGG TTAATTGAT TCATTACAAC AACCACTGTC TCCCTTTATT 31 phoglgape Emkkasneve pgmsaeyape Usipsglagae RHHLDPHEIE LSPORPSIMO BLUVHIRSSIT GTSDLWSSIX VDYGFGLSLE KRGHLABLEG KRGHLABLEG	GARAGCCCGC CCTTTTCTAT GGGGGTCACT CTGGGTTTTT CTGGGTTTTT GARARATAA 41 GDHDLLTCGQ GGLGEPSSY CPSGPPBGI RLGAEENALA RLLQPFQBG GEKPYKCNLC SALKSVVALC SALKSVALC SALKSVVALC SALKSVALC SALKSVVALC SALKSVVALC SALKSVVALC SALKSVVALC SALKSVVALC SALKSVVALC SALKSVVALC SALKSVALC SALKSVVALC SALKSVALC SALKSVALC SALKSVALC SALKSVALC SALKSVALC SALKSVALC SALKSVALC SALKSVALC SALKSVAL	TTTAGTCART TCCTGTAATG AITIATTATT TCTTTGTTT ATTGTATTG TGGCAGTTG TAGCAGTTG AAAAAATTAA 51 CQMPPLGDI CQMPPLGDI CQMPPLGDI TCTTCKQPFT HADNNPFNL THIBDSAPDRV KSPEIDFNL DHACTOASKL KSEMDPNLIP GAVVGVORDES AGESDR IDDG	5640 5760 5760 5820 5880 5940 60 120 240 300 480 540 600
50 55 60	TTAGATTGGA AAGTTTTTTTT AAAGCTGTTT GCTTATGTMC TATTTTTTT TTTCTMGTCT CTGCATTAAC A Seq ID NO: Protein Ac 1 MERREGGEPO LIFIENTRO CPKQBILIANK SAMPLLGIMA CRESSILIANK CRE	AAGAATTICA AAATGCATAACTA GTCGTAACTT CTGTTCAAA TTTATTIAGA TTGTTAACT TTGTTAACT 11 HLSKREPSPE LNGSLCLEKA LHHNGLESP ATGLACA ASGLACESC ASG	TATEGARAGE GCAGATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG SEQUENCE: PP_075044.1 21 PLEALLTDDE UNKPPSPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI LAGANTSSPP CGATTFROG GLSTASSPER APHOVIGERA APH	ATATTANAGA TIGITATIGG CTITACTAT TIGATTIGG TTAATTIGAT TCATTACAAC AACCACTATC TCCCTTTATT 31	GARAGCOGGE CCTTTTCTAT GGGGGTCACT CTTTTATTTT CTGGCTTTTT GTGTTTTTT GAAAAAATAA 41	TTTAGTCART TCCTGTAATG ATTTATTATT TCTTTGTTT ATTGTATTAG TGGGGGTIGT AAAAAATTAA 51 CUMMPPLGDI DCLSTSGRIT TCTTCKGPT HIADNINFINL TCTTCKGPT HIADNINFINL HIBSAPDRV KPPPLATPPL UNACTOAL KSENDPHLIP GAVVGVORD AGESDRIDGG AGESDRIDGG MTEMYSOML	5640 5760 5760 5820 5880 5940 120 180 240 360 420 420 420 660
50 55 60	TTAGATTGGA AAGTTTTTTTT AAAGCTGTTT GCTTATGTMC TATTTTTTT TTTCTMGTCT CTGCATTAAC A Seq ID NO: Protein Ac 1 MERREGGEPO LIFIENTRO CPKQBILIANK SAMPLLGIMA CRESSILIANK CRE	AAGAATTICA AAATGCATAACTA GTCGTAACTT CTGTTCAAA TTTATTIAGA TTGTTAACT TTGTTAACT 11 HLSKREPSPE LNGSLCLEKA LHHNGLESP ATGLACA ASGLACESC ASG	TATEGARAGE GCAGATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG SEQUENCE: PP_075044.1 21 PLEALLTDDE UNKPPSPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI LAGANTSSPP CGATTFROG GLSTASSPER APHOVIGERA APH	ATATTANAGA TIGITATIGG CTITACTAT TIGATTIGG TTAATTIGAT TCATTACAAC AACCACTATC TCCCTTTATT 31	GARAGCOGGE CCTTTTCTAT GGGGGTCACT CTTTTATTTT CTGGCTTTTT GTGTTTTTT GAAAAAATAA 41	TTTAGTCART TCCTGTAATG ATTTATTATT TCTTTGTTT ATTGTATTAG TGGGGGTIGT AAAAAATTAA 51 CUMMPPLGDI DCLSTSGRIT TCTTCKGPT HIADNINFINL TCTTCKGPT HIADNINFINL HIBSAPDRV KPPPLATPPL UNACTOAL KSENDPHLIP GAVVGVORD AGESDRIDGG AGESDRIDGG MTEMYSOML	5640 5760 5760 5820 5880 5940 120 180 300 420 480 600 600 600 600
50 55 60	TTAGATTGGA AAGTTTTTTTT AAAGCTGTTT GCTTATGTMC TATTTTTTT TTTCTMGTCT CTGCATTAAC A Seq ID NO: Protein Ac 1 MERREGGEPO LIFIENTRO CPKQBILIANK SAMPLLGIMA CRESSILIANK CRE	AAGAATTICA AAATGCATAACTA GTCGTAACTT CTGTTCAAA TTTATTIAGA TTGTTAACT TTGTTAACT 11 HLSKREPSPE LNGSLCLEKA LHHNGLESP ATGLACA ASGLACESC ASG	TATEGARAGE GCAGATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG SEQUENCE: PP_075044.1 21 PLEALLTDDE UNKPPSPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI LAGANTSSPP CGATTFROG GLSTASSPER APHOVIGERA APH	ATATTANAGA TIGITATIGG CTITACTAT TIGATTIGG TTAATTIGAT TCATTACAAC AACCACTATC TCCCTTTATT 31	GARAGCOGGE CCTTTTCTAT GGGGGTCACT CTTTTATTTT CTGGCTTTTT GTGTTTTTT GAAAAAATAA 41	TTTAGTCART TCCTGTAATG ATTTATTATT TCTTTGTTT ATTGTATTAG TGGGGGTIGT AAAAAATTAA 51 CUMMPPLGDI DCLSTSGRIT TCTTCKGPT HIADNINFINL TCTTCKGPT HIADNINFINL HIBSAPDRV KPPPLATPPL UNACTOAL KSENDPHLIP GAVVGVORD AGESDRIDGG AGESDRIDGG MTEMYSOML	5640 5760 5760 5820 5880 5940 120 180 240 360 420 420 420 660
50 55 60	TTAGATTGGA AAGTTTTTTTT AAAGCTGTTT GCTTATGTMC TATTTTTTT TTTCTMGTCT CTGCATTAAC A Seq ID NO: Protein Ac 1 MERREGGEPO LIFIENTRO CPKQBILIANK SAMPLLGIMA CRESSILIANK CRE	AAGAATTICA AAATGCATAACTA GTCGTAACTT CTGTTCAAA TTTATTIAGA TTGTTAACT TTGTTAACT 11 HLSKREPSPE LNGSLCLEKA LHHNGLESP ATGLACA ASGLACESC ASG	TATEGARAGE GCAGATATT GAAATTTTAT ACAGAGGCAC TGACCAAAGG SEQUENCE: PP_075044.1 21 PLEALLTDDE UNKPPSPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI RSAGGALPSPI LAGANTSSPP CGATTFROG GLSTASSPER APHOVIGERA APH	ATATTANAGA TIGITATIGG CTITACTAT TIGATTIGG TTAATTIGAT TCATTACAAC AACCACTATC TCCCTTTATT 31	GARAGCOGGE CCTTTTCTAT GGGGGTCACT CTTTTATTTT CTGGCTTTTT GTGTTTTTT GAAAAAATAA 41	TTTAGTCART TCCTGTAATG ATTTATTATT TCTTTGTTT ATTGTATTAG TGGGGGTIGT AAAAAATTAA 51 CUMMPPLGDI DCLSTSGRIT TCTTCKGPT HIADNINFINL TCTTCKGPT HIADNINFINL HIBSAPDRV KPPPLATPPL UNACTOAL KSENDPHLIP GAVVGVORD AGESDRIDGG AGESDRIDGG MTEMYSOML	5640 5760 5760 5820 5880 5940 120 180 300 420 480 600 600 600 600
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25	MAGAGPKRRA	LAAPAAEEKE	BAREKMLAAK	SADGSAPAGE	GEGVTLQRNI	TLLNGVAIIV	60 120
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30	GNIVLALYSG STROMLSSEA	LFAYGGWNYL VAVDFGNYHL	NPVTEEMINP GVMSWIIPVF	YRNLPLAIII VGLSCPGSVN	SLPIVTLVYV	LINLAYPITL	300 360
	SILSMIHPQL RKPELERPIK	LTPVPSLVPT VNLALPVFFI STTVLCQKLM	CVMTLLYAPS LACLFLIAVS	KDIFSVINFF	SFFNWLCVAL	AIIGMIWLRH	420 480
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50	CATGCCCCTC	ACTGCTCGTG CCATGGGGAG	GTCATGCACG	TGGCCTACCG	GGAGGTTCAG	GAGAAGAGGC	480
30	GTGGGCTCTG	GTGGACATAT	GTCTGCAGCC	TAGTGTTCAA	GGCGAGCGTG	GACATCGCCT	600
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55	TTTTCACCCT	CTTCATGGTG	GCCACAGCTG	AGTGCCTGGC	CCTGCTCAAC AGCAAGGAAA	GCTCAAGCCA	780 840
	TGTGCACAGG	TCATCACCCC	CACGGTACCA	CCTCTTCCTG	CAAACAAGAC	GACCTCCTTT	900 960
	GAGACCATGT	GAAGAAAACC	ATCTTGTGAG	GGGCTGCCTG	GACTGGTCTG	GCAGGTTGGG	1020
60	CATGAGGTAG	GGGCAGGCAA	GAGAGAGGAT	TCAGACGCTC	TGGGAGCCAG	TTCCTAGTCC	1140
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65	Protein Acc	89 Protein cession #: 1	₩P_005259.1				
	i	11	21 j	31 	1	51	
70	SNVCFDEFFP GKKRGGLWWT SEKNIFTLFM	SGVNKYSTAF VSHVRLWALQ YVCSLVFKAS VATAAICILL LGSDSHPPLL	LILVTCPSLL VDIAFLYVFH NLVELIYLVS	VVMHVAYREV SFYPKYILPP KRCHECLAAR	QEKRHREAHG VVKCHADPCP	ENSGRLYLNP	60 120 180 - 240
75	Sec ID NO.	90 DNA sequ	ience				
	Nucleic Ac:	ld Accession Lence: 26-49	1 #: NM_002:	391.1			
80	1	11	21 i	31 	1	51 	
85	CCCGGGGAGC CCGGCGTGGGT	AGCGCGGGCA GCGCTCACCT GAGTGCGCTG TTCCGCGAGG TGGAAGAAGG	CCGCGGTCGC AGTGGGCCTG GCACCTGCGG	CAAAAAGAAA GGGGCCCTGC GGCCCAGACC	GATAAGGTGA ACCCCCAGCA CAGCGCATCC	AGAAGGGCGG GCAAGGATTG GGTGCAGGGT	60 120 180 240 300
	TGCGTGTGAT	GGGGGCACAG	GCACCAAAGT	COGCCAAGGC	ACCCTGAAGA	AGGCGCGCTA	360

5	AAAGGCCAAA GCCCCTGGTG CACCAGTGCC ACTCCCCAGC TGAGCCTCCC	TGCCAGGAGA GCCAAGAAG TCACATGGG TTCTGTCTGC CCCACCCCTA CCAAAGCAAT AACACATCAA	GGAAGGAAA CCTGGCCACG TCGTTAGCTT AGTGCCCAAA GTGAGTCCCA	GGACTAGACG CCCTCCCTCT TAATCAATCA GTGGGGAGGG GAGCCCGCTT	CCAGGCCGG CCCAGGCCCG TGCCCTGCCT ACAAGGGATT TTGTTCTTCC	ATGCCAAGGA AGATGTGACC TGTCCCTCTC CTGGGAAGCT CCACAATTCC	420 480 540 600 660 720 780
10	Seq ID NO: Protein Ac	91 Protein cession #: 1	sequence: TP_002382.1				
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15	CGAOTORIRC	LLALLALTSA RVPCNWKKEP KAKAKAKKGK	GADCKYKFEN				60 120
20	Nucleic Ac Coding seq	92 DNA sequ id Accession uence: 98-80	1 ∯: NM_005: 02				
25	1	11	21	31	41	51 .	
23	CGTGTGCTCA	CACAGCTGCA GAACAAGGTG CTCCTACTGG CACAGCAAAG	AACGCCCAGC CTGCTCAGGT	TGCAGCCATG	AAGATCTGTA GAGGGGAAAA	GCCTCACCCT	120 180 240
30	TAAGCAGAAA	AGCAGGCCCG	GGAACAAAGG	CAAGTTTGTC	ACCAAAGACC	AAGCCAACTG	300
	GGACCATGAA TGAGAGAGTC	GCTACTGAGC TTTTCCTGTG TATTGGAAAC ACAGCTGTGA	TCTTTGCTGG	CAATCCAACC	TCATGCCTAA TCACAGAAAG	AGCTCAAGGA ACATCTGTAG	360 420 480 540
35	TAAGCTAGTC	AGCTCCACTC	TATTTGGGAA	CACAAAGCCC	AGGAAGGAGA	AAACAGAGAT	600
	GTCCCCCAGG	GAGCACATCA ACCAAAGCTC	AGGGCAAAGA	GACCACCCCC	TCTAGCCTAG	ACCAGAGGAA	660 720
	GACTGCCCTG	GAGTTCTGTG	GAGAGACTTG	GAGCTCTCTC	TGCACATTCT	TCCTCAGCAT	780
40	AGTGCAGGAC TGTCGTAAGT	ACGTCATGCT CCCTCTGTAT	ACTITAAAGC	TCTCTACAGT	CCCCCCAAAA	TATGAACTTT	840 900
	TGTGCTTAGT	GAGTGCAACG CTTATTTTC	AAATATTTAA	ACAAGTTTTG	TATTTTTTCC	TTTTGTGTTT	960 1020
	TTCCATGGCC	CACACAGCTA	TGTGTTTGAG	CAGCGAAGAG	TCTTTGAGCT	GAATGAGCCA	1080
45	GAGTGATAAT TTTTTCAAAA	TTCAGTGCAA AAAAAAAAAA	CGAACTTTCT AAA	GCTGAATTAA	TGGTAATAAA	ACTCTGGGTG	1140
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55	PSSLAVTOTM	KTAVKTRVCR ATKAPECVED	PDMANQRKTA	LEFCGETWSS	LCTFFLSIVO	DTSC	180
	Nucleic Ac	94 DNA sequid Accession	1 #: NM_0123	.01			
60							
	i	11	21 	31 	41 	51	
		GTGTGTCTCT					60 120
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		GGGGAAGGTA					360 420
70	GGAAGGCAAG	AGGTCGCCGT	ACGCAGGGCT	CCAGCTGGGG	GCTGCCAAGA	AGCCACCCGT	480
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75	CAAGCCCCAC	CTGGAGGGCG	CCGCCTTCCG	AGACCACCAG	CTGCTCGAGC	CCATCCGGGA	720 780
	CTTTGAGGCC	CGCAAGTGTC	CCGTGCATGG	CAAGACGATG	GAGCTCTTCT	GCCAGACCGA	840 900
	AGTGGAGGAG	GCCAAGGCCG	AGAAGGAGAC	GGAGCTGTCA	CTGCAAAAGG	AGCAGCTGCA	960
80	CAAGAGCTTC	ATTGAGATTG	AGAAGGCCAT	CCTGGAGCAG	AACTTCCGGG	ACCTGGTGCG	1020 1080
	GGACCTGGAG	AAGCAAAAGG	AGGAAGTGAG	GGCTGCGCTG	GAGCAGCGGG	AGCAGGATGC	1140
	GGACAAGCAG	GTGAAGGTGA ACCCGGGAGC	AGCTGCATAG	CATCAGCGAC	TCTGTGTTGT	TTCTGCAGGA	1200 1260
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	GAACCACATO	GAGAACGGTG	GTGACCATCG	CTATGTGAAC	AACTACACGA	ACAGCTTCGG	1500

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	TGGGAGGGAG	CCTGGTCCTG	CACCTGCCCT	CTGCAGCCCT	CTGCCAGCCT	CTTGGGGGCA	2040
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	CTATACACT	TTCTCTCCAA	CCCCCTATCC	CCCAATGTTG	TCAGCAGATG	CCTGGACAGC	2340
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25	GATGGGCCAG	CTTGCAGGGG	TTGGGGAGGG	AGACATCCAG	CTTGGGCTTT	CCCCTTTGGA	3000
	ATAAACCATT						

Seq ID NO: 95 Protein sequence: Protein Accession #: NP_036233.1

30 Protein Accession #: NP_036233

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35	PROPODONI.P	AGNEWRRPLI	OFVESCODEN	SNYPSMDSME	GKRSPYAGLO	LGAAKKPPVT	120
55	TA THE CHILD'S	IFSESRKPTV	OTMEDGETER	NEVERADTGL	PSRSKSGSEE	VLCDSCIGNK	180
	OVANNOCTIC	OF COCOLPINA	DATE OF THE	HOLLEPIRDE	EARKCPVHGK	TMELFCOTDO	241
	DOTON'S CHING	EHKNHSTVTV	PUDDOMETO	LSTOKECTOL	RITETEDEAE	KWOKEKDRIK	300
	ICICIDONEO	EONFROLVED	TENOPPERE	ALEXIPEDITAV	DOVKVIMDAL	DERAKVLHED	360
40	SPITNBRAID	ODGER DE OFF	CATHENVELD	DDI DTVUITI.	EGEGLGOSI A	NFKDDLLNVC	421
40	KOTKEQUASI	SUSVERIGER	CALIFICATION I SHE	INNIVENIERCE	PHEADDTMICE	YSMYLTPKGG	480
	MRHVERMCKA	DESKNYTERN	HMENOGENET	AMMENIATE ACC	eerowerum.	PVVQGSSSFS	540
	VRTSYQPSSP	OSPKAOPOTW	MENNLIGING	MITSKYWEIS	CICCHEAD	. v v goddod a	

45 Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: NM_080668.1
Coding sequence: 83-841

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75	AACCATCTAC	GGAGCCTTAG	TTGGGTCTCA	GACCATAAGT	GTGTACTACA	CAGAAGCTGT	1500
,,	ODDOOR OF A CT	TOTOCTOTO	TOTTONGATO	TTTYTTARAT	GCCAGGTTGA	TAGGGCGCTG	1560
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	CCTCATCCC	TOTAGACTICA	TCCCTTGCAC	AGGGCCCACG	CTGGAGTCTT	ACCACTCTGC	1680
	TO CONTROCTO	GANGGTGGCC	CCTCTTGTCA	CCCATACCCA	TTTCTTACAA	AATAAGITAC	1740
80	ACCURACIONA	CTTGGCCCTA	CAAGAGAAAG	TTGAAGAGTC	CCAGACCTAC	TAGCATTTTG	1800
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	CICATONICI	A DOGGOOD COCC	TGCCCCCCGAC	TOTOCTGOOD	CACCCCTGGC	CATTGTACCT	2040
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	LAGAGAATGC	TARTARA	GNGTGCTGGG	TCTGGGAGTG	CCAGGCCATC	TGCTCAACGC	2220
	MUSICUSCUS	TOUTHWATCH	- Cacade Consider				

TOTOMOTIO GOMAGACTO CAAGAACC CCCTGCTGG GAAGCCTAGG TGTCCTTGAG 2280 CTUAACGCA CTGAGGACT CTGGCTGAT CAGCGAGACT CTGGCGAAC 2240 CTUAACGCA CTGAGGACC CAGCGAGACT CTGGCGAAC 2240 AGTCTTAGTCC TGCAGAACA CTAGATCACCA GATGAGGACA ATGTAGGACA ATCATTCACA ATCATTC

Seq ID NO: 97 Protein sequence: Protein Accession #: NP_542399.1

10 1 21 31 41 51

MISGRITHSOG AAAGSOPPARP SPTKPLERSO RESOSELPSI LEHEMPKTPS AAAVRKPIVL
KAIVALAUVEV PÄNGSSPRED RISSPLERSON REPGERELTKE DIKKTEVEVA TRISTPURING
KAIVALAUVEV PÄNGSSPRED RISSPLERSON REPGERELTKE DIKKTEVEVA TRISTPURING
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SPWIGSKITT VORVOALDVA DOMILIPUIR PERENKRIKT MERELINGLIGUV 120 15

Seq ID NO: 98 DNA sequence

20		id Accession mence: 58-1		quence			
	1 -	11 CGGGTCCGGG	21	31 -	41 Checoconor	51 	60
25	accedent con	GAGCCGGTGT	accompagner	CTCCTCCCCC	TGCAGGAGAC	COOCOCCATO	120
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	AATACAACTC	ATCOTTCATT	CCCTGAAGTC	TTTACABCAT	ATATTACTOT	ACTTGCTGAC	5100
	ACTACARGIC	ATCOLCATT	DARCCCCCAR	CCTCTCACTC	TTOTTCCATT	CTTCACCAGC	5160
	ACAMAGC100	ALCIACATIT	CONNOCIONA	CONCERCTO	ACCACCECAT	COTTOCCTOLC	5220
	CTCACTGGAG	GCAGICIGGA	ADDRESS OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF T	coldificion	COMMONTANTA	TOT TOUTONG	5280
25	TTCCCCATGC	AGTCCAGGGA	ATTICCICA	GGAACTCCGC	GGTTCAATAA	CTTCACCAGC CGTTGCTCAC TTATGTGGAC GTTGGAATTG TCAATCCAGT GGAAAGCGTG	5340
23	TGCATGAAAA	AGTTTCTAGA	TGCATTGGAA	TTATCTCAAA	GCCCTATGTT	GTTGGMATTG	5400
	ATGACAGAAG	TTCTTTGTCG	GGAACAGCAG	CATGTCATGG	AAGAATTATT	TCAATCCAGT	5460
	TTCAGGAGGA	TTGCCAGAAG	GGGTTCATGT	GTCACACAAG	TAGGCCTTCT	GGAAAGCGTG	
	TATGAAATGT	TCAGGAAGGA	TGACCCCCGC	CTAAGTTTCA	CACGCCAGTC	CTTTGTGGAC	5520
20	CGCTCCCTCC	TCACTCTGCT	GTGGCACTGT	AGCCTGGATG	CTTTGAGAGA	CTTTGTGAC ATTCTTCAGC ARATGAATCT CGTGATGTAT AGTTTTCCAT GTGCTACGAT ACTTTACCAT	5580
30	ACAATTGTGG	TGGATGCCAT	TGATGTGTTG	AAGTCCAGGT	TTACAAAGCT	AAATGAATCT	5640
	ACCTTTGATA	CTCAAATCAC	CAAGAAGATG	GGCTACTATA	AGATTCTAGA	CGTGATGTAT	5700
	TCTCGCCTTC	CCAAAGATGA	TGTTCATGCT	AAGGAATCAA	AAATTAATCA	AGTTTTCCAT	5760
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	GCATTTACAG	AGAACATGGC	AGGAGAGAAT	CAGCTGCTGG	AGAGGAGAAG	ACTITACCAT	5880
35	TGTGCAGCAT	ACAACTGCGC	CATATCTGTC	ATCTGCTGTG	TCTTCAATGA	GTTAAAATTT TGAAAATCTG GGAAAGAAAG	5940
	TACCAAGGTT	TTCTGTTTAG	TGAAAAACCA	GAAAAGAACT	TGCTTATTTT	TGAAAATCTG	6000
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							6120
	CCTTCCTATA	TGTCTTCCCT	GTCATATTTG AGTTCAGAGC ACGGGAGCAG	GCAGACAGTA	CCCTGAGTGA	GGAAATGAGT	6180
40	CAATTOONT	TCTCAACCCC	ACTTCACAGC	TATTCATACA	GCTCCCAAGA	CCCTAGACCT	6240
-10	COCACTOCTC	GTTTTCGGAG	ACCIGGAGCAG	CGGGACCCCA	CGGTGCATGA	TGATGTGCTG	6300
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	BACCACAMOC	ACACAACCCT	CAATCGGCAT GGGCCCGCCT	CARCONCARO	AGGATTCAGE	CCCAAGAGAT	6420
	ANGCACATGC	COMMONDATION	CCTCCATCCC	PARCECCE A	ATCCARTACT	ACCATTABAT	6480
45	CITCCTTCTT	GGATGAGATT	CCTCCTTGGC	AAACIGGGAA	ALCOMING:	ACCULTANTI	6540
73	ATCOGTCTCT	TCTTMGCCM	GCTTGTTATT	ANTACAGANG	AGGICITICG	GCCAAGAGAT ACCATTAAAT CCCTTACGGG AGGAGAAGGA CTTGGCCACT CCTAATGAAA AAAGACCCTT AAAGTTTTCCC CATCGTGATG ATACTTCCAG TGCAGCAGAA GGAGTCTCTG CAAGTTTATT CATGAATGCT CATGATTGTC CATGATTGTC CATGATTGTC CATGATTGTC CATGATTGTC CATGAATGCT	6600
	AAGCACTGGC	TTAGCCCCTT	GCTGCAGCTG	GCTGCTTCTG	AAAACAATGG	AGGAGAAGGA	6660
	ATTCACTACA	TGGTGGTTGA	GATAGTGGCC	ACTATTOTT	CATGGACAGG	CFFGGCCACT	6720
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50	CATGTCTTTC	ATCCAAAAAG	AGCTGTGTTT	AGACACAACC	TIGAAATTAT	AAAGACCCTT	6780
30	GTCGAGTGCT	GGAAGGATTG	TTTATCCATC	CCTTATAGGT	TAATATTTGA	AAAGTTTTCC	6840
	GGTAAAGATC	CTAATTCTAA	AGACAACTCA	GTAGGGATTC	AATTGCTAGG	CATCGTGATG	6900
	GCCAATGACC	TGCCTCCCTA	TGACCCACAG	TGTGGCATCC	AGAGTAGCGA	ATACTTCCAG	6960
	GCTTTGGTGA	ATAATATGTC	CTTTGTAAGA	TATAAAGAAG	TGTATGCCGC	TGCAGCAGAA	7020
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55	TGTGAACTGG	TTGCGAAACA	ATTGAAGCAA	CATCAGAATA	CTATGGAGGA	CAAGTTTATT	7140
	GTGTGCTTGA	ACAAAGTGAC	CAAGAGCTTC	CCTCCTCTTG	CAGACAGGTT	CATGAATGCT	7200
	GTGTTCTTTC	TGCTGCCAAA	ATTTCATGGA	GTGTTGAAAA	CACTCTGTCT	GGAGGTGGTA	7260
	CTTTGTCGTG	TGGAGGGAAT	GACAGAGCTG	TACTTCCAGT	TARAGAGCAA	GGACTTCGTT	7320
	CAAGTCATGA	GACATAGAGA	TGATGAAAGA	CAAAAAGTAT	GTTTGGACAT	CATGAATGCT GGAGGTGGTA GGACTTCGTT AATTTATAAG	7380
60	ATGATGCCAA	AGTTAAAACC	AGTAGAACTC	CGAGAACTTC	TGAACCCCGT	TGTGGAATTC	7440
	GTTTCCCCATC	CTTCTACAAC	ATGTAGGGAA	CARATGTATA	ATATTCTCAT	TGTGGAATTC GTGGATTCAT ATTTAAGTTG	7500
	GATAATTACA	GAGATCCAGA	AAGTGAGACA	GATAATGACT	CCCAGGAAAT	ATTTAAGTTG	7560
							7620
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65	CTARATTCO	TATATTOM	AACTAGGTTA TAAGATAGAA GAGCCCAGAT	GTGCACTTTT	TAACTTTACC	AACAAATTTT	7740
05	CIMMITCCI	man acrea	CACCOCACAT	MA MOCA A A OC	COMPORTOR	CCATCCTCTC	7800
	CIGCILGAAA	ADMICCACICAT	AMAGECCAGAT	Chimomoreum	COCCUMACO	AAGTACTGTT CCGTACCCAG CCAGCAGCAG	7860
	TCAGAATGCG	AATTTCAGGA	ATATACCATT	GATTCIGATI	GGCGTTTCCG	AAGIACIGII	
	CTCACTCCGA	TGTTTGTGGA	GACCCAGGCC	TUCCAGGGCA	CICTCCAGAC	COGTACCCAG	7920
70	GAAGGGTCCC	TCTCAGCTCG	CTGGCCAGTG	GCAGGGCAGA	TAAGGGCCAC	CCAGCAGCAG	7980
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	AGCAGCACTG	ACCCGCTGGT	CGACCACACC	AGTCCCTCAT	CTGACTCCTT	GCTGTTTGCC	8100
	CACAAGAGGA	GTGAAAGGTT	ACAGAGAGCA	CCCTTGAAGT	CAGTGGGGCC	TGATTTTGGG	8160
	AAAAAAAGGC	TGGGCCTTCC	AGGGGACGAG	GTGGATAACA	AAGTGAAAGG	TGCGGCCGGC	8220
	CGGACGGACC	TACTACGACT	GCGCAGACGG	TTTATGAGGG	ACCAGGAGAA	GCTCAGTTTG	8280
75	ATGTATGCCA	GANAAGGCGT	TGCTGAGCAA	AAACGAGAGA	AGGAAATCAA	GAGTGAGTTA	8340
-	AAAATGAAGC	AGGATGCCCA	COTCOTTCTG	TACAGAAGCT	ACCGGCACGG	AGACCTTCCT	8400
	GACATTCAGA	TCAAGCACAG	CAGCCTCATC	ACCCCGTTAC	AGGCCGTGGC	CCAGAGGGAC	8460
	CCAATAATTY	CAAAACACCT	CTTTAGCAGC	TIGITITICIG	GAATTTTGAA	GCTCAGTTTG GAGTGAGTTA AGACCTTCCT CCAGAGGGAC AGAGATGGAT	8520
	ADATTTARGA	CACTGTCTCA	AAAAAACAAC	ATCACTCAAA	AGTTGCTTCA	AGACTTCAAT TCAGGACATT TGGTTGCCTG CCGCCTGCTG	8580
80	California Communication of the Communication of th	ATACCACCOT	Calcaladadadada	CCACCCTTTC	TCTCTTGTAT	TCAGGACATT	8640
30	ACCRATEGIA	ACCCACCCTT	COTCARCOTT	CACCCACCC	CTCTTAGCCC	TEGTTECCT	8700
	MOCTOT CAGC	ACCIOCACCCT	CCCCARCCCTC	COCCORDO	AGGCTCTCCC	1001100010	8760
	CONSCIPAC	MUCHUCCOTT	GOGGATUCGC	COCCANCOCCO	CCCTCTGCT	TOPACTOCIO	
	CUTGCTGAGC	TGCCTGCCAA	GCGAGTCCGT	GGGAAGGCCC	SCITCULFOC	TGATGTCCTC CCTCCGTGGG AGCAGAAGCC	8820
85	AGATGGGTGG	AGCTTGCTAA	GCTGTATAGA	TCAATTGGAG	AATACGACGT	CUTCCGTGGG	8880
60	ATTTTTACCA	GTGAGATAGG	AACAAAGCAA	ATCACTCAGA	GIGCATTATT	AGCAGAAGCC	8940
	AGAAGTGATT	ATTCTGAAGC	TGCTAAGCAG	TATGATGAGG	CTCTCAATAA	ACAAGACTGG CCTTGACTGT	9000
	GTAGATGGTG	AGCCCACAGA	AGCCGAGAAG	GATTTTTGGG	AACTTGCATC	CCTTGACTGT	9060

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	CTGACATTTA	TTGACAAAGC	TATGCACGGG	GAGCTCCAGA	AGGCGATTCT	AGAGCTTCAT	9300
5	TACACTCAAC	AGCTGAGTCT	COTTACCTC	CTCCAAGATG	ATGTTGACAG	AGCCAAATAT	9360
_	TACAGICAAG	ATGGCATTCA	GCTTTACCTC	CI CLA A TOTAL TOTAL	OWN CONTROLS	TOTOTOTO	9420
	TACATTCAAA	ATGGCATTCA	GAGTTTTATG	CAGAATTATT	CIAGIATION	moreone control	9480
	CACCAAAGTA	GACTCACCAA	ATTGCAGTCT	GTACAGGCTT	TAACAGAAAT	TCAGGAGTTC	
	ATCAGCTTTA	TAAGCAAACA	AGGCAATTTA	TCATCTCAAG	TTCCCCCTTAA	GAGACITUIG	9540
	AACACCTGGA	CAAACAGATA	TCCAGATGCT	AAAATGGACC	CAATGAACAT	CTGGGATGAC	9600
10	ATCATCACAA	ATCGATGTTT	CTTTCTCAGC	AAAATAGAGG	AGAAGCTTAC	CCCTCTTCCA	9660
	CARGATANTA	GTATGAATGT	GGATCAAGAT	GGAGACCCCA	GTGACAGGAT	GGAAGTGCAA	9720
	CACCACCARAC	AAGATATCAG	CTCCCTCATC	AGGAGTTGCA	ACTITICCAT	DAADTAAAAD	9780
	CAGCAGGAGG	GTGCCCGGAA	CICCCIONIC	MOONOT FOOL	CONTRACTOR	BOTCH BOCKE	9840
	ATGATAGACA	AGTCAAAAAC	GCAGAACAAT	TICICACTIC	CIAIGMOCCI	Charmound	9900
15	CTGCATAAAG	AGTCAAAAAC	CAGAGACGAT	TUGCTGGTGA	GCIGGGIGCA	CHIGCIACIGC	
13	CGCCTGAGCC	ACTGCCGGAG	CCGGTCCCAG	GGCTGCTCTG	AGCAGGTGCT	CACTGIGGIG	9960
	AAAACAGTCT	CTTTGTTGGA	TGAGAACAAC	GTGTCAAGCT	ACTTAAGCAA	AAATATTCTG	10020
	GCTTTCCGTG	ACCAGAACAT	TCTCTTGGGT	ACAACTTACA	GGATCATAGC	GAATGCTCTC	10080
	ACCACTGACC	CAGCCTGCCT	TOCTOARATC	GAGGAGGACA	AGGCTAGAAG	AATCTTAGAG	10140
	ACCUSTORION OF THE PARTY OF THE	CCAGTTCAGA	COMMONONCAC	ANCOTONTOO	CCCCTCTCTA	CCAGAGAGCA	10200
20	CTTTCTGGAT	TCTCTGAGGC	MONTH CAUAG	AMOGIGATES	#CCCCC+CCC	TOCOTOCTO	10260
20	TTCCAGCACC	TCTCTGAGGC	TGTGCAGGCG	GCIGAGGAGG	AGGCCCAGCC	TCCCTCCTGG	10200
	AGCTGTGGGC	CTGCAGCTGG	GGTGATTGAT	GCTTACATGA	CGCTGGCAGA	TITCIGIGAC	10320
	CAACAGCTGC	GCAAGGAGGA	AGAGAATGCA	TCAGTTATTG	ATTCTGCAGA	ACTGCAGGCG	10380
	TATCCAGCAC	TTGTGGTGGA	GAAAATGTTG	AAAGCTTTAA	AATTAAATTC	CAATGAAGCC	10440
	AGATTGAAGT	TTCCTAGATT	ACTTCAGATT	ATAGAACGGT	ATCCAGAGGA	GACTTTGAGC	10500
25	CTCATCACAA	AAGAGATCTC	TTCCCTTCCC	TOCTOGCAGE	TOATCAGCTG	GATCAGCCAC	10560
23	* MOCORCOCO	TACTGGACAA	ACACCAACCC	CTTCCTCTC	ACCACTOTO	GGBAGBARTC	10620
	ATGGTGGCCT	ACCCGCAGGC	AGACCAAGCC	GIIGCIGIIC	MOCACICIGI	A A COMPA MECC	10020
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	TTCAAGGATA	CTTCTACTGG	TCATAAGAAT	AAGGAGTTTG	TGGCAAGGAT	TAAAAGTAAG	10740
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	******	ACATTGAAAA	AATOTATOTA	CYPATENTAADA	CAGCCTTGGG	TGACCCAAAG	10920
	GCTCCAGGCC	TGGGGGCCTT GGAAAGGAGG	TAGAAGGAAG	TTTATTCAGA	CTTTTGGAAA	AGAATTTGAT	10980
	A A COMMONT	CCANAGGAGG	TTCTAAACTA	CTCACAATCA	AGCTCAGTGA	CTTCAACGAC	11040
	AMACATITIG	GGANAGGAGG	IICIAACIA	**********	ACCOCCCCCCC	CRATCTCARA	11100
35	ATTACCAACA	TGCTACTTTT CCTGGATGAG	MOUNTGANG	AMMONCTON	MOCCCCCTGG	OWNICIONAL	11100
33	GAATGTTCAC	CCTGGATGAG	CUACTTCAAA	GTGGAGTTCC	TGAGAAATGA	GCTGGAGATT	11160
	CCCGGTCAGT	ATGACGGTAG	GGGAAAGCCA	TTGCCAGAGT	ACCACGTGCG	AATCGCCGGG	11220
	TTTGATGAGC	GGGTGACAGT	CATGGCGTCT	CTGCGAAGGC	CCAAGCGCAT	CATCATCCGT	11260
	GGCCATGACG	AGAGGGAACA	CCCTTTCCTG	GTGAAGGGTG	GCGAGGACCT	GCGGCAGGAC	11340
	CAGCGCGTGG	AGCAGCTCTT	CCAGGTCATG	AATGGGATCC	TGGCCCAAGA	CTCCGCCTGC	11400
40	*CCC*C*CCC	CCCTGCAGCT	CACCACCTAT	ACCOPTICATOR	CCATGACCTC	CAGGTTAGGA	11460
-10	MOCCHOROGO	GGCTTGAAAA	TACTOTTACC	TTGAAGGACC	TTCTTTTTTGAA	CACCATGTCC	11520
	TIMMIIGAGI	AGGCGGCTTA	COMO COMO CO	accar coccare	OCCUPATION.	AMBURARAGAT	11600
	CAAGAGGAGA	AGGCGGCTTA	CCTGAGTGAT	CCCAGGGCAC	CGCCGIGIGA	ATATAAAAA	11500
	TGGCTGACAA	AAATGTCAGG	AAAACATGAT	GTTGGAGCTT	ACATGCTAAT	GTATAAGGGC	TIPEO
	GCTAATCGTA	CTGAAACAGT	CACGTCTTTT	AGAAAACGAG	AAAGTAAAGT	GCCTGCTGAT	11700
45	CTCTTANAGC	GGGCCTTCGT	GAGGATGAGT	ACAAGCCCTG	AGGCTTTCCT	GGCGCTCCGC	11760
	TCCCACTTCG	CCAGCTCTCA	CGCTCTGATA	TGCATCAGCC	ACTGGATCCT	CGGGATTGGA	11820
	GACAGACATC	TGAACAACTT	TATGGTGGCC	ATGGAGACTG	GCGGCGTGAT	CGGGATCGAC	11880
	MARCOCCATO	CGTTTGGATC	CCCTACACAG	TTTCTGCCAG	TOCCTGAGTT	GATGCCTTTT	11940
	11100000010	GCCAGTTTAT	COCTACATON CO	mma cca a mca	BACABACCCC	CCTTATCTAC	12000
50	CGGCTAACTC	TACACGCACT	CARICIGATO	TIMECAMIGA		GL GGL LGLAG	12000
20	AGCATCATGG	TACACGCACT	CCGGGCCTTC	CGCTCAGACC	Croscerser	CACCAACACC	12060
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	AAAAAAGGAG	GGTCATGGAT	TCAAGAAATA	AATGTTGCTG	AAAAAAATTG	GTACCCCCGA	12180
	CAGAAAATAT	GTTACGCTAA	GAGAAAGTTA	GCAGGTGCCA	ATCCAGCAGT	CATTACTTGT	12240
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55	COLCONACCA	AAGATCACAA	CATTOGTGCC	CAACAACCAG	AGAGTGGGCT	TTCAGAAGAG	12360
23	CONGONNOCN	AGTGCCTGAT	CALLCOLOGG	*************	N CAMOCOMOCO	CACAACCTCC	12420
	ACTCAAGTGA	AGCCCTGGAT	GONCONGCO	magan cooms	GRANGE CELL	COMMERCATO	12490
	GAAGGATGGG	AGCCCTGGAT	GTGAGGTCTG	TOGGAGICIG	CHGATAGAAA	GCATIACATI	12460
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	TOATCAGCTT	TCAAAGCATT	TACAACTGCT	CCAAGTTAGT	GAAACAGCTG	TCTCCGTAAA	12780
	magacan and	GTGGGGAAGC	CTTCCA ATCC	CONTONOR	CTCCCACATT	CCAAACCACA	12840
	TOGAGGAAAA	TTCATCACCA	2020000000	**********	TANGTATAGT	TOATOTAACA	12900
65	CICAGAAGGC	TICATCACCA	AGAL ITTGGG	MUMU TANAGE	IMMGTATAGI	TOUTOTOUCK	12300
03	TTGTAGAAGC	AGCATAGGAA	CAATAAGAAC	AATAGGTAAA	GCTATAATTA	TOGCTTATAT	14960
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	CATACATAAA	AGTGCTTTGC	ATTCAATTTC	GGATAACTTC	AAAAATCCCA	TOGTTOTTGT	13200
70	GULACATAOA	ACTAAGCATT	man connected	CACRATARA	CARACTECCTA	TTTYZABATYZA	13260
70	INGGGATAGT	TGGAGGAAAA	- CAULLCCAU	- COUNTY AND	DOMESTICCIA	ATTATOTA -	13330
	ATTCCTCATT	TGGAGGAAAA	AAAGCATGCA	TICTAGCACA	ACANGATGAA	ALIATUGAAT	13350
	ACAAAAGTGG	CTCCTTCCCA	TGTGCAGTCC	CIGICCCCCC	CCGCCAGTCC	TUCACACCCA	T3380
	AACTGTTTCT	GATTGGCTTT	TAGCTTTTTG	TIGITITIT	TTTTCCTTCT	AACACTTGTA	13440
	TTTGGAGGCT	CTTCTGTGAT	TTTGAGAAGT	ATACTCTTGA	GTGTTTAATA	AAGTTTTTTT	13500
75	CCAAAAGTA						

Seq ID NO: 99 Protein sequence:

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80		11	21	31	41	51	
	ī	ī	ī	1	1	1	
	MAGSGAGVRC	SLLRLOETLS	AADROGAALA	GHOLIRGIGO	ECVLSSSPAV	LALQTSLVFS	60
	RDFGLLVFVR	KSLNSIEFRE	CREETLKFLC	IPLEKMGQKI	APYSVEIKNT	CTSVYTKDRA	120
	AKCKIPALDL	LIKLLOTERS	SRLMDEPKIG	ELFSKFYGEL	ALKKKIPDTV	LEKVYELLGL	180
85	LGEVHPSEMI	NNAENLPRAP	LGELKTOMTS	AVREPKLPVL	AGCLKGLSSL	LCNPTKSMEE	240
	DPOTSREIFN	PVLKAIRPOI	DLKRYAVPSA	GLRLFALHAS	QFSTCLLDNY	VSLPEVLLKW	300
	CAUTAINET NY	BALCAL POPT.	KUAGNWAYM	ARMHENKLOY	PMROFYGIIR	NVDSNNKELS	360

	IAIRGYGLFA	GPCKVINAKD	VDPMYVRLIO	RCKOMPLTOT	DTGDDRVYOM	PSFLOSVASV	420
		YTPVLEHLVV					480
		CSKPVVLPKG					540
		FSVNSSSESL					600
5		NLHPAKPKDF					660
,							720
		SITVRNAKKI					
		TPLLSLPHNI					780
		DILPCLDGYL					840
		IRIRVVQMLG					900
10	MKPV I PLDVP	LPRVTELALT	ASDROTKVAA	CELLHSMVMF	MLGKATOMPE	GGQGAPPMYQ	960
	LYKRTPPVLL	RLACDVDOVT	ROLYEPLVMO	LIHWPTNNKK	PESQDTVALL	EAILDGIVDP	1020
		RCIREPLKWS					1080
	APPRITATED	EEESLVEOFV	PRALUTYMES	LALAHADEKS	LGTTOOCCDA	TOHT-CRITEK	1140
		RRLPRGFPPS					1200
15	MINDENOUS.	VLKEEGVSFL	ASSCRIPTION	ODGGGTI LODG	TAUT DODGE	OME ON DEL	1260
13	NKSPNLWLKD	IGERTVGALQ	INTERGOGCG	QPSGILMQPI	LLILEGPPSL	CALICAPORT	1320
		NYSKCTVVVR					1380
		VMAHLPDVCV					1440
	AQVDRSRLAA	VVSACKQLHR	AGLLHNILPS	QSTDLHHSVG	TELLSLVYKG	IAPGDERQCL	1500
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		LLKNLDLAVL					1620
	TILOHWKKCD	SWWAKDSPLE	TKMAVLALLA	KILOIDSSVS	FNTSHGSFPE	VFTTYISLLA	1680
		QAVILLPPPT					1740
		ELSOS PMLLE					1800
25		RLSFTROSFV					1860
		MGYYKILDVM					1920
		NOLLERRRLY					1980
	DAFTENMAGE	PVEVEVPMER	aconincats	VICCVPNBDR	CDCIOCOCT CV	PERMUUTEN	2040
	PIDPKKKKND	PARABANEK	KKKYIBIKKB	AKEAAMGUSD	GPSIMSSLSI	DOSTUSEEN	
30	SQFDFSTGVQ	SYSYSSQDPR	PATGRPRRRE	CKDPLAHDDA	PEPEMBERNS	HECMAPLITAL	2100
30	VKHMHRSLGP	POGEEDSVPR	DLPSWMKFLH	GKLGNPIVPL	NIRLPLAKEV	INTEEVERPY	2160
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	KHVFHPKRAV	PRHNLEIIKT	LAECAKDCF3	IPYRLIFEKF	SCKOPNSKON	SVGIQLLGIV	2280
	MANDLPPYDP	QCGIQSSEYF	VERMINVLAO	RYKEVYAAAA	EVLGLILRYV	MERKNILEES	2340
	LCELVAKQLK	QHQNTMEDKF	IVCLNKVTKS	FPPLADRFMN	AVFFLLPKFR	GVLKTLCLEV	2400
35	VLCRVEGMTE	LYFOLKSKDF	VOVMRHRDDE	ROKVCLDIIY	KMMPKLKPVE	LRELLNPVVE	2460
	PUSHDSTTCP	EQMYNILMWI	HONVROPESE	TONDSOFTEK	LAKDVLIOGL	IDENEGROLI	2520
	TONDWCUCTO	LPSNTLDRLL	ALMST-VSDET	EVERTISTATIV	PLUENTSMSP	DYPNPMPERP	2580
	LODODDODVA	IDSDWRFRST	THE TOMPTOTO	A COCTL OFFT	OPCCI.CARWD	VACOTRATOO	2640
	OUDDET TOWN	DGRSSPDWLT	COCCEDE AND	Tencenerin	PRESENTATION	PDIACOUCEDE	2700
40		EVDNKVKGAA					2760
70							2820
		LYRSYRHGDL					
		NITOKLLODE					2880
	LASLQQPVGI	RLLEEALLRL	LPAELPAKRV	RGKARLPPDV	LRWVELAKLY	RSIGEYDVLR	2940
	GIFTSEIGTK	QITQSALLAB	ARSDYSEAAK	QYDEALNKQD	WVDGEPTEAR	KDFWELASLD	3000
45		LEYCSTASID					3060
		GELQKAILEL					3120
	LHOSRLTKLQ	SVQALTEIQE	PISPISKQGN	LSSQVPLKRL	LNTWINRYPD	AKMOPMNIWD	3180
	DIITNRCFFL	SKIEEKLTPL	PEDNSMNVDQ	DGDPSDRMEV	QEQUEDISSL	IRSCKPSMKM	3240
	KMIDSARKON	NESLAMKLLK	ELHKESKTRD	DWLVSWVQSY	CRLSHCRSRS	QGCSEQVLTV	3300
50	LETURLICIEN	NVSSYLSKNI	LAPRDONTLI.	GTTYRIIANA	L-SSEPACLAR	IEEDKARRIL	3360
••		EKVIAGLYOR					3420
	DOOL DADEDA	ASVIDSAELQ	PADDITIONERM	TABLETHENE	PBI'KEBBI'IU	TIEDVDEETI.	3480
	er remembrasen	PCWQFISWIS	WILLIAM LANDO	PATRICALCATED	TEDATEDOSTU	VNUTTOCKEV	3540
	SUMIKSISSV	NKEFVARIKS	MANAGEDROO	AAVERDVAN	TIDRITECATA	DIMANUAL TO	3600
55							
"		ERMYAALGDP					3660
		NKDSKPPGNL					3720
	GFDERVTVMA	SLRRPKRIII	RGHDEREHPP	LVKGGEDLRQ	DÜKARÖFLÖA	MNGILAQDSA	3780
		YSVVPMTSRL					3840
	DWLTKMSQKH	DVGAYMLMYK	GANRTETVTS	FRKRESKVPA	DLLKRAPVRM	STSPEAFLAL	3900
60		ICISHWILGI					3960
						FDWKNFEQKM	4020
		INVAEKNWYP					4080
	ARGSKOHNTR	AQEPESGLSE	ETOVKCLMDO	ATDPNILGRT	WEGWEPWM		
65							

65 Seq ID NO: 100 DNA sequence Nucleic Acid Accession #: NM_000673

	Coding seq	ience: 10	1-1225				
70	1	11 ·	21 	31 	41	51 1	
	ATGTGAAGGC	ACAAGCTG	CT GTTATATAC	A ACAGAGTGAA	CTGAGCATCA	GTCAGAAAAA	60
	GTCTATGTTT	GCAGAAAT	AC AGATCCAAG	A CAAAGACAGG	ATGGGCACTG	CTGGAAAAGT	120
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	AGAAGTTGCC	CCACCAAA	GA CTARAGARG	T TCGCATTAAG	ATTTTGGCCA	CAGGAATCTG	240
75	TOGCACAGAT	GACCATGT	GA TAAAAGGAA	C AATGGTGTCC	AAGTTTCCAG	TGATTGTGGG	300
			TG TAGAGAGCA				360
	TGACAAAGTC	ATCCCTCT	CT TTCTGCCAC	A ATGTAGAGAA	TGCAATGCTT	GTCGCAACCC	420
			TA GGAGCGATA				480
	CACCAGATTT	ACATGCAA	GG GCAAACCAG	T ACACCACTTC	ATGAACACCA	GTACATTTAC	540
80	CGAGTACACA	GTGGTGGA	TG AATCTTCTG	T TGCTAAGATT	GATGATGCAG	CTCCTCCTGA	600
			CT GTGGGTTTT				660
	CAAGGICAAA	CCTGGTTC	CA CTTGCGTCG	T CTTTGGCCTG	GGAGGAGTTG	GCCTGTCAGT	720
			AG CTGGTGCAT				780
0.5			GG CTGTAGGTG				840
85			GC TGTCAGAAA				900
			AA CCATGATTG				960
	GACCAGCCTV	GTTGTAGG	AG TICCICCAT	C AGCCAAGATG	CYCACCTATG	ACCCGATGTT	1020

		000445					
	GCTCTTCACT	GGACGCACAT	GGAAGGGATG	TGTCTTTGGA	GGTTTGAAAA	GCAGAGATGA	1080
	TOTCCCAAAA	CTAGTGACTG	AGTTCCTGGC	AAAGAAATTT	GACCTGGACC	AGTTGATAAC	1140
	TCATGTTTTA	CCATTTAAAA	AAATCAGTGA TTTGAGATCC	AGGATTTGAG	CTGCTCAATT	CAGGACAAAG	1200
5	CARCECCACE	TTOTOTOTO	ACACTTCCCT	CATCTGAAAT	CATCTATCTC	TOTCACABAT	1320
	ACABGCATAA	GTAGAAGATT	TGTTGAAGAC	ATAGAACCCT	TATAAAGAAT	TATTAACCTT	1380
	TATAAACATT	TAAAGTCTTG	TGAGCACCTG	GGAATTAGTA	TAATAACAAT	GTTAATATTT	1440
	TTGATTTACA	TTTTGTAAGG	TGAGCACCTG CTATAATTGT	ATCTTTTAAG	AAAACATACA	CTTGGATTTC	1500
10							1560
10	CAGATATAGC	GTATAAAGAT	ATAGTAAATG ATTTGAATAT	CATCTCCCAG	AGTAATATTC	ACTTAACACA	1620
	TIGAAACTAT	TATTTTTTAG	AATCAGTTCA	TOCATCATC	CATATTACTO	CATTACATTA	1740
	BGBBBGBCBG	ABABGATTAA	GGGACGGGCA	CATTTTTCAA	CHIATTANGAA	TCATCATTAC	1800
	ATAACTTGGT	GAAACTGAAA	GGGACGGGCA AAGTATATCA	TATGGGTACA	CAAGGCTATT	TGCCAGCATA	1860
15	TATTATTATT	TTACAAAATA	THEFT	AATACTGAAT	DATABACATAG	AGCTAGAGTC	1920
	ATATTATCAT	ACTTATCATA	ATGTTCAATT GTGACTCCAT	TGATACAGTA	GAATTGCAAG	TCCCTAAGTC	1980
	CCTATTCACT	GTGCTTAGTA	GTGACTCCAT	TTAATAAAA	GTGTTTTTAG	TTTTTAACAA	2040
	CTAAACCG						
20	n vn vn.	101 Protein					
20	Brotein Acc	ession #: N	D 000664				
	PIOCEIN ACC	caaton w. r					
	1	11	21	31	41	51	
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25	MGTAGKVIKC	KAAVLWEQKQ	PFSIEBIEVA	PPKTKEVRIK	ILATGICATO	DHVIKGTMVS	60
	KPPVIVGHEA	TGIVESIGEG	VTTVKPGDKV	IPLPLPQCRE	CNACRNPDGN	LCIRSDITGR	120 180
	GVLADGTTRP	TCKGKPVHHP	MNTSTPTEYT GGVGLSVIMG	OVOESSVAKI	DDAAPPEKVC	LIGCOPSIGY	240
	TOPKNOTERI	SEVI-SEMTGN	NVGYTFEVIG	HLETMIDALA	SCHWINGTSV	VVGVPPSAKM	300
30	LTYDDMLLET	GRTWKGCVPG	GLKSRDDVPK	LVTEPLAKKE	DLDOLITHVL	PFKKISEGFE	360
	LLNSGQSIRT	VLTP					
	Seq ID NO:	102 DNA 600	quence				
35	Nucleic Ac	ld Accession	#: NM_0067	83.1			
33	Coding sequ	ence: 176	36				
		11	21	31	41	51	
	ī	1	ī	ĭ	i	ĭ	
	ATGGATTGGG	GGACGCTGCA	CACTITICATO	GGGGGTGTCA	ACAAACACTC	CACCAGCATC	60
40	GGGAAGGTGT	GGATCACAGT	CATCTTTATT GCAAGAGGAC	TTCCGAGTCA	TGATCCTAGT	GGTGGCTGCC	120
	CAGGAAGTGT	GGGGTGACGA	GCAAGAGGAC	TTCGTCTGCA	ACACACTGCA	ACCGGGATGC	180
	AAAAATGTGT	GCTATGACCA	CTTTTTCCCCG	GTGTCCCACA	TCCGGCTGTG	GGCCCTCCAG	240
	CTGATCTTCG	TCTCCACCCC	AGCGCTGCTG	GTGGCCATGC	ATGTGGCCTA	CTACAGGCAC	300 360
45	GARACCACTC	GCAAGTTCAG	GCGAGGAGAG GATAGAGGGG	AAGAGGAATG	ATTTCAAAGA	CATAGAGGAC	420
43	ATTAAAAAGC	ACAAGGTTCG	ACCACCCCTTT	TCGCIGIGGI	TOTAL CTTCCT	TTECANTOCC	480
	TACCACCICC	CCTCCCTCTT	AGCAGCCTTT GAAATGTGGG	ATTGACCCCT	GCCCCAACCT	TGTTGACTGC	540
							600
	ATTTGCATGC	TGCTTAACGT	GGCAGAGTTG GCAAAAAAAT	TGCTACCTGC	TGCTGAAAGT	GTGTTTTAGG	660
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	CAGAATGAAA	TGAATGAGCT	GATTTCAGAT	AGTGGTCAAA	ATGCAATCAC	AGGTTTCCCA	780
	AGCTAA						
55	Seq ID NO:	103 Protein cession #: 1	sequence:				
33	Procein Ac	session #: 1	WP_006//4.1				
	1	11	21	31	41	51	
	ī	1	1	1	1	Ī	
	MDWGTLHTFI	GGVNKHSTSI	ĠKVWITVIFI	PRVMILVVAA	QEVWGDEQED	PVCNTLOPGC	60
60	KNVCYDHFFP	VSHIRLWALQ	LIFVSTPALL	VAMHVAYYRH	ETTRKFRRGE	KRNDFKDIED	120
	IKKHKVRIEG	SLWWTYTSSI	PFRIIPEAAP	MYVFYFLYNG	YHLPWVLKCG	IDPCPNLVDC HPNHALKESK	180
	FISRPTEKTV	PTIPMISASV SGQNAITGPP	ICMLLINVAEL	CYLLLKYCFR	RSKRAQTQKN	HPNHALKBSK	240
	GNEWNET I 2D	SGUNALTGPP	5				
65	Seg ID NO:	104 DNA sec	quence				
	Nucleic Ac	id Accession	1 #: NM_0204	11			
	Coding seq	uence: 86-5:	26				
						51	
70	1	11	21	31	41	27	
70	COLOGOGGG	1 NGCNGCNTNG	GACAGGGCAA	GGCGGGATAA	GUNGGGGGG	CACAGOCCOM	60
	AACCOACCAC	CONNECTED	TGCGCATGCT	CCTTTCGTGC	CCACCTCAGT	GCGCATGTTC	120
	ACTIGOGGGGGG	TTCCCATCGG	CCCCTTCCCC	AGTGTGGGGA	ACGCGGCGGA	GCTGTGAGCC	180
	GGCGACTCGG	GTCCCTGAGG	TCTGGATTCT	TTCTCCGCTA	CTGAGACACG	GCTGTGAGCC GCGGACACAC	240
75	ACAAACACAG	AACCACACAG	CCACTCCCAG	GAGCCCAGTA	ATGGAGAGCC	CCAAAAAGAA	300
	GBACCAGCAG	CTICALAGTICG	GGATCCTACA	CCTGGGCAGC	AGACAGAAGA	AGATCAGGAT	360
	ACAGCTGAGA	TCCCAGTGCG	CGACATGGAA	GGTGATCTGC	AAGAGCTGCA	TCAGTCAAAC	420
	ACCGGGGATA	AATCTGGATT	TGGGTTCCGG	CUTCAAGGTG	AAGATAATAC	CTAAAGAGGA	480 540
80	ACACTGTAAA	A TGCCAGAAG	ATATTROAT	THE TOTAL CHARACTERS A	ACTATOTOS	AGACAAGCTG TAAAGTTTTG	600
00		CAAAAAAAA		unciinn			
	CACITICAL	CAMMANA					
	Seq ID NO:	105 Protei	n sequence:				
85	Protein Ac	cession #: 1	NP_065144.1				
	1		21	31	41	51	
		11	41	31	**	31	

	. 11 0 02/	080443					
5	PRSPVMESPK	CSLGVFPSAP KKNQQLRVGI EEHCKMPEAG	LHLGSRQKKI	 EPATRVPEVW RIQLRSQCAT	MKAICKSCIS ITSETTEHGG	HTQTQNHTAS QTPGINLDLG	60 120
3	Nucleic Ac	106 DNA sec id Accession Lence: 99-58	#: J04129				
10	1 CATCCCTCTG	11 GCTCCAGAGC CGTGGCCCTG	21 TCAGAGCCAC	31 CCACAGCCGC	41 AGCCATGCTG	51 TGCCTCCTGC	60 120
15	AGACCTGGA ACATCTCCCT CCACCCCGA AGAAGAAGGT TGGCGAACGA	GCTCCCAAAG CATGGCGACA GGACAACCTG CCTTGGAGAG GGCCACGCTG	TTGGCAGGGA CTGAAGGCCC GAGATCGTTC AAGACTGGGA CTCGATACTG	CCTGGCACTC CTCTGAGGGT TGCACAGATG ATCCAAAGAA ACTACGACAA	CATGGCCATG CCACATCACC GGAGAACAAC GTTCAAGATC TTTCCTGTTT	GCGACCAACA TCACTGTTGC AGCTGTGTTG AACTATACGG CTCTGCCTAC	180 240 300 360 420
20	AGGACACCAC AGGACGATGA GGTACTTGCT CCAGGAAGAC TTTCAAAGAA	CACCCCATC GATCATGCAG GGACTTGAAA CAGACTCCCA TAACCACAGC	CAGAGCATGA GGATTCATCA CAGATGGAAG CCCTTCCACA TCAGAAGACG	TGTGCCAGTA GGGCTTTCAG AGCCGTGCCG CCTCCAGAGC ATGACGTGGT	GCCCTGCCC TTTCTAGCTC AGTGGGACTT CATCTGTGTC	AGGCACCTAT ACCTCCGCCT CCTCCTGCCC GCCATCCCCT	480 540 600 660 720
25	TCCTGCTGCA GCAGAGGTTA	CACCTGCACC	ATTGCCATGG CTTGGAGCAT	GGAGGCTGCT G	CCCTGGGGGC	AGAGTCTCTG	780
30	Protein Ac	107 Protein	RAA60147				
	1	11	21 	31	41 	51	
35	WENNSCVEKK	ELPKLAGTWH VLGEKTGNPK EIMQGPIRAF	KFKINYTVAN	EATLLDTDYD	NFLFLCLQDT	EDNLEIVLHR TTPIQSMMCQ	60 120
40	Nucleic Ac	108 DNA sec id Accession uence: 48-7	n #: Eos se	quence			
-10	1	11	21	31	41	51	
	1	CAGTTAGCCC	1	1			60
	GTCTGATCCA	GAAGGCCAAG	CTGGCAGAGC	AGGCCGAACG	CTATGAGGAC	ATGGCAGCCT	120
45	TCATGAAAGG	CCCCGTGGAG	AAGGGCGAGG	AGCTCTCCTG	CGAAGAGCGA	AACCTGCTCT	180
45	TCATGAAAGG	CGCCGTGGAG	AAGGGCGAGG GTGGGCGGCC	AGGGGGGGGG	CTGGAGGGTG	CTGTCCAGTA	180 240
45	TCATGARAGG CAGTAGCCTA TTGAGCAGAA GGGAGAAGGT	CGCCGTGGAG TAAGAACGTG AAGCAACGAG GGAGACTGAG	AAGGGCGAGG GTGGGCGGCC GAGGGCTCGG CTCCAGGGCG	AGGEGGTGC AGGAGAAGGG TGTGCGACAC	CGAAGAGCGA CTGGAGGGTG GCCCGAGGTG CGTGCTGGGC	CTGTCCAGTA CGTGAGTACC CTGCTGGACA	180
	TCATGAAAGG CAGTAGCCTA TTGAGCAGAA GGGAGAAGGT	CGCCGTGGAG TAAGAACGTG AAGCAACGAG GGAGACTGAG	AAGGGCGAGG GTGGGCGGCC GAGGGCTCGG CTCCAGGGCG	AGCTCTCCTG AGAGGGCTGC AGGAGAAGGG TGTGCGACAC AGAGCYGGGT	CGAAGAGCGA CTGGAGGGTG GCCCGAGGTG CGTGCTGGGC	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGAAGG	180 240 300 360 420
50	TCATGAAAGG CAGTAGCCTA TTGAGCAGAA GGGAGAAGGT	CGCCGTGGAG TAAGAACGTG AAGCAACGAG GGAGACTGAG	AAGGGCGAGG GTGGGCGGCC GAGGGCTCGG CTCCAGGGCG	AGCTCTCCTG AGAGGGCTGC AGGAGAAGGG TGTGCGACAC AGAGCYGGGT	CGAAGAGCGA CTGGAGGGTG GCCCGAGGTG CGTGCTGGGC	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGAAGG	180 240 300 360 420 480
	TCATGAAAGG CAGTAGCCTA TTGAGCAGAA GGGAGAAGGT GCCACCTCAT GTGACTACTA ACTCAGCCCG CCAACCCCAT	CGCCGTGGAG TANGAACGTG AAGCAACGAG GGAGACTGAG CAAGGAGGCC CCGCTACCTG GTCAGCCTAC CCGCCTAGCTG	AAGGGCGAGG GTGGGCGGCG GAGGGCTCGG GTCAGGGCG GCGAGGTCG CAGGAGGCCA CTGGCCCTGA	AGCTCTCCTG AGAGGGCTGC AGGAGAAGGG TGTGCGACAC AGAGCCGGGT CCACCGGTGA TGGACATCAG ACTTTTCCGT	CGAAGAGCGA CTGGAGGTG GCCCGAGGTG CGTGCTGGGC CTTCTACCTG CGACAAGAAG CAAGAAGAG CTTCCACTAC	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGAAGG CGCATCATTG ATGCCGCCCA GAGATCGCCA	180 240 300 360 420 480 540
	TCATGARAGG CAGTAGCCTA TTGAGCAGAA GGGAGAAGGT GCCACCTCAT GTGACTACTA ACTCAGCCCG ACACCCCAT ACAGCCCCCAT	CECCTGGAG TANGANCTG ANGCANCGAG GGAGACTGAG CANGGAGGCC CCGCTACCTG GTCAGCCTAC CCGCTGGGC GGAGGCCATC	AAGGGCGAGG GTGGGCGCC GAGGGCTCGG CTCCAGGGCG GGGGACGCCG GCCGAGGTGG CAGGAGGCCA CTGGCCCTGA TCTCTGGCCA	AGTOTICETG AGAGGGCTGC AGGAGAAGGG TGTGCGACAC AGAGCCGGTGA TGGACATCAG ACTTTTCCGT AGACCACTTT	CGAAGAGCGA CTGGAGGTG GCCCGAGGTG CGTGCTGGGC CTTCTACCTG CGACAAGAAG CAAGAAGAG CTTCCACTAC CGACGAGGCC	ARCCIGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA ARGATGAAGG CGCATCATTG ATGCCGCCA ARGATGACCA ATGGCTGATC	180 240 300 360 420 480 540 600
50	TCATGARAGG CAGTAGCCTA TTGAGCAGAA GGGAGAAGGT GCACCTCAT GTGACTACTA ACTCAGCCCG CCAACCCCAT ACAGCCCGGA TGCACACCCTAT	CGCCGTGGAG TARGAACGTG AAGCAACGAG GGAGACTGAG CAAGGAGGCC CCGCTACCTG GTCAGCCTAC GGCCTACCTG GGAGGCCATC CAGCGAGGCCATC CAGCGAGGCCATC CAGCGAGGAGAC	AAGGCCAGG GTGGGCGCG GAGGCTCGG GCGAGGCCG GCCGAGGTCG CAGGAGGCCA TCTCTGGCCCA TCTCTGGCA TCTCTGGCA	AGCTCTCCTG AGAGGGCTGC AGGAGAAGGG TGTGGGACAC AGAGCCGGGT CCACCGGTGA TGGACATCAG ACTTTTCCGG AGACCACTTT AGACCACTTT ACAGCACCCCT	CGAAGAGCGA CTGGAGGGTG GCCCGAGGTG CCTGCTGGGC CTTCTACCTG CGACAAGAAG CAAGAAGAAG CTTCCACTAC CGACGAGGCC CATCATGCAG	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGAAGG CGCATCATTG ATGCCGCCCA GAGATCGCCA AAGGCTGATC CTGCTGCGAG	180 240 300 360 420 480 540
	TCATGRAGG CAGTAGCCTA TTGAGCAGAA GGGAGAAGGT GCCACCTCAT GTGACTACTA ACTCAGCCCG ACACCCCTA ACACCCCGA TGCACACCCT ACAACCTGAC	CECCSTGGAG TARGAACGTG AAGCAACGAG GGAGACTGAG CAAGGAGGCC CCGCTACCTG GTCAGCCTAC CCGCCTGGGC GGAGGCCATC CAGCGAGGAC ACTGTGGAC ACTGTGTGTG	AAGGCGAGG GTGGCGGCC GAGGGCTCGG CTCCAGGGCG GCGAGGTGG CAGGAGGCCA CTGGCCTGA TCTCTGGCA TCTTACAAG GCCGACAACG CCCGCCACCG	AGCTCTCCTG AGAGGGCTGC AGAGGAGGG TGTGCGACAC AGAGCCGGGT CGACATCAG ACTTTTCCGT AGACCACTTT ACAGCACCT CCGGGGGAAG CCCCGGGGGAAG CCCCGGCGCAG	CGAAGAGCGA CTGGAGGGTG GCCGAAGGTG CGTGCTGGGC CTTCTACCTG CGACAAGAAG CAAGAAGGAG CTTCCACTAC CGACGAGGGCC CATCATGCAG GGGGGGGGAG CCCCCTCCAG	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGAAGG CGCATCATTG ATGCCGCCA ATGCTGATC ATGCCGCA ATGGCTGATC CTGCTGCGAG GCTCCCCAGG GCTCCCCAGC	180 240 300 360 420 480 540 600 720 780 840
50	TCATGRAGG CAGTAGCCTA TTGAGCAGAA GGGAGAAGGT GCCACCTCAT GTGACTACTA ACTCAGCCCG ACACCCCTA ACACCCCGA TGCACACCCT ACAACCTGAC	CECCSTGGAG TARGAACGTG AAGCAACGAG GGAGACTGAG CAAGGAGGCC CCGCTACCTG GTCAGCCTAC CCGCCTGGGC GGAGGCCATC CAGCGAGGAC ACTGTGGAC ACTGTGTGTG	AAGGCGAGG GTGGCGGCC GAGGGCTCGG CTCCAGGGCG GCGAGGTGG CAGGAGGCCA CTGGCCTGA TCTCTGGCA TCTTACAAG GCCGACAACG CCCGCCACCG	AGCTCTCCTG AGAGGGCTGC AGAGGAGGG TGTGCGACAC AGAGCCGGGT CGACATCAG ACTTTTCCGT AGACCACTTT ACAGCACCT CCGGGGGAAG CCCCGGGGGAAG CCCCGGCGCAG	CGAAGAGCGA CTGGAGGGTG GCCGAAGGTG CGTGCTGGGC CTTCTACCTG CGACAAGAAG CAAGAAGGAG CTTCCACTAC CGACGAGGGCC CATCATGCAG GGGGGGGGAG CCCCCTCCAG	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGAAGG CGCATCATTG ATGCCGCCA ATGCTGATC ATGCCGCA ATGGCTGATC CTGCTGCGAG GCTCCCCAGG GCTCCCCAGC	180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	TCATGARAGG CAGTAGGCTA TTGAGCAGAA GGGAGAAGGT GCACCTCAT GTGACTACTA ACTCAGCOCG CCAACCCCAT ACACCCCAT ACACCCTGAC AGCCCCAGAG TGCCCAGAGG CTCCCAAGGG CTCCCAAGGG CACCCTGTCC	CSCCSTGGAG TANGANCTIC ANGCANCIANG GAGANCTAGG GAGANCTAGG CANGGAGCC CCGCTACCTIG GTCAGCCTAC CCGCTCTGGGC GGAGGCCATC CAGCAGGAGA ACTGTGGACG CTGAGTGTTG ACTAGTATAGG CTCCGTGGAG CGAGCTGTTG	AAGGCGAGG GTGGGCGGG GAGGCTCGG GCCGAGGGG GCCGAGGTGG CAGAAGCCA CTGCCCAAAAG CCCAACAAAG CCCGCAAAAG CCCGCAACAG AGGACTGG	AGCTCTCCTE AGAGGGCTGC AGGAGAAGGG TGTGGGACAC AGAGCCGGGT CCACCGGTGA AGACCACCTT ACAGCACCCT CCGGGGAAGA CCCCGCCCTG CCACCCTTC AGAGCACCTTC AGAGCACCTTC AGAGCACCTTC AGAGCTGAGA ACCACTTGCACCTTC AGAGCTGAGA ACCACTGGTAC AGAGCTGGTA	CGARGAGCGA CTGGAGGGTG GCCCGAGGTG GCCCGAGGTG CGTGCTGCGC CGACAAGAAG CAAGAAGAG CTTCCACTAC CGACGAGGCC CAT CATCCAG CCCCTCCAG TCCCCTAGGC CCCCTCCAG ATGCCCCCAC ATGCCCCAGGA ATGCCCCCAC	AACCTGCTCT CTGTCCAGTA CGTGGGTACA AAGATGAAGG CGCATCATTG ATGCCCCA GAGATCGCCA ATGGCTGATC CTGCCGAG GCTCCCCAGG GCTGCCCAGG CCCGCTGTTCTTG CCCCGGGGATCC CCCTGCTTCTTC	180 240 300 360 420 420 540 660 720 780 840 900 900 91020
50	TCATGARAGG CAGTAGGCTA TTGAGCAGAA GGGAGAAGGT GCACCTCAT GTGACTACTA ACTCAGCOCG CCAACCCCAT ACACCCCAT ACACCCTGAC AGCCCCAGAG TGCCCAGAGG CTCCCAAGGG CTCCCAAGGG CACCCTGTCC	CSCCSTGGAG TANGANCTIC ANGCANCIANG GAGANCTAGG GAGANCTAGG CANGGAGCC CCGCTACCTIG GTCAGCCTAC CCGCTCTGGGC GGAGGCCATC CAGCAGGAGA ACTGTGGACG CTGAGTGTTG ACTAGTATAGG CTCCGTGGAG CGAGCTGTTG	AAGGCGAGG GTGGGCGGG GAGGCTCGG GCCGAGGGG GCCGAGGTGG CAGAAGCCA CTGCCCAAAAG CCCAACAAAG CCCGCAAAAG CCCGCAACAG AGGACTGG	AGCTCTCCTE AGAGGGCTGC AGGAGAAGGG TGTGGGACAC AGAGCCGGGT CCACCGGTGA AGACCACCTT ACAGCACCCT CCGGGGAAGA CCCCGCCCTG CCACCCTTC AGAGCACCTTC AGAGCACCTTC AGAGCACCTTC AGAGCTGAGA ACCACTTGCACCTTC AGAGCTGAGA ACCACTGGTAC AGAGCTGGTA	CGARGAGCGA CTGGAGGGTG GCCCGAGGTG GCCCGAGGTG CGTGCTGCGC CGACAAGAAG CAAGAAGAG CTTCCACTAC CGACGAGGCC CAT CATCCAG CCCCTCCAG TCCCCTAGGC CCCCTCCAG ATGCCCCCAC ATGCCCCAGGA ATGCCCCCAC	AACCTGCTCT CTGTCCAGTA CGTGGGTACA AAGATGAAGG CGCATCATTG ATGCCCCA GAGATCGCCA ATGGCTGATC CTGCCGAG GCTCCCCAGG GCTGCCCAGG CCCGCTGTTCTTG CCCCGGGGATCC CCCTGCTTCTTC	180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55	TCATGAAGG CAGTAGCCTA TTGAGCAGAA GGGAGAGGGT GCACCTCAT GGACTACTA ACTCAGCCCG CAACCCCAT ACACCCCAT ACACCCCAT ACACCCCGAGAG TGCCAGAGG TGCCAGAGG CACTCTTCTT GGACCCGCTGC CAACCCCCTCCCCCCCCCC	GSCOTGGAG TARGAACGTG AGCAACGAG GGAGACTGAG GCAGGAGGCC CCGCTACCTG GTCAGCCTAC CGGCTGGGC GGAGGCCTAC CAGGAGGAC ACTOTGGAG CTAGGTGTG ACTAGTATAG GCAGCTGTTG TCCCCGAC TGCCTGTTT TCCCCGAC	AAGGGGGAGG GTGGGGGCC GAGAGCCG GCGAAGTGG CAGAAGTGG CAGAAGTGA TCCTTGCACA TCCTTACAAAG CCCGACAACG GCCGACAACG GCCGACAACG GCCGACAACG GAGACAACG GCCGACAACG GAGACAACG GAGACACG GGCGACACG AGGGACTGGC AGGGCACCT CCCAGGACCA CGTAGGACACT CCCAGGACCA GGTAGGAAATT CCCAGGACCA GGTAGGAAATT CCCAGGACCA GGTAGGAAATT CCCAGGACCA GGTAGGAAATT CCCAGGACCA GGTAGGAACT GGTAGGAACT CCCAGGACCA GGTAGGAACT CCCAGGACCA GGTAGGAACT CCCAGGACCA GGTAGGAACT CCCAGGACCA GGTAGGAACT CCCAGGACCA GGTAGGAACT CCCAGGACCA GGTAGGAATT	AGCTCTCTES AGAGGCTNC AGGAGAAGGG TGTGCGACAC AGAGCCGGGT CCACCGGTGA ACTTTTCCGT AGACCACTTT ACAGCACCTT CCAGCGGAAGA CCCGGCGCT CCGGGGAAGA ACCACTTC CCGGGGAAGA ACCACTTG CCACCCTTC AGAGCTTGCG AGAGCTTACGGGTACTTCT GGCTACTTCT GGCTACTTCT AGAGGAGTGTC AGAGGTGTTC AGAGGAGTTTC AGAGGAGTGTC AGAGGAGTGTC	CGARGAGCCA CTGGAGGGTG GCCCGARGATG GCCCAACAGAG CTTCCTACCTG GCACAACAAG CTTCCACTAC CGACGAGGCC CATCATCAC GGGGGGCGAG CCCCCTCCAG TCCCCTAGGC CACCTCCCAG CCCCCCCAC CCCCCCCCCC	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGAAGG CGCATCATTG ATGCCGCCA AAAATCGCCA AAAATCGCCA AAAATCGCCA CTGCTGCAAC CTGCTGCAAC CCTGCTCCTC CTGCTCCTC CCCTGCTCTT CCCCTGCTCTT CCCCTCCCT	180 240 300 360 420 420 540 660 720 780 840 900 900 91020
50 55	TCATGAAGG CAGTAGCAGA TIGAGCAGAA GGGAGAGGT GCACCTCAT GGACTACTA ACTCAGCCCG CAACCCCAT ACAACCCCAT ACAACCCCAT ACACCCCAT ACACCCCAGAG GCCCAGAGG GCCCAGAGG GCCCAAAGGG CTCCAAAGGG CACTCTTCTT GGACCCCGT GGACAGTGGC GGACAGTGGC	GSCOTGGAR TARGAACGTG AGCAACGAG GGAGACTGAG GGAGACTACTG GTCAGCCTACCTG GTCAGCCTACCTG GGAGGCCTAC CAGCGAGGAG CAGCGTGGAG CTGAGTGTT ACTAGTATGAG GCAGCTGTTG TCCTCCGGAG GCAGCTGTTT TCCTCCGGAG TGCCTGTGAA AGGGCTGGA AGGGCTGGAA AGGGCTGGAA	AAGGGCGAGG GTGGGCGCC GAGGGCTCGGCCGGGCGCCAGGTCG CCGAGGTCG TCCTACAAAG CCCGCCACAGCCCG TCCTACAAAG CCCGCCACACGCCG GTGGGAGGCA TCCTACAAAG CCCGCCACACACG GTGGGAGGC AGGGCACCTA CCAGGACCA AGGGACTAG AGGACTAG AGGACTAG AGGACTAG AGGACTAG	AGCTCTCTES AGAGGCTNC AGGAGAAGGG TGTGCGACAC AGAGCCGGGTA AGAGCCGGTGA ACTTTTCCGT AGACCCTT ACAGCACCTT ACAGCACCTT CCAGCGGAAGA ACACTGAGCACCTT CCAGCCTTC CCAGCGTACACCTT CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCACCTTC CCACTTC CCACCTTC CCACCTTC CCACCTTC CCACCTTC CCACCTTC CCACCTTC CCACCTT	CGARGAGCGA CTGGAGGGTG GCCCIAGGTG GCCCIAGGTG GCCCAAGAGA CAAGAAG CAAGAAGAG CTCCACTAC CGACCAAGGAG CACCCTCCAG CCCCCCCCAG ATGCCCCCCC CCCCCCCTCCT CCCCCTCTCT CCCCCTCTCT CCCCCTCTCT CCCCCTCTCT CCCCCTCTTT CCCCCTTGT CCTTGTGTT CTGTGTTTT	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGACG CGCATCATTG ATGCCCCCA GAGATCCCCA GAGATCCCCA GCTCCCAGG TCCCCAGG TCCCCAGG CCCTGCTCTC CTGGGGATC CCCGCCCCC CCCGCCCCC CCCGCCCCC CCCGCCCCC CCCGCCTCTC CTGGCGACCC CCTGTCTTG	180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	TCATGAAGG CAGTAGCAGA TIGAGCAGAA GGGAGAGGT GCACCTCAT GGACTACTA ACTCAGCCCG CAACCCCAT ACAACCCCAT ACAACCCCAT ACACCCCAT ACACCCCAGAG GCCCAGAGG GCCCAGAGG GCCCAAAGGG CTCCAAAGGG CACTCTTCTT GGACCCCGT GGACAGTGGC GGACAGTGGC	GSCOTGGAR TARGARCTIG ARGCARCAGA GGAGACTGAG CAAGGAGGCC CCGCTACCTG GGAGGCCTAC CGGCCTGGGG CACGTGGGG ACTGGGG ACTGGGG ACTGGTGATGTG ACTAGTGTTG ACTAGTGTTG ACTAGTGTTG ACTAGTGTGAC TCCGTGGAG TCCCCGTGGAG TCCCCGTGGAG TCCCCGGAC TGCCTCTGAT TGCCCCGAC TGCCTCTGAT	AAGGGCGAGG GTGGGCGCC GAGGGCTCGGCCGGGCGCCAGGTCG CCGAGGTCG TCCTACAAAG CCCGCCACAGCCCG TCCTACAAAG CCCGCCACACGCCG GTGGGAGGCA TCCTACAAAG CCCGCCACACACG GTGGGAGGC AGGGCACCTA CCAGGACCA AGGGACTAG AGGACTAG AGGACTAG AGGACTAG AGGACTAG	AGCTCTCTES AGAGGCTNC AGGAGAAGGG TGTGCGACAC AGAGCCGGGTA AGAGCCGGTGA ACTTTTCCGT AGACCCTT ACAGCACCTT ACAGCACCTT CCAGCGGAAGA ACACTGAGCACCTT CCAGCCTTC CCAGCGTACACCTT CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCACCTTC CCACTTC CCACCTTC CCACCTTC CCACCTTC CCACCTTC CCACCTTC CCACCTTC CCACCTT	CGARGAGCGA CTGGAGGGTG GCCCIAGGTG GCCCIAGGTG GCCCAAGAGA CAAGAAG CAAGAAGAG CTCCACTAC CGACCAAGGAG CACCCTCCAG CCCCCCCCAG ATGCCCCCCC CCCCCCCTCCT CCCCCTCTCT CCCCCTCTCT CCCCCTCTCT CCCCCTCTCT CCCCCTCTTT CCCCCTTGT CCTTGTGTT CTGTGTTTT	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGACG CGCATCATTG ATGCCCCCA GAGATCCCCA GAGATCCCCA GCTCCCAGG TCCCCAGG TCCCCAGG CCCTGCTCTC CTGGGGATC CCCGCCCCC CCCGCCCCC CCCGCCCCC CCCGCCCCC CCCGCCTCTC CTGGCGACCC CCTGTCTTG	180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140
50 55	TCATGARAGG CAGTAGCCTA TTGAGCAGA GGGACATCAT ACTCAGCCGG CCACCCCAT ACAGCCCGAA ACACCCCAA ACACCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCC	GSCOTGGAR TARGAACGTG AGCAACGAG GGAGACTGAG GGAGACTACTG GTCAGCCTACCTG GTCAGCCTACCTG GGAGGCCTAC CAGCGAGGAG CAGCGTGGAG CTGAGTGTT ACTAGTATGAG GCAGCTGTTG TCCTCCGGAG GCAGCTGTTT TCCTCCGGAG TGCCTGTGAA AGGGCTGGA AGGGCTGGAA AGGGCTGGAA	AAGGGGAGG GTGGGGGGG GAGGACCCG GAGAACCCG GAGAACCCG GAGAACCCG CTGCACCCCCAC CTGCCCCCAC CCTGCCCCCCAC GCCACACC CCCACACAC GCCACACC CCCACACAC GCCACCCC CCACACAC GCCACCCC CCACACAC CCCACACAC CCCACAC	AGCTCTCTES AGAGGCTNC AGGAGAAGGG TGTGCGACAC AGAGCCGGGTA AGAGCCGGTGA ACTTTTCCGT AGACCCTT ACAGCACCTT ACAGCACCTT CCAGCGGAAGA ACACTGAGCACCTT CCAGCCTTC CCAGCGTACACCTT CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCAGCCTTC CCACCTTC CCACTTC CCACCTTC CCACCTTC CCACCTTC CCACCTTC CCACCTTC CCACCTTC CCACCTT	CGARGAGCGA CTGGAGGGTG GCCCIAGGTG GCCCIAGGTG GCCCAAGAGA CAAGAAG CAAGAAGAG CTCCACTAC CGACCAAGGAG CACCCTCCAG CCCCCCCCAG ATGCCCCCCC CCCCCCCTCCT CCCCCTCTCT CCCCCTCTCT CCCCCTCTCT CCCCCTCTCT CCCCCTCTTT CCCCCTTGT CCTTGTGTT CTGTGTTTT	AACCTGCTCT CTGTCCAGTA CGTGAGTACC CTGCTGGACA AAGATGACG CGCATCATTG ATGCCCCCA GAGATCCCCA GAGATCCCCA GCTCCCAGG TCCCCAGG TCCCCAGG CCCTGCTCTC CTGGGGATC CCCGCCCCC CCCGCCCCC CCCGCCCCC CCCGCCCCC CCCGCCTCTC CTGGCGACCC CCTGTCTTG	180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140
50 55 60	TCATGARAGG CAGTAGCCTA TTGAGCAGA GGGACATCAT ACTCAGCCGG CCACCCCAT ACAGCCCGAA ACACCCCAA ACACCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCAA ACACCCCCC	GECCYTGGAG TAAGAACGTG AAGCAACGAG GGAGACTGAG CAAGGAGGAC CAGCTACCTG GTCAGCTAC CAGCAGGAGAC CAGCAGGAGAC CAGCAGGAGAC CTGAGTGGAGA ACTOTTGGAAG CCAGCTGTTG ACTAGTATGGA CCAGCTGTTG ACTAGTATGGAG ACTCCTGGAT TCCTCCCGAC TCCCTCGAT TCCTCCCGAC TCCCTCTGAT TAAAGTTCCC 109 Protein cession #: 1	AAGGGCGAGG GTGGGGCGGGGGACGCCG GGGGACGCCG CTCCAGGGCG GGGAACGCCG CTGGCCCTGA TCTCTGGCAA TCTCTGGCAA TCTCTGGCACA GCCGACAACG GGGGACACCG GGTGGAGGCCA AGGGACTGGC AGGGACTGGC CCAGGGACCA CGTAGGAACTGGC CGTAGGACA CGTAGGAACTGGC GTTGGACA	AGCTOTOTIS AGAGGGTNC AGGAGAAGGG TGTGGGACAC AGAGCCGGTGA TGGACACCAG AGACCACTAT ACACCACCTTC CCGGGGAAGA ACCACCTTC CCGGGGAAGA ACCACTGGTC CCACCTTC CCACGGGAAGA ACCACTGGTC CCACCTTTC GAGAGATGTC CCACCTTTC TGTGTGTTTTT GGAAAGCATC C	CGARGAGGGA CTGGAGGGTG GCCCJAGGTG GCCCJAGGTG GCCCJAGGTG GCCCACAGAGAG CACAGAGAG CACAGAGAG CACCACTAC GGCGAGGGCGAG CCCCCTCCAG CCCCCTCCAG CCCCCTCCAG TCCCCTCCAG TCCCCTCTCCAG TCCCCTTCCAG TCCCCTTCCAG TCCCCTTCCAG TCCCCTTCCAG TCCCCTTCTC	AACCHGCTCT CTGTCCAGTA CGTGAGTACA CGGAGTACA AACATGAAGG GCGCACCATTG ATGCGGCCA ATGGCTGATC CTGCTGCGAG GCTCCCCACC GCTGTTTCTTG CCCCCACC CCTGGTGCTCT CCCCTGCTCT CGCTGCCTCT CGCTGCTCT CGCTGCTCT CGCTGCTCT CGCTGCTCT CGCTGCTCT CGCTGCT	180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140
50 55 60	TCATGARAGG CAGTAGCCTA TTGACAGAA GGAGAAGGT GCACCTCAT GTGACTACTA ACAACCCCTA TGACACCCCT TCACACCCCAGA GCCACCCCAGA GCCACACCCC ACACCCCTTCT CGCACCCCGC GCACCCCCTC GCACCCCCT TCCCCCCCCC GCACCCCCCC TCCCCCCCCCC	GECCYTGGAR TANGANGUTG ANGCANGUNG GNAGACTUNG CANGGARGACC CONSCINACTUNG CO	AAGGGCGAGG GTGGGGGGCCCCCCCCCCCCCCCCCCCCC	AGCICTOCTIS AGGAGGOTOC AGGAGAAGGA TGTGCGACAC AGAGCCGGGT AGGACCGGGT AGAGCCGGGT AGACCGGGT AGACCCGTT AGAGCACCTT AGAGCACCTT AGAGCACCTT AGAGCACCTT AGAGCACCTT AGAGCTGAGG ACCACTGGGGAAGA CCCAGCCTTC GGCTACTTCT GGGTACTTCT TGTGTTGTT	CGARGAGCA TOGAGGGTA GCCCIAGGTA GCCCIAGGTA GCCCIAGGTA GCCCIAGGTA GCCCIAGGTA GCCCIAGGTA GCCCIAGGTA CTTGCACTA GCCCIACCA GCACAGAGA GCCCCCCCCCCA GGGGGGGGA TCCCCTCAGC CCCCCCCCA GGGGGGGA TCCCCTCAGCC CCCCCCCCA TCCCCCCCC CCCCCCCC	AACCRGCTCT CTGTCAGGTA CGTGAGTACA AAGATGAACG AAGATGAACG AAGATGAACG AAGATGAACG AAGATGAACG AAGATGACG AAGATGACG CGTGCTGAGAG CCCCCACG CGTGTTCTTG CCCGGGATC CCCTGCTCCT CGCTGCTCT TGCTCCTCT TGCTCCTCT TGCTCCTCT TGCTCCTCT TGCTCCTCT TGTTGTGTGT TGTTGTGTGT TGTTGTGTGT TGTTGT	180 240 300 360 420 480 540 660 720 780 900 9102 1140 1200 1260
50 55 60 65	TCATGARAGO CASTAGOCTA TTGAGCAGAA GGGGAGAAGOT GCCACTCAT GCCACTCAT ACAGCCCGA TCGAGCCCGA TCGAGCCCGA TCGAGCCCGA TCGAGCCCGA TCGAGCCGAGAGAG TCGCAGAGAGAG TCGCAGAGAGAG TCGCAGAGAGAG TCGCAGAGAGAG TCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CSCCTTGGMS TARGAGGTIS AGCAACGMS GGGACCTGMS CCGCCTGGGG GGACCTGMS CCGCCTGGGG GGACCTGAC CCGCCTGGGG GGAGCCTAC CCGCCTGGGG GGAGCCTAC CCGCCTGGGG ACTGTCGAC ACTGTCGAC ACTGTCGAC ACTGTCGAC ACTGTCGAC ACTGTCGAC ACTGCTGGAC ACTGCTGGAC ACTGCTGGAC ACTGCAC ACTGCTGGAC ACTGCAC ACTG	ANGGGCCARG GROUNG CONGRETCH GROUNG CONGR	AGCTCTCCTA AGGGGTCCC AGGAGAAGGG TTTGGGGACA AGAGGCTCG AGAGGATCA AGAGCCGGT AGACCACTT AGACCTTT AGACCTTTC AGACCTTACC CCCACCCTTC AGACCTTTC AGACCTTACC CCCACCCTTT AGACCTTACC CCCACCCTTT AGACCTTACC CCCACCCTTC AGACCTTACC CCCACCCTTC AGACCTTACC AGACCTTACC CCCACCCTTC AGACCTTACC AGACCTACC AGACCTTACC AGACCTACC AGACCTTACC AGACCTACC AGACCTTACC AGACCTACC AGACCTACC AGACCTACC AGACCTACC AGACC	COARGAGCA CTRORAGGGTA GCCCIAGUTA CTROCTAGCTA CTROCTAGCA CTROCTAGCA CARCAGAGA CARCAGAGA CARCAGAGA CARCAGAGA CARCAGAGA CARCAGAGA CARCAGAGA CARCAGAGA CARCAGAGA CARCAGAGA CARCAGAGA CARCAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGAGA CARCAGAGAGAGAGA CARCAGAGAGAGA CARCAGAGAGAGAGA CARCAGAGAGAGAGA CARCAGAGAGAGAGA CARCAGAGAGAGAGAGAGAGAGA CARCAGAGAGAGAGAGAGAGA CARCAGAGAGAGAGAGAGAGAGAGA CARCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA CARCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	AACCTGCTCT COTOTCOMGTA COTOTCO	180 240 300 160 420 480 540 600 660 720 840 900 900 1080 1140 1200 1260
50 55 60 65	TCATURARGO CASTAGOCTA TTGAGCAGAA GOGAGAAGGT GCACATCAT TGAGCACACA ACACCCC ACAGCCCCACA TGCACACCCT ACACCCCCC ACACCCCC TGCCCCCCCC GGACAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAA	CECCTTGGMS TARGAGGTIS GROGACTURE CANGERCE GROGACTURE CUCCTGGAC GROGACTURE CUCCTGGAC GROGACTURE CUCCTGGAC TACTGCTGGAC ACTGCACTGGAC ACTGCACTGGAC ACTGCACTGGAC ACTGCACTGGAC ACTGCACTGGAC ACTGCACTGAC ACTGCACTGGAC TACTGCACTGAC TACTGCACTCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTCAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTGAC TACTGCACTCACTGAC TACTGCACTGAC TACTGCACTCACTCAC TACTGCACTCACTCAC TACTGCACTCACTCACTCAC TACTGCACTCACTCACTCAC TACTGCACTCACTCACTCACTCAC TACTGCACTCAC	ANGGICCIACG GROUNT CONTROL OF THE CO	AGCTCTCCTG AGGAGAAGGG TTTGCGACAG AGGAGCAGGG AGAGGGACGGG AGAGGGACGGGGACGGGCAGGGGAAGGGCTTTTGTGGACAGG 31 31 31 31 31 31 31 31 31 31 31 31 31	COARGAGCA CTRORAGGOTT GCCCUAGGTT GCCCUAGGTT GCCCUAGGTT GCCCUAGGTT CTTGCTACCT GCCCCCCCCCCCCCCCCCCCCCC	AACCHICTCT COTGACTAT COTGACTAC TAGGETACC TEGETGGAC ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA COCTGACTAC TOCGACACA COCTGACTAC TOCGACACA TOTGAT	100 240 300 360 420 480 540 660 720 780 900 91020 1140 1200 1260
50 55 60 65	TCATURARGO CASTAGOCTA TTGAGCAGAA GOGAGAAGGT GCACATCAT TGAGCACACA ACACCCC ACAGCCCCACA TGCACACCCT ACACCCCCC ACACCCCC TGCCCCCCCC GGACAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAAGGG CTCCAAA	CSCCTTGGMS TARGAGGTIS AGCAACGMS GGGACCTGMS CCGCCTGGGG GGACCTGMS CCGCCTGGGG GGACCTGAC CCGCCTGGGG GGAGCCTAC CCGCCTGGGG GGAGCCTAC CCGCCTGGGG ACTGTCGAC ACTGTCGAC ACTGTCGAC ACTGTCGAC ACTGTCGAC ACTGTCGAC ACTGCTGGAC ACTGCTGGAC ACTGCTGGAC ACTGCAC ACTGCTGGAC ACTGCAC ACTG	ANGGICCIACG GROUNT CONTROL OF THE CO	AGCTCTCCTG AGGAGAAGGG TTTGCGACAG AGGAGCAGGG AGAGGGACGGG AGAGGGACGGGGACGGGCAGGGGAAGGGCTTTTGTGGACAGG 31 31 31 31 31 31 31 31 31 31 31 31 31	COARGAGCA CTRORAGGOTT GCCCUAGGTT GCCCUAGGTT GCCCUAGGTT GCCCUAGGTT CTTGCTACCT GCCCCCCCCCCCCCCCCCCCCCC	AACCHICTCT COTGACTAT COTGACTAC TAGGETACC TEGETGGAC ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA COCTGACTAC TOCGACACA COCTGACTAC TOCGACACA TOTGAT	180 240 300 160 420 480 540 600 660 720 840 900 900 1080 1140 1200 1260
50 55 60 65 70	TCATGRAGGE CAGTIAGCTA GARAGGE GGACACTGAT GTACTACTA ACACCTGAC ACACT	CECCYTGAM TARABACKTE TARABACKTE TARABACKTE GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA ACTACTA ACTACTA TCCTCCTGAT TCCTCCTGAT TCCTCCTGAT TCCTCCTGAT TARAGTICCC TARAGTICC TARAGTICCC ARAGTICCC TARAGT	ANGESCHARE GROUNDESCHARE GROUN	AGCNETICETS AGGISTATION AGGISTATION AGGISTATION TOGACATCAI AGGISTATION AGGISTATION AGGISTATION AGGISTATION AGGISTATION COMPANIA COMPANIA AGGISTATION COMPANIA COMPANIA AGGISTATION COMPANIA AGGISTATIO	COARGAGCA CTRORAGGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGO GCCCCTCA GGGGGGGGA CCCCTCCA GCCCCTCA GCCCCCTCA GCCCCTCA GCCCCTCA GCCCCCTCA GCCCCCTCA GCCCCCTCA GCCCCCCTCA GCCCCCCCCC GCCCCCCC GCCCCCCC GCCCCCCC GCCCCCC	AACCHICTCT COTGACTAT COTGACTAC TAGGETACC TEGETGGAC ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA COCTGACTAC TOCGACACA COCTGACTAC TOCGACACA TOTGAT	100 240 300 160 420 480 540 660 660 780 780 900 1020 1100 1100 1200 1260
50 55 60 65 70 75	TCATGRAGGE CAGTIAGCTA GARAGGE GGACACTGAT GTACTACTA ACACCTGAC ACACT	CECCITIGNA TARANACTIA	ANGESCHARE GROUNDESCHARE GROUN	AGCNETICETS AGGISTATION AGGISTATION AGGISTATION TOGACATCAI AGGISTATION AGGISTATION AGGISTATION AGGISTATION AGGISTATION COMPANIA COMPANIA AGGISTATION COMPANIA COMPANIA AGGISTATION COMPANIA AGGISTATIO	COARGAGCA CTRORAGGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGO GCCCCTCA GGGGGGGGA CCCCTCCA GCCCCTCA GCCCCCTCA GCCCCTCA GCCCCTCA GCCCCCTCA GCCCCCTCA GCCCCCTCA GCCCCCCTCA GCCCCCCCCC GCCCCCCC GCCCCCCC GCCCCCCC GCCCCCC	AACCHICTCT COTGACTAT COTGACTAC TAGGETACC TEGETGGAC ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA COCTGACTAC TOCGACACA COCTGACTAC TOCGACACA TOTGAT	100 240 300 160 420 480 540 660 660 780 780 900 1020 1100 1100 1200 1260
50 55 60 65 70	TCATGRAGGE CAGTIAGCTA GARAGGE GGACACTGAT GTACTACTA ACACCTGAC ACACT	CECCYTGAM TARABACKTE TARABACKTE TARABACKTE GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA GRACIACTA ACTACTA ACTACTA TCCTCCTGAT TCCTCCTGAT TCCTCCTGAT TCCTCCTGAT TARAGTICCC TARAGTICC TARAGTICCC ARAGTICCC TARAGT	ANGESCHARE GROUNDESCHARE GROUN	AGCNETICETS AGGISTATION AGGISTATION AGGISTATION TOGACATCAI AGGISTATION AGGISTATION AGGISTATION AGGISTATION AGGISTATION COMPANIA COMPANIA AGGISTATION COMPANIA COMPANIA AGGISTATION COMPANIA AGGISTATIO	COARGAGCA CTRORAGGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGOTI GCCCIAGO GCCCCTCA GGGGGGGGA CCCCTCCA GCCCCTCA GCCCCCTCA GCCCCTCA GCCCCTCA GCCCCCTCA GCCCCCTCA GCCCCCTCA GCCCCCCTCA GCCCCCCCCC GCCCCCCC GCCCCCCC GCCCCCCC GCCCCCC	AACCHICTCT COTGACTAT COTGACTAC TAGGETACC TEGETGGAC ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA ARACHTOACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA GETTOACACA COCTGACTAC TOCGACACA COCTGACTAC TOCGACACA TOTGAT	100 240 300 160 420 480 540 660 660 780 780 900 1020 1100 1100 1200 1260
50 55 60 65 70 75	TCATTGRANGS GCAGTTGLT GGGAGAGGT GCAGTTGLT GGGAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCT ACAGTTGCAGCCCT ACAGTTGCAGCCT GCC	CECCYTEGMS TAGABACTTAG TAGABACTTAG GAGAACTTAG CACACTTAG TAGAACTTAG ACTTAG TAGAACTTAGAACTTAG TAGAACTTAG	AAGGGCCTAC GCOMACCA AGGGACTGGC GCOMACCA AGGGACTGGC GCOMACCA CCTCCAGAGCG GCOMACCA AGGGACTGGC CCTCCAGAGCGC AGGGACTGGC CCTCCAGAGCGC AGGGACTGGC CCTCCAGAGCGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGGC CCTCGAGCCTA CCCAGAGCGC CCTCGAGCCTA CCCAGAGCGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGCC AGGGACTGGC AGGGACTGC AGGGACT AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACT AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACT AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACT	AGCHTTCHTG AGGGGGACAC AGGGGGGACAC AGGGGGGGACAC AGGGGGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGCGAC AGGGCGACAC AGGGCGCGAC AGGGCGACAC AGGGCACAC AGGCACAC AGGGCACAC AGGCACAC AGGGCACAC AGGCACAC AGGGCACAC AGGCACAC AGGGCACACAC AGGGCACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGCACACAC AGGGCACACAC	CORAGAGOS CONGAGOS CONGAGOS CONTROLOS CO	AACCHICATOR OTTORADOR OTTO	180 240 3100 480 480 600 540 600 7720 900 1020 1020 1220 1260
50 55 60 65 70 75	TCATTGRANGS GCAGTTGLT GGGAGAGGT GCAGTTGLT GGGAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCCT ACAGTTGCAGCCT ACAGTTGCAGCCCT ACAGTTGCAGCCT GCC	CECCYTEGMS TAGABACTTAG TAGABACTTAG GAGAACTTAG CACACTTAG TAGAACTTAG ACTTAG TAGAACTTAGAACTTAG TAGAACTTAG	AAGGGCCTAC GCOMACCA AGGGACTGGC GCOMACCA AGGGACTGGC GCOMACCA CCTCCAGAGCG GCOMACCA AGGGACTGGC CCTCCAGAGCGC AGGGACTGGC CCTCCAGAGCGC AGGGACTGGC CCTCCAGAGCGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGGC CCTCGAGCCTA CCCAGAGCGC CCTCGAGCCTA CCCAGAGCGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGGC AGGGACTGCC AGGGACTGGC AGGGACTGC AGGGACT AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACT AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACT AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACTGC AGGGACT	AGCHTTCHTG AGGGGGACAC AGGGGGGACAC AGGGGGGGACAC AGGGGGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGGGACAC AGGGCGCGAC AGGGCGACAC AGGGCGCGAC AGGGCGACAC AGGGCACAC AGGCACAC AGGGCACAC AGGCACAC AGGGCACAC AGGCACAC AGGGCACAC AGGCACAC AGGGCACACAC AGGGCACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGGCACACAC AGGCACACAC AGGGCACACAC	CORAGAGOS CONGAGOS CONGAGOS CONTROLOS CO	AACCHICATOR OTTORADOR OTTO	100 240 300 160 420 480 540 660 660 780 780 900 1020 1100 1100 1200 1260
50 55 60 65 70 75	TCATTGRANGS CONTRACTOR GORACTOR GORACTOR GORACTOR TGATACTOR ACACCTOR TGATACTOR ACACCTOR TGATACTOR ACACCCGOT TGATACTOR ACACCCGOT TGATACTOR ACACCCGOT TGATACTOR ACACCCGOT TGATACTOR ACACCCGOT TTATTCTTCTCA TCATACCCG TTCTTCTT TCATCTATA TCATACCG TCTTTCT TCTTCTCAT TCATACCG TCTTTCT TCTTCTCTCAT TCATACCG TCTTTCT TCTTCTCTCAT TCATCTATAC TCATACCG TCTTTCTT TCATCTATACCG TCTTTCTT TCATCTATACCG TCTTTCTT TCATCTATACCG TCATCTTTCT TCATCTATACCG TCATCTTTCT TCATCTATACCG TCATCTTTCT TCATCTATACCG TCATCTTCTTCT TCATCTATACCG TCATCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	CECCYTGAM TAGRACTIC TAGRACTIC GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA GARGACTGA CONCECTIGAC GARGACTGA GARGACTGA CONCECTIGAC GARGACTGA CONCECTIGA GARGACTGA CONCECTIGA GARGACTGA CONCECTIGA CONCECTIGA GARGACTGA TOCCCGA CONCECTIGA TOCCCGA CONCECTIGA TOCCCGA CONCECTIGA TOCCCGA CONCECTIGA TOCCCGA TOCCCGA TOCCCGA TOCCCGA TOCCCGA TOCCCGA TOCCGA TOCCCGA TOCCCCGA TOCCCCGA TOCCCCGA TOCCCCGA TOCCCCGA TOCCCCGA TOCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	AAGGGCCTATG GCCAATTUAG TOTAGGCA TOTAGGCA GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC AGGGACTAGCC AGGGACTAGCC CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTAGCA CCCAGGACTACCA CCCAGGACCACCAC CCCACACAC C CCCACACACAC CCCA	AGCHTTCHTO AGGGGACA AGGGGTGA AGGGGGACA AGGGGGGACA AGGGGGGACA AGGGCGGGACA AGGGCGGGACA AGGGCGGGACA AGGGCGGGACA AGGGCGGGACA AGGGCACGTT AGGCACACTTT AGGACACTTT AGGGACGACTT AGGGCACTTA AGGGCACTT AGGGCACTTA AGGGCACTTA AGGGCACTTA AGGGCACTTA AGGGCTACGAC AGGGCTACTA AGGGCTACGAC AGGGCTACTTA AGGGCTAGGAC AGGGCTACTTA AGGGCTAGGAC AGGACTTACT AGGGCTAGGAC AGGGCTACTTACT AGGGCTAGGAC AGGGCTACTTACT AGGGCTAGGAC AGGGCTACTTACT AGGGCTAGGAC AGGGCTACTTACT AGGGAGGAT AGGGAGAT AGGGAGGAT AGGGAGGAT AGGGAGAGAT AGGGAGGAT AGGGAGAT AGGGAGGAT AGGAGGAT AGGGAGGAT AGGGAGGAT AGGGAGGAT AGGGAGGAGAT AGGGAGGAT AGGGAG	CORAGIAGOS CORORAGOS CONTROLOS	AACCHGCTCH COTTAMISTAC CTGGCTGGGAC AAGATGAAG CCCACCTGCTGGAC AAGATGAAG CCCACCTGCTGCAG CCCACCTGCTGCAG CCCCCCACCTG CCCCCCACCTG CCCCCACCTG CCCCCACCTG CCCCCACCTG CCCCCACCTG CCCCCACCTG CCCCACCTGCT CCCCACCTC CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCCACCTGCT CCCCACCTGCT CCCCCACCTGCT CCCCCACCTGCT CCCCCCACCTGCT CCCCCACCTGCT CCCCCACCTGCT CCCCCCACCTGCT CCCCCCCACCT CCCCCCCACCT CCCCCCCCACCT CCCCCCCC	100 240 300 400 400 400 500 600 600 600 100 900 1140 1200 1200 1200 1200 1200 1200 12
50 55 60 65 70 75	TCATTGRANGS CONTRACTOR GORACTOR GORACTOR GORACTOR TGATACTOR ACACCTOR TGATACTOR ACACCTOR TGATACTOR ACACCCGOT TGATACTOR ACACCCGOT TGATACTOR ACACCCGOT TGATACTOR ACACCCGOT TGATACTOR ACACCCGOT TTATTCTTCTCA TCATACCCG TTCTTCTT TCATCTATA TCATACCG TCTTTCT TCTTCTCAT TCATACCG TCTTTCT TCTTCTCTCAT TCATACCG TCTTTCT TCTTCTCTCAT TCATCTATAC TCATACCG TCTTTCTT TCATCTATACCG TCTTTCTT TCATCTATACCG TCTTTCTT TCATCTATACCG TCATCTTTCT TCATCTATACCG TCATCTTTCT TCATCTATACCG TCATCTTTCT TCATCTATACCG TCATCTTCTTCT TCATCTATACCG TCATCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTATACCG TCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	CECOTYGRAD TAMACACCAM ANACACCAM ANACACCAM GAGAACTAM GAGAACTAM GAGAACTAM GAGAACTAM CONCENTRATION TO THE CONCENTRATI	AAGGGCCTATG GCCAATTUAG TOTAGGCA TOTAGGCA GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC GCCAAGATGGC AGGGACTAGCC AGGGACTAGCC CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTA CCCAGGACTAGCA CCCAGGACTACCA CCCAGGACCACCAC CCCACACAC C CCCACACACAC CCCA	AGCHTTCHTO AGGGGACA AGGGGTGA AGGGGGACA AGGGGGGACA AGGGGGGACA AGGGCGGGACA AGGGCGGGACA AGGGCGGGACA AGGGCGGGACA AGGGCGGGACA AGGGCACGTT AGGCACACTTT AGGACACTTT AGGGACGACTT AGGGCACTTA AGGGCACTT AGGGCACTTA AGGGCACTTA AGGGCACTTA AGGGCACTTA AGGGCTACGAC AGGGCTACTA AGGGCTACGAC AGGGCTACTTA AGGGCTAGGAC AGGGCTACTTA AGGGCTAGGAC AGGACTTACT AGGGCTAGGAC AGGGCTACTTACT AGGGCTAGGAC AGGGCTACTTACT AGGGCTAGGAC AGGGCTACTTACT AGGGCTAGGAC AGGGCTACTTACT AGGGAGGAT AGGGAGAT AGGGAGGAT AGGGAGGAT AGGGAGAGAT AGGGAGGAT AGGGAGAT AGGGAGGAT AGGAGGAT AGGGAGGAT AGGGAGGAT AGGGAGGAT AGGGAGGAGAT AGGGAGGAT AGGGAG	CORAGIAGOS CORORAGOS CONTROLOS	AACCHGCTCH COTTAMISTAC CTGGCTGGGAC AAGATGAAG CCCACCTGCTGGAC AAGATGAAG CCCACCTGCTGCAG CCCACCTGCTGCAG CCCCCCACCTG CCCCCCACCTG CCCCCACCTG CCCCCACCTG CCCCCACCTG CCCCCACCTG CCCCCACCTG CCCCACCTGCT CCCCACCTC CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCACCTGCT CCCCCACCTGCT CCCCACCTGCT CCCCCACCTGCT CCCCCACCTGCT CCCCCCACCTGCT CCCCCACCTGCT CCCCCACCTGCT CCCCCCACCTGCT CCCCCCCACCT CCCCCCCACCT CCCCCCCCACCT CCCCCCCC	180 240 190 240 190 240 240 480 660 660 190 190 190 1100 1100 1100 110

	CGTGCTGGCC	CAGGACCTGC	ATAAGCCAGC	TTTCGAGGCA	GACATATCTG	AGCTCATCCT	360
	TTGCCAGAAC	GAGGTTGACT	ACCCTCTCAA	GAACCTTCAG	GCCTGGATGA	AGGATGAACC	420
	ACGGTCCACG	AACCTGTTCA	TGAAGCTGGA	CTCGGTCTTC	ATCTGGAAGG	AACCCTTTGG	480
_	CCTGGTCCTC	ATCATCGCAC	CCTGGAACTA	CCCATTGAAC	CTGACCCTGG	TGCTCCTGGT	540
5		CCCGCAGGGA					600
		CTGGCTGAGG					660
	GCTGGGCGGA	CCCCAGGAGA	CAGGGCAGCT	GCTAGAGCAC	AAGTTGGACT	ACATCTTCTT	720
	CACAGGGAGC	CCTCGTGTGG	GCAAGATTGT	CATGACTGCT	GCCACCAAGC	ACCTGACGCC	780
		GAGCTGGGGG					840
10		AACCGCGTGG					900
	CCCTGACTAC	GTCCTGTGCA	GCCCCGAGAT	GCAGGAGAGG	CTGCTGCCCG	CCCTGCAGAG	960
		CGTTTCTATG					1020
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		AACGAGAGCG					1140
15		GTGATGCAGG					1200
		GAGGCCATCA					1260
		AGCAGACAGG					1320
		GAGGGCTTCA					1380
~~		ATGGGCCGGT					1440
20		CTCGCCCCCT					1500
		AACCAGCAGC					1560
		CACCCGCCTC					1620
		CCAACTCACA					1680
~~		ACATGACTGC					1740
25		GCTGCTCGAG					1800
		TCCCCAATTC					1860
		GTGTCACCCT					1920
		GAGCGTGGAG					1980
		GCCCCATCCC					2040
30		TCTCTGCACC					2100
	AGCTCCATCC	ACTGGGAAAA	CTGGGGTTTG	CATCACTCCA	CIGCACAGIG	TTAGTGGGAC	2160
	CTGGGGGCAA	GTCCCTTGAC	TTCTCTGAGC	CTCAGTTTCC	TTATGTGAAA	GTTGCTGGAA	2220
	CCAAAATGGA	GTCACTTATG	CCAAACTCTA	ATAAAATGGA	GTCGGGGGGG	CACATAGAAG	2280
0.5		CACATGCCCG					2340
35	AGACA CAGGG	CGTATGGAAA	AGCACGTCCT	CAAAGACTGT	AGTATTCCAG	ATGAGCTGCA	2400
	GATGCTTACC	TACCACGGCC	GTCTCCACCA	GAAAACCATC	GCCAACTCCT	GCGATCAGCT	2460
						TAAAACGTTC	
					AAGCACTCAT	AGCCCAGATA	2580
40	GGAATCCTCT	GCTCCTCCCA	AATAAATTCA	TCTGTTC			
40			•				

Seq ID NO: 111 Protein sequence: Protein Accession #: NP_000686

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		1	1	1	1	1	1	
			PMKLDSVFIW					60
		ISOGTEKVLA	EVLPOYLDOS	CFAVVLGGPQ	ETGOLLEHKL	DYIFFTGSPR	VGKIVMTAAT	120
_	_	KHLTPVTLEL	GGKNPCYVDD	NCDPQTVANR	VAMPCYFNAG	QTCVAPDYVL	CSPEMQERLL	180
5	0		YGDDPQSSPN					240
		VDVQETEPVM	QEEIFGPILP	IVNVQSVDBA	IKPINRQEKP	LALYAPSNSR	QVVNQMLERT	300
		SSGSFGGNEG	FTYISLLSVP	FGGVGHSGMG	RYHGKPTFDT	PSHHRTCLLA	PSGLEKLKEI	360
		RYPPYTDWNQ	QLLRWGMGSQ	SCTLL				

Seq ID NO: 112 DNA sequence Nucleic Acid Accession #: NM_004456 Coding sequence: 58-2298

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	1	11	21	31	41	51	
60	1	1	1	I	Į.	1	
		CGACGCGCGG					60
		GGAAGAAATC					120
		GACTGAGACA					180
		ATCGTCAGAA					240
65		TACAGCCTGT					300
		TGACCAGTGA					360
		CTTCAGTACC					420
		AAACTGTTTT					480
~~		TCATTGAAGA					540
70		TTATAAATGA					600
		ACGATGATGA					660
		ATCACCGAGA					720
		AGGCCATTTC					780
	GAAAAATATA	AAGAACTCAC	CGAACAGCAG	CTCCCAGGCG	CACTTCCTCC	TGAATGTACC	840
75		ATGGACCAAA					900
		TCTGTAGGCG					960
	ACACCCAACA	CTTATAAGCG	GAAGAACACA	GAAACAGCTC	TAGACAACAA	ACCTTGTGGA	1020
		ACCAGCATTT					1080
	CGGATAAAGA	CCCCACCAAA	ACGTCCAGGA	GGCCGCAGAA	GAGGACGGCT	TCCCAATAAC	1140
80 ·		CCAGCACCCC					1200
	AGGGAAGCAG	GGACTGAAAC	GGGGGGAGAG	AACAATGATA	AAGAAGAAGA	AGAGAAGAAA	1260
	GATGAAACTT	CGAGCTCCTC	TGAAGCAAAT	TCTCGGTGTC	AAACACCAAT	DAAGATGAAG	1320
	CCAAATATTG	AACCTCCTGA	GAATGTGGAG	TGGAGTGGTG	CTGAAGCCTC	AATGTTTAGA	1380
	GTCCTCATTG	GCACTTACTA	TGACAATTTC	TGTGCCATTG	CTAGGTTAAT	TGGGACCAAA	1440
85	ACATGTAGAC	AGGTGTATGA	GTTTAGAGTC	AAAGAATCTA	GCATCATAGC	TCCAGCTCCC	1500
	GCTGAGGATG	TGGATACTCC	TCCAAGGAAA	AAGAAGAGGA	AACACCGGTT	GTGGGCTGCA	1560
		AGATACAGCT					1620

CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTTGTGTGAT A TTTTGTGAAA AGTTTTGTCA ATGTAGTTCA GAGTGTCAAA ACGGCTTTCC G TGCAAAGCAC AGTGCACACC CAAGCAGTGC CCGTGCTACC TGCGTACCG A CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATTGGA ACAGTAAAAA	AGCACAAAAT	1680
TGCAAAGCAC AGTGCAACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG A		
COTGACCTOT GTCTTACTTG TGGAGCCGCT GACCATTGGG ACAGTAAAAA 1	DOGNIGCUGC	1740 1800
	TOTOTOTOC	1860
5 AAGAACTICA GTATTCAGCG GGGCTCCAAA AAGCATCTAT TGCTGGCACC A	ATCTGACGTG	1920
GCAGGCTGGG GGATTTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT (CTCAGAATAC	1980
TGTGGAGAGA TTATTTCTCA AGATGAAGCT GACAGAAGAG GGAAAGTGTA 1	TGATAAATAC	2040
ATGTGCAGCT TTCTGTTCAA CTTGAACAAT GATTTTGTGG TGGATGCAAC	CCGCAAGGGT	2100
10 AACAAAATTC GTTTTGCAAA TCATTCGGTA AATCCAAACT GCTATGCAAA A	AGTTATGATG	2160 2220
10 GTTMACGGTG ATCACAGGAT AGGTATTTTT GCCAAGAGAG CCATCCAGAC C CTGTTTGTTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCGG	CATCGABAGA	2280
GANATGGANA TCCCTTGACA TCTGCTACCT CCTCCCCCTC CTCTGANACA		2340
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15 GCCTTCTCAC CAGCTGCAAA GTGTTTTGTA CCAGTGAATT TTTGCAATAA 1	TGCAGTATGG	2520
TACATTTTTC AACTITGAAT AAAGAATACT TGAACTTGAA AAAAAAAAAA	AAAAAA	
Seq ID NO: 113 Protein sequence:		
20 Protein Accession #: NP_004447		
= -		
1 11 21 31 41	51	
MGOTGKKSEK GPVCWRKRVK SEYMRLRQLK RFRRADEVKS MFSSNRQKIL I	PROPERTY NO.	60
25 KQRRIQPVHI LTSVSSLRGT RECSVTSDLD PPTQVIPLKT LNAVASVPIM		120
MVEDETVLHN IPYMGDEVLD QDGTFIEBLI KNYDGKVHGD RECGFINDEI	FVELVNALGO	180
VNDDDDDDD DDPERREEKO KDLEDHRDDK ESRPPRKFPS DKILEAISSM I	FPDKGTAEEL	240
KEKYKELTEQ QLPGALPPEC TPNIDGPNAK SVQREQSLHS FHTLFCRRCF I	KYDCFLHPFH	300
_ ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP (GGRRRGRLPN	360
30 NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEEEK KDETSSSSEA I KPNIEPPENV EWSGABASMP RVLIGTYYDN PCAIARLIGT KTCRQVYEFR V		420 480
PAEDVDTPPR KKKRKHRLWA AHCRKIQLKK DGSSNHVYNY QPCDHPRQPC	DESCRIVE	540
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CKNCSIQRGS KKHLLLAPSD VAGWGIFIKD PVQKNEFISE YCGEIISQDE	ADRRGKVYDK	660
35 YMCSFLFNLN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI I	FAKRAIQTGE	720
ELFVDYRYSQ ADALKYVGIE REMBIP		
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40 Nucleic Acid Accession #: NM_001827 Coding sequence: 96-335	51	
40 Nucleic Acid Accession 8: NM_001827 Coding sequence: 96-335 1 11 21 31 41 1	1	
40 Nucleic Acid Accession 8: Nu_001827 Coding sequence: 96-335 1 11 21 31 41	COGCTCTTCG	60
Nuclaic Acid Accession 8: NM_001827 Coding sequence: 96-315 1	CCGCTCTTCG ATCTACTACT	60 120 180
Nuclaic Acid Accession 8: NN_001827	CCGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC	120 180
Nucleic Acid Accession 8: INI, 001827	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT	120 180 240 300
Nuclaic Acid Accession 8: NN_001827	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT CGTCAAATCT	120 180 240 300 360
Nucleic Acid Accession 8: NN_001827	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT CGTCAAATCT TGAGAAATGT	120 180 240 300 360 420
Nucleic Acid Accession 8: IN 001827	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTTTCC ATTCTTCTCT CGTCAAATCT TGAGAAATGT GAGCTCAGTT	120 180 240 300 360 420 480
Nucleic Acid Accession 8: NM_001827	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT CGTCAAATCT TGAGAAATGT GAGCTCAGTT CCAGTCAGTT	120 180 240 300 360 420 480 540
40 Suclaic Acid Accession 8: 101,001827 Coding sequence: 96-0155 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT CGTCAAATCT TGAGAAATGT GAGCTCAGTT CCAGTCAGTT	120 180 240 300 360 420 480
Nucleic Acid Accession 8: IN\$_001827	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT CGTCAAATCT TGAGAAATGT GAGCTCAGTT CCAGTCAGTT	120 180 240 300 360 420 480 540
Nucleic Acid Accession 8: IN 001827	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT CGTCAAATCT TGAGAAATGT GAGCTCAGTT CCAGTCAGTT	120 180 240 300 360 420 480 540
Nucleic Acid Accession 8: IN\$_001827	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT CGTCAAATCT TGAGAAATGT GAGCTCAGTT CCAGTCAGTT	120 180 240 300 360 420 480 540
Nucleic Acid Accession 8: NN_001827 Coding sequence: 96-015 1 1 1 1 1 45	COGCTCTTCG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT CGTCAAATCT TGAGAAATGT GAGCTCAGTT CCAGTCAGTT	120 180 240 300 360 420 480 540
40 Coding sequence: \$6-135 1 1 21 31 41 AGTECTORS SEQUENCE: \$6-135 45 COCINETE TOWNS THE SEQUENCE CONSIGNATION OF SEQUENCE CONSINCATION OF SEQUENCE CONSIGNATION OF SEQUENCE CONSIGNATION OF SEQU	COGCTCTTOG ATCTACTACT AGAGAACTTT CTTGGTGTTC CTTGCTTCTCT CGTCAAATCT GAGAAATGT GAGCTCAGTT ATAAAGTTTG 51	120 180 240 300 360 420 480 540 600
40 Coding sequence \$6-315 1 1 1 1 1 1 1 1 1 1 1 4 1 1 1 4 1 1 1 1	COGCTCTTOG ATCTACTACT AGAGAACTTT CTTGGTGTTC CTTGCTTCTCT CGTCAAATCT GAGAAATGT GAGCTCAGTT ATAAAGTTTG 51	120 180 240 300 360 420 480 540
40 Coding sequence: \$6-135 1 1 21 31 41 AGTECTORS SEQUENCE: \$6-135 45 COCINETE TOWNS THE SEQUENCE CONSIGNATION OF SEQUENCE CONSINCATION OF SEQUENCE CONSIGNATION OF SEQUENCE CONSIGNATION OF SEQU	COGCTCTTOG ATCTACTACT AGAGAACTTT CTTGGTGTTC CTTGCTTCTCT CGTCAAATCT GAGAAATGT GAGCTCAGTT ATAAAGTTTG 51	120 180 240 300 360 420 480 540 600
Nucleic Acid Accession 8: NN_001827 Coding sequence: \$6-315 1	COGCTCTTOG ATCTACTACT AGAGAACTTT CTTGGTGTTC CTTGCTTCTCT CGTCAAATCT GAGAAATGT GAGCTCAGTT ATAAAGTTTG 51	120 180 240 300 360 420 480 540 600
Nucleic Acid Accession 8: NN_001827 Coding sequence: 96-015 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	COGCTCTTOG ATCTACTACT AGAGAACTTT CTTGGTGTTC CTTGCTTCTCT CGTCAAATCT GAGAAATGT GAGCTCAGTT ATAAAGTTTG 51	120 180 240 300 360 420 480 540 600
Nucleic Acid Accession 8: IN 001827 Coding sequence: 96-015 1 1 1 21 31 41 AGTICTOCOS AGRITORIUG CROOGCODA COTROTTETA TECTROTROCO CONTENTATION CARGOGOGO CORROTTETA TECTROTROCO CONTENTATION CARGOGOGO CORROTTETA TECTROTROCO COMMANDE ACCEMANCE CARCURATE CROMANDO CROOTTETA CONTENTATION COMMANDE CONTENTATION COMMANDA ANTOMOTE TATROTROCA CAMATATION CONTENTATION CONTENTA	COGCTCTTCG ATCTACTACT ATCTACTACT ATCTACTACT CTTGGTOTCC CGTCAAATCT TGAGAAATCT TGAGAAATCT TGAGAAATCT CAGTCAGTT ATAAAGTTTG 51 SLGWVEYMIH	120 180 240 300 360 420 480 540 600
Nucleic Acid Accession 8: IN 001827 Coding sequence: 96-015 1 1 1 21 31 41 AGTICTOCOS AGRITORIUG CROOGCODA COTROTTETA TECTROTROCO CONTENTATION CARGOGOGO CORROTTETA TECTROTROCO CONTENTATION CARGOGOGO CORROTTETA TECTROTROCO COMMANDE ACCEMANCE CARCURATE CROMANDO CROOTTETA CONTENTATION COMMANDE CONTENTATION COMMANDA ANTOMOTE TATROTROCA CAMATATION CONTENTATION CONTENTA	COGCTCTTOG ATCTACTACT AGAGAACTTT CTTGGTGTCC ATTCTTCTCT CGTCAAATCT TGAGAAATGT GAGCTCAGTT ATAAAGTTTG	120 180 240 300 360 420 480 540 600
40 Coding sequence: \$6-315 1 1 21 31 41 45 COCINETS SEQUENCE: \$6-315 46 COCINETS SEQUENCE: \$6-315 47 COCINETS SEQUENCE: \$6-315 48 COCINETS SEQUENCE: \$6-315 49 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 41 1 1 21 31 41 41 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 41 COCINETS SEQUENCE: \$6-315 42 COCINETS SEQUENCE: \$6-315 43 COCINETS SEQUENCE: \$6-315 44 COCINETS SEQUENCE: \$6-315 45 COCINETS SEQUENCE: \$6-315 46 COCINETS SEQUENCE: \$6-315 47 COCINETS SEQUENCE: \$6-315 48 COCINETS SEQUENCE: \$6-315 49 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 41 COCINETS SEQUENCE: \$6-315 41 COCINETS SEQUENCE: \$6-315 42 COCINETS SEQUENCE: \$6-315 43 COCINETS SEQUENCE: \$6-315 44 COCINETS SEQUENCE: \$6-315 45 COCINETS SEQUENCE: \$6-315 46 COCINETS SEQUENCE: \$6-315 47 COCINETS SEQUENCE: \$6-315 48 COCINETS SEQUENCE: \$6-315 49 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 41 COCINETS SEQUENCE: \$6-315 41 COCINETS SEQUENCE: \$6-315 42 COCINETS SEQUENCE: \$6-315 43 COCINETS SEQUENCE: \$6-315 44 COCINETS SEQUENCE: \$6-315 45 COCINETS SEQUENCE: \$6-315 46 COCINETS SEQUENCE: \$6-315 47 COCINETS SEQUENCE: \$6-315 48 COCINETS SEQUENCE: \$6-315 49 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 41 COCINETS SEQUENCE: \$6-315 41 COCINETS SEQUENCE: \$6-315 42 COCINETS SEQUENCE: \$6-315 43 COCINETS SEQUENCE: \$6-315 44 COCINETS SEQUENCE: \$6-315 45 COCINETS SEQUENCE: \$6-315 46 COCINETS SEQUENCE: \$6-315 47 COCINETS SEQUENCE: \$6-315 48 COCINETS SEQUENCE: \$6-315 49 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCINETS SEQUENCE: \$6-315 40 COCI	COGCTCTTOG ATCTACTACT ATCTACTACT ATCTACTACT CTTGGTGTCC ATCTACTCTCGTCAAATCT CGTCAAATCT CGTCAAATCT GAGAATCT ATCAGAATTT ATAAAGTTTG 51	120 180 240 300 360 420 480 540 600
Nucleic Acid Accession 8: NN_001827 Coding sequence: 96-0155 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	COGCICTTOG ATCHACHACH ANGARACTIT CTTGGTGTCC ATTCHACTGTCC CGTCAAATCT CGCAGAATCT CGCCAGTCAGTT ATAAAGTTTG 51 SLGNVEYMIH 51 CTCCTCCTCGT	120 180 300 360 420 480 540 600
1	COGCICTTOG ATCHACHACH ANGAGACTIT CTTGGTGTC ATCHACTACT CGTCAAATCT TGAGAAATCT TGAGAATCT TGAGAATCT CGTCAATCT CGTCAATCT TGAGAATCT	120 180 300 360 420 480 540 600
40 Coding sequence: \$6-315 1 1 1 21 31 41 45 CODING sequence: \$6-315 46 CODING SEQUENCE: \$6-315 47 CODING SEQUENCE: \$6-315 48 CONTINUED CONTROLLED SEQUENCE CONCOUNTED TO TOTAL CONCOUNT OF THE SEQUENCE CONCOUNTED CON	COGCTCTCG ATCTACTACT ARCAGACTTC CTTGGTGTCC ATCTACTGTCC CTGGTGTCC CATCACTC CCAGTCAGTT CCAGTCAGTT CCAGTCAGTT ATAAAGTTTG 51	120 180 240 300 360 420 480 540 600
40 Coding sequence: \$6-315 1 1 1 1 1 1 1 1 1 1 1 1 41 41 41 41 41 4	COGCICTICG ATCTACTACT ATCTACTACT ATCTACTACT CTTGGTGTCC ATCTACTCTCGTGTCC ATCTACTCTCTCGTGTCC ATCTACTCTCTCTCGACAAATGT CCAGTCAGTT CCAGTCAGTT CCAGTCAGTT ATAAAGTTTG 51	120 180 240 300 480 480 600 600
40 Coding sequence: \$6-315 1 1 1 1 1 1 1 1 1 1 1 1 41 41 41 41 41 4	COGCICTICG ATCTACTACT ATCTACTACT ATCTACTACT CTTGGTGTCC ATCTACTCTCGTGTCC ATCTACTCTCTCGTGTCC ATCTACTCTCTCTCGACAAATGT CCAGTCAGTT CCAGTCAGTT CCAGTCAGTT ATAAAGTTTG 51	120 180 240 300 360 420 480 540 600
1	CGGCTCTGG ATCTACTACT AGGAGACTTCA ATCTACTACT ATTCTTCTCC CGTCAAATCT CAATCAGTT ATAAATTT CCAATCAGTT ATAAATTT S1 I CTCTCTCCTG CCTCATCAGT ATAAAGTTTG CCATTCAGT ATAAAGTTTG CTCTCTCCTG CCTCATCAGT ACCAGCGCG CGGAGGATCGGC CTCGAATTTGA	120 180 240 300 420 480 540 600
1	CCGCTCTTGG ATCTACTACT AGGGAGGATTTGA ATCTACTACT AGGGAGGATTGA ATCTACTACT ATCTACTACT ATCTACTACT CCGCTCAATCT CCACTACATCT CCACTACATCT ATCACTACT ACCACTACT ACCAC	120 180 300 420 420 480 600 60 120 180 240 300 480
1	CCGCTCTTGG ATCTACTACT AGGGAGGATTTGA ATCTACTACT AGGGAGGATTGA ATCTACTACT ATCTACTACT ATCTACTACT CCGCTCAATCT CCACTACATCT CCACTACATCT ATCACTACT ACCACTACT ACCAC	120 180 240 300 360 420 420 450 600 600 600
1	COGCICTION ACTACHACIA ANGONACTI ANGONACTI COTTORNA ANGOLICATI ANGOLICANI SI I I I I I I I I I I I I I I I I I	600 120 240 3000 240 3000 240 3000 240 3000 240 3000 240 3000 240 3000 240 3000 240 3000 240 3000 300
40 Coding sequence 9:6-315 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	COCCTOTOG ANCHACTACT ANCHACTACT COCCTOTOGATOR COTTOGATOR COTTOGATOR COTTOGATOR TOTOGATOR SI SI SI CTCTCAATOR COCCTOCATT ATAAAGTTTG SI SI CTCTCTCTC GCAATTGGA GCAATGGA TGGGAATGGA TGGAATGGA TGGGAATGGA TGGAATGGA TGGAATGGA TGGAATGAAT	120 180 240 300 360 420 420 450 600 600 600
40 Coding sequence: \$6-315 1 1 1 21 31 41 45 COCINETE SEQUENCE: \$6-315 46 COCINETE SEQUENCE: \$6-315 47 COCINETE SEQUENCE: \$6-315 48 COCINETE SEQUENCE: \$6-315 49 COCINETE SEQUENCE: \$6-315 40 COCINETE SEQUENCE: \$6-315 40 COCINETE SEQUENCE: \$6-315 40 COCINETE SEQUENCE: \$6-315 41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CONTROL OF THE PROPERTY OF T	120 180 300 360 420 480 540 600 600 600 240 300 340 340 600 720 780 780 780
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1	CONTROL OF THE PROPERTY OF T	120 240 360 360 360 420 480 540 600 600
40 Coding sequence 9:6-315 1 1 1 21 31 41 45 CODING SEQUENCE 9:6-315 46 CODING SEQUENCE 9:6-315 47 CODING SEQUENCE 9:6-315 48 CODING SEQUENCE 9:6-315 48 CODING SEQUENCE 9:6-315 49 CODING SEQUENCE 9:6-315 40 CODING SEQUENCE 9:6-315 40 CODING SEQUENCE 9:6-315 50 THARGARD TOTTOLOGIA CONTROLLED CONTROLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROL	CONTROL OF THE PROPERTY OF T	120 240 300 360 420 480 540 600 600 240 300 240 300 420 780 600 600 600 600 600 600 600 600 600 6
1	COCCTOTOGO ATCHACTACT ATCHACTACT ATCHACTACT ATCHACTACT ATCHACT ATCHACTACT ATCHACT ATCH	120 240 360 360 480 540 660 660 660 672 480 540 660 720 660 720 660 720 960 960 960
40 Coding sequence 9:6-315 1 1 1 21 31 41 45 CODING SEQUENCE 9:6-315 46 CODING SEQUENCE 9:6-315 47 CODING SEQUENCE 9:6-315 48 CODING SEQUENCE 9:6-315 48 CODING SEQUENCE 9:6-315 49 CODING SEQUENCE 9:6-315 40 CODING SEQUENCE 9:6-315 40 CODING SEQUENCE 9:6-315 50 THARGARD TOTTOLOGIA CONTROLLED CONTROLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROLLED CONTROL	CONTROL OF THE PROPERTY OF T	120 240 300 360 420 480 540 600 600 240 300 240 300 420 780 600 600 600 600 600 600 600 600 600 6

	CTTCTCATTT	GTTTGGGATC	TGGCCACCAA	GTTCCAGAAT	GATACACGGA	TCAGTGCAGA	1200
	AGTTCATCAG	GCTCTCGGAC	CTTAGGGCTG	TTGGAGAAGG	CTTCAGCAGC	AGAACTGATG	1260
	GTGAAGGCTC TTGGAAGGGC	GTGTTCTCCA	TCCTCAACTT	TCTTTGCTTC	GATCATACAC	AAGAATACAT	1320 1380
5	ACAGTCTGCT	AAAAAAATGAA	CACTGTCGTT	CATTGCAGCC	AGTCCATGCC	ACACAGATGC	1440
,	GCTTCATGAG	AGACTGACAG	CTATCAGGGG	TTGTGGCACT	TAGTGAGGAC	TCTCCTCCCC	1500
	GCTTCATGAG CAGTGTGTGC	TGATGACACA	TACACACCTG	ACAATAGCTT	GAGTCTTCTC	TGTTCCTTTT	1560
	ACTOTOTAGO CTTGTCCAAA	CAACATACAC	AAATTTADTA	ACCCTTTCTA	AATATCTATC	ATGGTTCATC	1620
10	CTTGTCCAAA	TGCAGAGTCA TTTGCAAAAA	GAGCTATTTG	TACTICATTA	TTATTTCCAA	GGCGAATAGT	1680 1740
10	AAACAAAAAA	111000000	170111700001	1111GIAIG1	100000000	200000000	2,40
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15	Nucleic Aci	ence: 204-2	285	70.1			
	courting and						
	1	11	21	31	41	51	
	1	GCGGCGCTGG	i common or i		TOTOTOTOTO	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	60
20	TEGOGGCTGG	CTCCTCTCCG	CTGCCGGCTG	CTCCTCGACC	AGGCCTCCTT	CTCAACCTCA	120
	GCCCGCGGCG	CCGACCCTTC	CGGCACCCTC	CCGCCCCCTC	TCGTACTGTC	GCCGTCACCG	180
	CCGCGGCTCC	GCCCTGGCC	CCGATGGCTC	TGTGCAACGG	AGACTCCAAG	CTGGAGAATG	240
	CTGGAGGAGA	CCTTAAGGAT GTACGGGAAA	GGCCACCACC	ACTATGAAGG	AGCTGTTGTC	ATTCTGGATG	300 360
25	A A ATTTTCCC	CTTCCABACA	CCACCATTIVE	CTATABAGGA	ACAAGGATTC	COTOCTATTA	420
	TCATCTCTGG	AGGACCTAAT TGGCAAGCCT	TCTGTGTATG	CTGAAGATGC	TCCCTGGTTT	GATCCAGCAA	480
	TATTCACTAT	TGGCAAGCCT	GTTCTTGGAA	TTTGCTATGG	TATGCAGATG	ATGAATAAGG	540
	TATTTGGAGG	TACTGTGCAC ATGTTCATTA	AAAAAAAGTG	TCAGAGAAGA	TGGAGTTTTC	AACATTAGIG	600 660
30	ATCCACATAC	TGTAGACAAA	GTAGCTGATG	GATTCAAGGT	TGTGGCACGT	TCTGGAAACA	720
	TAGTAGCAGG	CATAGCAAAT	GAATCTAAAA	AGTTATATGG	AGCACAGTTC	CACCCTGAAG	780
	TTGGCCTTAC	AGAAAATGGA	AAAGTAATAC	TGAAGAATTT	CCTTTATGAT	ATAGCTGGAT	840
	GCAGTGGAAC	CTTCACCGTG GTCAAAAGTT	CAGAACAGAG	AACTTGAGTG	TATTCGAGAG	ATCAAAGAGA	900 960
35	CAGCTTTGCT	AAATCGTGCT	TTGAACCAAG	AACAAGTCAT	TGCTGTGCAC	ATTGATAATG	1020
	CCTTTATGAG	AAAACGAGAA	AGCCAGTCTG	TTGAAGAGGC	CCTCAAAAAG	CTTGGAATTC	1080
	AGGTCAAAGT	GATAAATGCT	GCTCATTCTT	TCTACAATGG	AACAACAACC	CTACCAATAT	1140
	CAGATGAAGA	TAGAACCCCA AAGAAAAATC	ATTRICICATA	CTTTTCTTA	GATTGCCAAT	GAAGTAATTG	1260
40	GAGAAATGAA	CTTGAAACCA	GAGGAGGTTT	TCCTTGCCCA	AGGTACTITA	OGGCCTGATC	1320
	TAATTGAAAG	TCCATCCCTT	GTTGCAAGTG	GCAAAGCTGA	ACTCATCAAA	ACCCATCACA	1380
	ATGACACAGA	GCTCATCAGA AGATGAAGTG	AAGTTGAGAG	AGGAGGGAAA	AGTAATAGAA	CCTCTGAAAG	1440 1500
	ATTITICATAA	TCCATTTCCA	GGTCCTGGCC	TOTOTATOR	AGTAATATGT	GETGAAGAAC	1560
45	CTTATATTTG	TAAGGACTTT	CCTGAAACCA	ACAATATTTT	GAAAATAGTA	GCTGATTTTT	1620
	CTGCAAGTGT	TAXAAAGCCA	CATACCCTAT	TACAGAGAGT	CAAAGCCTGC	ACAACAGAAG	1680
	AGGATCAGGA	GAAGCTGATG	CAAATTACCA	GTCTGCATTC	ACTGAATGCC	TTCTTGCTGC	1740 1800
	CCAGTAAAGA	TGTAGGTGTG TGAACCTGAC	TGGGAATCAC	TTATTTTTCT	GGCTAGGCTT	ATACCTCGCA	1860
50							1920
	CAGATGTTAC	TCCCACTTTC	TTGACAACAG	GGGTGCTCAG	TACTTTACGC	CAAGCTGATT	1980
	TOATTTTTAC	TAACATTCTC	TTTGATCGGG	ACCCACTTCA	BARGCAGCCT	TCATGCCAGA	2100
	GATCTGTGGT	TATTCGAACC	TTTATTACTA	GTGACTTCAT	GACTGGTATA	CCTGCAACAC	2160
55	CTGGCAATGA	TATTCGAACC GATCCCTGTA	GAGGTGGTAT	TAAAGATGGT	CACTGAGATT	AAGAAGATTC	2220
	CTGGTATTTC	TCGAATTATG	TATGACTTAA	CATCAAAGCC	CCCAGGAACT	ACTGAGTGGG	2280
	AGTAATAAAC	TTCTTGTTCT	ATTAAAA				
60	Seq ID NO:	118 Protei	n sequence:				
	Plotein Acc	centron #:	MILIZATO. 1				
	1	11	21	31	41	51	
65	J	 ENAGGDI.KDG	<u></u>	1	1	- CONTRACT DED	60
03	MALCNGDSKL	ATTTSCCDMS	HHHYEGAVVI	PATPTTGKPV	TORKVERTEV	NKVFGGTVHK	120
	KSVREDGVFN	ISVPNTCSLF	RGLQKESVVL	LTHGDSVDKV	ADGFKVVARS	GNIVAGIANE	180
	SKKLYGAOFH	PEVGLTENGK	VILKNELYDI	AGCSGTFTVQ	NRELECTREI	KERVGTSKVL	240
70	VLLSGGVDST	VCTALLNRAL	NQEQVIAVHI	DNGFMRKRES	QSVEBALKKL	GIQVKVINAA	300 360
70	HSPYNGTITL PUPI ACCTT.P	PISDEDKTPK DDLTEGACLU	REISELLMAI	HUNDTELIER	LREEGEVIER	VIGENNLKPB LKDPHKDEVR	420
	TIGREIGLPE	ELVSRHPFPG	PGLATRVICA	EEPYICKDFP	BTNNILKIVA	DFSASVKKPH	480
	TLLQRVKACT	TERDORKLMO	ITSLHSLNAF	PP-BIKIAGAÖ	GDCRSYSYVC	GISSKDEPDW ADFEAHNILR ATPGNEIPVE	540
75	ESLIFLARLI	PRMCHNVNRV	VYIFGPPVKE	PPTDVTPTFL	TTGVLSTLRQ	ADFEAHNILR	600 660
13	ESGYAGKISQ	KIPGISRIMY	DEDPLOKOPS	CORPASIELL	TTSDFMTGIP	ATPGNEIPVE	660
	Seq ID NO:	119 DNA se	quence				
80	Nucleic Ac	id Accessio uence: 27	1 #: NM_UU6:	500.1			
50	ouring sad	wente: 4/					
	1	11	21	31	41	51	
	!	<u> </u>		1	I	GCCTTCTTGC	60
85	TOGOCCCTG	CTGCTGCTGT	CCTCGCGTCG	CGGGTGTGCC	CGGAGAGGCT	GAGCAGCCTG	120
	CCCCTGAGCT	GGTGGAGGTG	GAAGTGGGCA	GCACAGCCCT	TCTGAAGTGC	GGCCTCTCCC	180
	AGTCCCAAGG	CAACCTCAGC	CATGTCGACT	GGTTTTCTGT	CCACAAGGAG	AAGOGGACGC	240

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	TCATCTTCCG	TOTTOTOTAG	GGCCAGGGCC	AGAGOGAACC	TGGGGAGTAC	GAGCAGCGGC	300
	TCAGCCTCCA	GGACAGAGGG	GCTACTCTGG	CCCTGACTCA	AGTCACCCCC	CAAGACGAGC	360
	CCATCTTCTT	GTGCCNGGGC	AAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	COTOCCAGGA	GTACCGCATC	CAGCTCCGCG	420
-	TCTACAAAGC	TCCGGAGGAG	CCAAACATCC	AGGTCAACCC	CCTGGGCATC	CCTGTGAACA	480
5	GTAAGGAGCC	TGAGGAGGTC	GCTACCTGTG	TAGGGAGGAA	CGGGTACCCC	ATTCCTCAAG	540
	TCATCTGGTA	CAAGAATGGC	CGGCCTCTGA	AGGAGGAGAA	GAACCGGGTC	CACATTCAGT	600
	CGTCCCAGAC	TGTGGAGTCG	AGTGGTTTGT	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	660
	TGGTTAAAGA	AGACAAAGAT	GCCCAGTTTT	ACTGTGAGCT	CAACTACCGG	CIGCCCAGIG	720 780
10	GGAACCACAT TGTGGCTGGA	GAAGGAGTCC	AGGGAAGTCA	CCGTCCCTGT	TFTCTACCCG	ACAGAAAAAG	840
10	GTTTGGCTGA	AGTGGAGCCC	GIGGGAATGC	TUNNUGARUG	CARCCACARG	COCRCCACCA	900
	GGGAGGCAGA	TOGCAACCCT	CONCORCACACT	*COCCCTCCT	CCTCCTCCAAC	CCCAGCACCA	960
	GGGAGGCAGA	DOGGGGGGGGGGGG	GAATGTCAGG	ACGGGGGTCCT	CONCACCATO	ATATOGCTGC	1020
	AGGAACACAG	1GGGCGCIAI	CTGGTGAACT	PARAMETERS A	COTCOCACTG	ACTCCCCCAG	1080
15	COCCOTCACAC	ACAGGAACIA	AGCAGCCTCA	CCCCGACCTG	TGAGGCAGAG	ACTACCCAGG	1140
13	CCCCTGMGMG	CONCRETE	AGAGAAGAGA	CAGACCAGGT	CCTCCGAAAGG	GGGCCTGTGC	1200
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	BACKBORCCA	AGATOCACAG	CCACTCCTGA	GCACCCTGAA	TGTCCTCGTG	ACCCCGGAGC	1500
	TGTTGGAGAC	AGGTGTTGAA	TGCACGGCCT	CCAACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
	TCTTCCTGGA	GCTGGTCAAT	TGCACGGCCT TTAACCACCC	TCACACCAGA	CTCCAACACA	ACCACTGGCC	1620
							1680
25	TGCCGGAGCC	GGAGAGCCGG	GGCGTGGTCA CTCTATTTCC	TCGTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740.
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							1860
	TTAAGTCAGA	TAAGCTCCCA	GAAGAGATGG	GCCTCCTGCA	GGGCAGCAGC	GGTGACAAGA	1920
30	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
30	CAGCTCCCTT	CCCTGCCTGG	ACCATTCCCA	GCTCCCTGCT	CACTOTTOTO	TCAGCCAAAG	2100
	CCTCCAAAGG	GACTAGAGAG	AAGCCTCCTG AGGACCTCAC	CTCCCCTCAC	CIGCACACCC	TC1TTCAGAG	2160
	GGCCACTGGG	TTAGGACCTG	CGTTGAGTGA	TIGGCCCTGC	ANGCOGCITI	COCCACTOR	2220
	GICCACCACC	ACCIOCICCA	CTTGCAGAAC	CHARTETTE	TTTACACACA	TTATGGCTGT	2280
35	BARTA CODOC	WOOMONO!!!	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCCTCCCC	2340
33	CANAGGCTGG	CTTCCACCAT	CCAGGTGCAC	CACTGAAGTG	AGGACACACC	GGAGCCAGGC	2400
	GCCTGCTCAT	GTTGAAGTGC	GCTGTTCACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCAGTGTTGC	TGCCACCACC	CTCCTGCTCG	CCTCTTCAAA	GTCTCCTGTG	2520
	ACATEMPTTC	TTTCCTCACA	ACCCAGGAAC	TGGTGTCATT	CCTTAAAAGA	TACGTGCCGG	2580
40	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC CATCCTGGCT	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGTC	AGGACGAGAC	CATCCTGGCT	AACACGGTGA	AACCCTGTCT	CTACTAAAAA	2700
	TACAAAAAAA	AATTAGCTAG	GCGTAGTGGT	TGGCACCTAT	AGTCCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAGG	AGAATGGTAT	GAATCCAGGA	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
4.5	CACTGCACTC	CAGCCTGGGC	AACACAGOGA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAG	2880
45							2940
	TCCCCGTGTT	CACTTGCTCC	CATAGCCCTC	TTGATGGATC	ACGTAAAACT	GAAAGGCAGC	3000
	GGGGAGCAGA	CAAAGATGAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGGTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAAGGG	CCCAAATGAG	3120 3180
50	AGAATGGTAC	TTAGGGATGG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3240
30	CTGTGTGTAT	GCATACATAT	GTGTGTATAT TGTATATATA	ATGGTTTTGT	TARGETOTOTA	MATTIGUAGA	3300
	TIGTITCCIT	TATATATGTA	AATCATACAT	TATATORARA	THIMINIALA	CERCCACAGG	3360
	AAAGCTTAAT	TGTCCCAGAA	TACAACCAAA	ACCCACACAA	AACCOPPTCC	ACTTOCCAGC	3420
							3480
55	AGAGATCAGG	TTTCACCACC	AAAACGTCCC CTTCCTATCG	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
55	TOTTACONG	AGCTATGTCC	CTTCCTATCG	TTTCCGTCCA	CTT		
	IGIINGCAGO	A0011110100	01100111100				
60	Seq ID NO: Protein Acc	120 Protein cession #: 1	n sequence: NP_006491.1				
	1	11	21	31	41	51	
	1	1	1			1	
65	MGLPRLVCAP	LLAACCCCPR	VAGVPGEAEQ	PAPELVEVEV	GSTALLKOGL	SQSQGNLSHV	60
	DWFSVHKEKR	TLIFRVRQGQ	GOSEPGEYEO	RLSLQDRGAT	LALTQVTPQD	BRIFLCQGKR	120
	PRSQEYRIQL	RVYKAPERPN	IQVNPLGIPV	NSKEPBEVAT	CVGRNGYPIP	QVIWYKNGRP	240
	LKEEKNRVHI	QSSQTVESSG	LYTLOSILKA	QLVKEDKDAQ	PACETNAKTA	SGNHAKESKE	300
70	VTVPVFYPTE	KVWLEVEPVG	MLKEGDRVEI	RCLADGNPPP	HESTREGUES	TREABBETIN	360
70	DNGVLVLEPA	RKEHSGRYEC	QAWNLDTMIS	PPREACHER	NIVSDVRVSP	AAPERQEGSS VPSIPGLNRT	420
	LTLTCRAESS	ODPREGMPKR	WVKENMVLNL	VIQUADURES	MUGGIRCVAB	ANDUNDONA	480
	QUVKIMAPGP	VANISATANWA	MAKETIMATIKE	TT DT DT INT O	TI THOCKTO	GLSTSTASPH	540
	PRITTINGENERAL	BLLBIGVECT	ASNULGANIS	TOP DED VIOLE	PLYVYCYIDC	RRSGKQEITL	600
75	DOCUMENT IN	KLIPEPESKGV	MGLLQGSSGD	ADVACOUGER	VIN.DU	ratoongus 12	
15	PPSKKIEDVV	PAKSDYDAPP	Mannyagan	MOTOPOOL	110000		
	Com TO MO.	121 DNA se	mionoo				
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	ATAGTCTACA	CAGAGCTCCC	CTTGCTGCCC	AGACAAGCTG	AAGGACCACA	GGAAAAGCCA	60
0.5	TGGAGACTTC	AGCATCCTCC	TCCCAGCCTC	AGGACAACAG	TCAAGTCCAC	AGAGAAACAG	120
85	AAGATGTAGA	CTATGGAGAG	ACAGATTTCC	ACAAGCAAGA	CGGGAAGGCT	GGACTCTTTT	180
	CCCAAGAACA	ATATGAGAGA	AACAAGTCTT	CTTCCTCCTC	CTTCTCTTCC	TCCTCATCCT	240
	CCTCATCTTC	TTCATCCTCC	TCCTCCTCAG	GTCCTGGGCA	TGGGGAGCCT	GACGTTTTGA	300

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	WO 02	/086443				000011mo10	360
	GACTCCGAAG	TCAACTCTAT	GACCCAGCAA	CTGGAGAGGT	GGAGGCCTCT	CAGTTAAGAA	420
	GACTGAATAT	AAAGAAAGAT	GATGAGTTTT	TCCATTTCGT	CCTCCTGTGC	TTTGCCATCG	480
-	GGGCCTTGCT	GGTGTGTTAT	CACTATTACG	CAGACTGGTT	CATGTCTCTT	GGGGTCGGCC	540
5	TGCTCACCTT	CGCCTCCCTG	GAAACCGTTG	GCATCTACTT	CGGACTAGTG	TACCGTATCC	600 660
	ACAGOGTCCT	CCAAGGCTTC AGGCCACTTC	CAGGTGGGCA	CCAGAAGTT	GCCCCAGTGT	GACCACCACT	720
	GCGACCCCTG	AGCCCACAAG	GGCAGAGCAG	CATTCTGAGA	GACGCACAGG	AGACCAAGCC	780
	AGACCAATAA	ACAGAACACT	TTTCCTTCCA	TGTGGTCTGA	ATGTTGGCAC	CAGCCCGGGC	840
10	AGGGGCATCT	CATTTGGGCA	GTACTGCTGT	GCAACCCAGC	TGCAAGGATG	GAAGGCAGAG	900
	GGTGGGTGTG	GGGCCTGAGG GAGGACAGCA	PACCACAGTA	CCTGGACCAG	CAGGAAGATT	CIGGGAGGIC	960 1020
	ATGGTTTTTC	TCARATCCCA	GGCTATCTGC	ATGCGCTCTC	AGGTGCTACC	GAGCCATCCT	1080
	GGGAGAGATG	GATGGTCCAC CAGGTAAGAT	TGCTTTGAGG	CAGGGAGCCA	TOGGGCTGGG	GCCCCTTGGT	1140
15	GAACCTGATG	CAGGTAAGAT	GCTGAGGACT	AAAACCATTT	TTTTTGCACC	CAAAAAAAA	1200 1260
	GGCAGGAAAA	TGATCATCAG	Chartanate	GUAGUUAGGU	COMPAGEMENT	CARGACCAAC	1320
	CTGGGCAACA	TAGTGAGACC	CCCATCTCTA	CAATTTTTTT	TTAATGACCA	AATGTGGCGG	1380
	TACATACCTG	TACATACCTG	CGGTTCCAGC	TACTCAAGAG	GCTGAGGCAG	GAGGACTGCT	1440
20	TGAGCCCAGG	AGTTCAGGGC	TGCAGTGAGG	TACGATCAAG	CCACTGCACT	CCAGCCTGGG	1500
	CGACAGAGCA	AGATCGTTTC	TCTAAAATT				
25		122 Protei: cession #: 1					
	1	11	21	31	41	51	
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20	METSASSSOP	ODNSOVHRET	EDVDYGETDF	HKQDGKAGLF	SOEQYERNKS	SSSSFSSSSS	60
30	8888888888	GPGHGEPDVL	KDELQLYGDA	PGEVVPSGES	GLRRRGSDPA	SGEVEASQLR	120 180
		FHFVLLCFAI FOKFRLTGFR		ADWPMSLGVG	DETFASEETV	GITFGLVIKI	180
35	Seq ID NO:	123 DNA sec	quence	_			
33	Nucleic Ac	id Accession uence: 243.	1 #: BC02254	12			
	couring seq	dence: 243.	.030				
	1	11	21	31	41	51	
40	l mmoomaaa	AGCCGATAAA	TOTOGGGGGG		Charmona	CGGCCAGGCC	60
70	CCTTCCTGCG	TCCGCACCTG	GCCCCGCGCG	CCCCTCTCGG	GCGTCCGGCT		120
	TGGCGGCTCG	GGTGGCGGCG	GTTCGGGCGG	COGCCTGGCT	GCTCCTCGGG	GCGGCGACGG	180
	GGCTCACGCG	CGGGCCCGCC	ACGGCCTTCA	ccccccccc	CTCTGACGCC	GCATAAGGG	240 300
45	CCATGTGTTC	TGAAATTATT AGTGAAGTTT	TTGAGGCAAG	TOTAL	AGATGGTTTC GCACACGTTGC	CACAGAGACC	360
73	TTAAACAGGA	CATTCCTGCA	GGACTTTATG	TGGATCCGTA	TGAGTTGGCT	TCATTACGAG	420
	AGAGRAACAT	AACAGAGGCA	GTGATGGTTT	CAGAAAATTT	TGATATAGAG	GCCCCTAACT	480
	ATTTGTCCAA	GGAGTCTGAA	GTTCTCATTT	ATGCCAGACG	AGATTCACAG	TGCATTGACT	540 600
50	GTTTTCAAGC	CTTTTTGCCT	GTGCACTGCC	GCTATCATCG	TTOTOLOGA	GARGATOGGA	660
50	TTTTGAAATG	CTGGGCTCAC	TCAGAAGTGG	CAGCCCCTTG	TGCTTTGGAT	AATGAGGATA	720
	TATCCCAATG	GAACAAGATG	AAGTATAAAT	CAGTATATAA	GAATGTGATT	CTACAAGTTC	780
	CAGTGGGACT	GACTGTACAT	ACCTCTCTAG	TATGTTCTGT	GACTCTGCTC	ATTACAATCC	840 900
55	TATGTAGTTA	ATTGATCCTT	AGAAACCTAA	ATAAGATCTA	TTAATTTCTG	ACGAGAGGTG	960
-	TTCTTCTAGA	ATTAATTACT	TTTATCTTTT	GTCTTCATTT	GTGGCCAAAA	TTATGTTTAC	1020
	TAGAGGAAAT	TTGGGATCAT	TCTCAGCTAA	TTCCAAAATG	TAGTGCTCTA	TTGCATGGAT	1080
	CCTTGGTAAT	CCTCAAGCAT	CAGATGCCAT	AAGGGGAAAC	TTAATTCTGC	TAAATTAATG	1140
60	GTAGAGACAA	ATTATTCTCA	TTTTGCAAGT	ACTITICAATT	TAAGCTACAA	ATTGAGAAAA	1260
00	COGTTATAAA	AAATAADAAT	ATAGGCCAGG	CACAGTGGCT	CACACCTGTA	ATCCCAGCAC	1320
	TTTGGGAGGC	CGAGGTGGGC	GGATCACCAG	AGGTCAAGAG	TTTGAGACCA	GCTTGGTGAA	1380
	ACCCTGTCTC	TACTAAAAAT GAAGGGTGAG	ACAAAAGTTA	GCTGGGGCTG	GTGGTGGGCA	TCTGTAGTCC	1440
65	CAGCTAATIG	CGCACCACTG	CACTACAGCC	TGGGGGACAG	AACGAGACCC	TOTCTCCAAA	1560
0.5	GGAAAAACAA	AAAAGAAGAA	TAAAATAATT	TGGATGAAAA	TCATGTTTAT	TTAAATAGTA	1620
	ATTOTOATOAG	ACTATTABAC	ATCTCCCACA	GTTTCAATGA	ABATCATTAA	ACTACCACAG	1680
	CTAAGAAATT	AATATTAATA	TAAAAAATTAT	TGATAATCTT	ADTTATTOA	G AATTGGCAAA	1740 1800
70	GGACTCC	A TICICCITI	ACAITITAT	G GTACAGAGT	A TGTCAGGAA	G ACAACTCAGA	1860
,,,	TTGCCATTT	T AAATAAAGT	GTACATGAA	C AAAAAAAA	A AAAAAA		
	Seg ID NO:	124 Protei	n sequence:				
75	Protein Ac	cession #:	AAH22542				
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90	MCSBIILRQE	VLKDGFHRDL	LIKVKPGESI	EDLHTCRLLI	KQDIPAGLYV	DPYELASLRE	60
80	RNITEAVMVS	ENFOIEAPNY LMFCDQAGSR	LSKESEVLIY	ARRDSQCIDO	FQAPLPVHCR	YHRPHSEDGE	120 180
	WINNEARGUA	ENVILOVEVG	LTVHTSLVCS	VILLITIES	KKKKK	CADEMEDICO	100
85	Seq ID NO:	125 DNA se	quence				
63	Nucleic Ac	id Accessio	n. #: NM_004	994.1			
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	1	11 	21	31	41	51 1	
	AGACACCTCT	GCCCTCACCA	TGAGCCTCTG	GCAGCCCCTG	GTCCTGGTGC	TCCTGGTGCT	60
5	CCTGAGAACC	TTTGCTGCCC	ACAGGCAGCT	GGCAGAGGAA	TACCTGTACC	GCTATGGTTA	120 180
	CACTCGGGTG	GCAGAGATGC	GTGGAGAGTC	GARATCTCTG	GGGCCTGCGC	TGCTGCTTCT	240
	CCAGAAGCAA	CTGTCCCTGC CGGTGCGGGG	TOCCAGACCT	TGAGCTGGAT	CANACCTTTG	AGGGGGACCT	300 360
10	CAAGTGGCAC	CACCACAACA	TCACCTATTG	GATCCAAAAC	TACTCGGAAG	ACTTGCCGCG	420
10	GGCGGTGATT	GACGACGCCT	TTGCCCGCGC	CTTCGCACTG	TGGAGCGCGG	TGACGCCGCT	480 540
	GCACGGAGAC	GGGTATCCCT	TCGACGGGAA	GGACGGGCTC	CTGGCACACG	CCTTTCCTCC	600
	TGGCCCCGGC	ATTCAGGGAG	ACGCCCATTT	CGACGATGAC	GAGTTGTGGT	CCCTGGGCAA	660 720
15	CATCTTCGAG	GCCGCTCCT	ACTCTGCCTG	CACCACCGAC	GGTCGCTCCG	ACGGCTTGCC	780
	CTGGTGCAGT	ACCACGGCCA	ACTACGACAC	CGACGACCGG	TTTGGCTTCT	GCCCCAGCGA	840
	GAGACTCTAC	ACCOGGGACG TCCTACTCCG	CCTGCACCAC	TGGGAAACCC	TCCGACGGCT	ACCICTGGTG	900 960
	CGCCACCACC	GCCAACTACG	ACCGGGACAA	GCTCTTCGGC	TTCTGCCCGA	CCCGAGCTGA	1020
20	CTCGACGGTG	ATGGGGGGCA TACTCGACCT	ACTCGGCGGG	GGAGCTGTGC	GTCTTCCCCT	TCACTTTCCT	1080
	TACCACCTCG	AACTTTGACA	GCGACAAGAA	GTGGGGCTTC	TGCCCGGACC	AAGGATACAG	1200
	TTTGTTCCTC	GTGGCGGCGC	ATGAGTTCGG	CCACGCGCTG	GGCTTAGATC	ATTCCTCAGT	1260
25	CGACGTGAAT	GGCATCCGGC	ACCTCTATGG	TCCTCGCCCT	GAACCTGAGC	CACGGCCTCC	1320
	AACCACCACC	ACACCGCAGC TCAGAGCGCC	CCACGGCTCC	CCCGACGGTC	TGCCCCACCG	GACCCCCCAC	1440
	TOTCCACCCC	TCAGAGCGCC ACTGCTGGCC	CCACAGCTGG	CCCCACAGGT	CCCCCCTCAG	CTGGCCCCAC	1500 1560
	TGCCTGCAAC	GTGAACATCT	TCGACGCCAT	CGCGGAGATT	GGGAACCAGC	TGTATTTGTT	1620
30	CAAGGATGGG	AAGTACTGGC GACAAGTGGC	GATTCTCTGA	GGGCAGGGGG	AGCCGGCCGC	AGGGCCCCTT	1680 1740
	GCTCTCCAAG	AAGCTTTTCT	TCTTCTCTGG	GCGCCAGGTG	TGGGTGTACA	CAGGCGCGTC	1800
	GGTGCTGGGC	CCGAGGCGTC	TGGACAAGCT	GGGCCTGGGA	GCCGACGTGG	CCCAGGTGAC	1860
35	CGGGGCCCTC	CGGAGTGGCA AAGGCGCAGA	TGGTGGATCC	CCGGAGCGCC	AGCGGGGGGG AGCGAGGTGG	ACCGGATGTT	1920
	CCCCGGGGTG	AAGGCGCAGA CCTTTGGACA	CGCACGACGT	CTTCCAGTAC	CGAGAGAAAG	CCTATTTCTG	2040
	CCAGGACCGC	TTCTACTGGC	GCGTGAGTTC	CCCGGAGTGAG	TAGGGCTCCC	TGGACCAAGT	2100
40	GCAGTGCCAT	ACCTATGACA GTAAATCCCC	ACTGGGACCA	ACCCTGGGGA	AGGAGCCAGT	TTGCCGGATA	2220
40		TTCTGTTCTG					2280
	Seq ID NO:	126 Protein	sequence:	ninutci i co		••••	
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	1	11	21	31	41	51 1	
	KSLWOPLVLV	LLVLGCCFAA	PROROSTLVL	PPGDLRTMLT	DRQLAESYLY	RYGYTRVAEM	60
50	RGESKSLGPA	DLPRAVIDDA	PETGELDSAT	LKAMRTPRCG	VPDLGRFQTF	EGDLKWEHEN	120
50	PDGKDGLLAH	APPPGPGIOG	DAHPDDDDELW	SLCKGVVVPT	REGNADGAAC	HFPFIFEGRS	240
	YSACTTDGRE	DGLPWCSTTA	NYDTDDRFGF	CPSERLYTRD	GNADGKPCQF	PPIFQGQSYS	300
	CTSEGRGDGR	LWCATTSNFD	DRDKLFGFCP SDKKWGPCPD	OGYSLPLVAA	HEFGHALGLD	HSSVPEALMY	360 420
55	CTSEGRGDGR PMYRFTEGPP	LWCATTSNFD LHKDDVNGIR	SDKKWGPCPD HLYGPRPEPE	QGYSLFLVAA PRPPTTTTPQ	HEFGHALGLD PTAPPTVCPT	HSSVPEALMY GPPTVHPSER	360 420 480
55	CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS PSSEGRGSPP	LWCATTSNFD LHKDDVNGIR AGPTGPPTAG OGRELIADKW	SDKKWGPCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV	QGYSLFLVAA PRPPTTTTPQ PVDDACNVNI PREPLSKKLP	PERCHALGED PTAPPTVCPT FDAIAEIGNO PPSGROVWYY	HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	360 420 480 540
55	CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV	LWCATTSNFD LHKDDVNGIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG	SDKKWGPCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGKMLLFSGR	QGYSLFLVAA PRPPTTTTPQ PVDDACNVNI FEEPLSKKLF RLWRFDVKAQ	HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FPSGRQVWVY MVDPRSASEV	HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	360 420 480
	CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV	LWCATTSNFD LHKDDVNGIR AGPTGPPTAG OGRELIADKW	SDKKWGFCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGKMLLFSGR	QGYSLFLVAA PRPPTTTTPQ PVDDACNVNI FEEPLSKKLF RLWRFDVKAQ	HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FPSGRQVWVY MVDPRSASEV	HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	360 420 480 540 600
55 60	CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK Seq ID NO:	LWCATTSNFD LHKDDVNGIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG AYPCQDRFYW 127 DNA Sec	SDKKWGPCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGKMLLFSGR RVSSRSELNQ HUENCE	QGYSLPLVAA PRPPTTTTPQ PVDDACNVNI PEEPLSKKLP RLWRFDVKAQ VDQVGYVTYD	HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FPSGRQVWVY MVDPRSASEV	HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	360 420 480 540 600
60	CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK Seq ID NO: Nucleic Ac:	LWCATTSNFD LHKDDVNGIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRFYW	SDKKWGPCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGKMLLFSGR RVSSRSELNQ Quence	QGYSLPLVAA PRPPTTTTPQ PVDDACNVNI PEEPLSKKLP RLWRFDVKAQ VDQVGYVTYD	HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FPSGRQVWVY MVDPRSASEV	HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	360 420 480 540 600
	CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK Seq ID NO: Nucleic Ac:	LWCATTSNFD LHKDDVNGIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRFYW 127 DNA Bed id Accession	SDKKWGPCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGKMLLFSGR RVSSRSELNQ Quence	QGYSLPLVAA PRPPTTTTPQ PVDDACNVNI PEEPLSKKLP RLWRFDVKAQ VDQVGYVTYD	HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FPSGRQVWVY MVDPRSASEV	HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR	360 420 480 540 600
60	CTSEGREDER PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK Seq ID NO: Nucleic Ac. Coding seq	LWCATTSNFD LHKDDVNGIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG AYPCQDRFYW 127 DNA see id Accession uence: 32-6	SDKKMGPCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGKMILFSGR RVSSRSELNQ PUENCE #1 NM_0041 70	QGYSLPLVAA PRPPTTTTPQ PVDDACNVNI PEEPLSKKLP RLWRFDVKAQ VDQVGYVTYD 81	HEFGHALGLD PTAPPTVCPT FDAIABIGNQ PPSGRQVWVY MVDPRSASEV ILQCPED	HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR DRMFPGVPLD	360 420 480 540 600 660
60	CTSEGREDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK Seq ID MO: Mucleic Ac. Coding seq 1 GCAGAAATAG GGTCGCCGGC	LMCATTSNFD LHKDDVNGIR AGPTGPTTAG QOPFLIADKW AQVTGALRSG AYPCQDRFYW 127 DNA see id Accession uence: 32-6*	SDKKNGFCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGKNILFSGR RVSSRSELNQ Quence 1 H: NM_0041 70 21 TCAACCCCGA TCGTGGAGGT	GGYSLFLVAA PRPPTTTTPG PVDDACAVNI PSEPLSKKLF RLMRFDVKAQ VDQVGYVTYD 81 31 GATGCTGAAC GCTGGGGCTG	HEFGRALGLD PTAPPTVCPT FDATAEIGNQ PPSGRQVWYY MVDPRSASEV ILQCPED 41 AAAGTGCTGT GAAGAGGAGT	HSSVPEALMY GPPTVHPBER LYLPKDGKYW TGASVLGPRR DRMPPGVPLD 51 CCCGGCTGGG	360 420 480 540 600 660
60 65	CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGRR RFSEGRGRR LDKLGLGGADV THDVFQYREK Seq ID MO: Nucleic Ac. Coding seq 1 GCAGAAATAG GGTGGCCGCG GGTGCCCGCGGG	LMCATTSNFD LHKDDVNGIR AGPTGPFTAG QGPFLIADKW AQVTGALRS AYFCQDRFYW 127 DNA see id Accession sence: 32-6' 11 CCTAGGGAGA CATTGGGGT CCTGCTGGG	SDIKNGFCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGKMLLPSGR RVSSRSELNQ Juence 1 H: NM_0041 70 21 	GGYSLFLVMA PRPPTTTTPQ PVDDACAVNI PEEPLSKKLP RLNRFDVKLP RLNRFDVKLP 81 31 1 GATGCTGAAC GCTGGGGCTG GCTGTTTCCC	HEFGRALGLD PTAPPTVCPT PDATAEIGNQ PFSGRQVWYY MVDPRSASEV ILQCPED 41 AAAGTGCTGT GAAGAGGAGT CTCACGGCCC	HSSVPEALMY GASYLGPRE LYLPKOGKYW TGASYLGPRE DRMFPGVPLD 51 } CCCGGCTGGG CTCTGGGCTC AGCATGAGAA	360 420 480 540 600 660
60	CTSEGRGDGR PMYRFTEOPP PTAGPTGPPS RFSEGRGRP RFSEGRGRP LDKLGLGGADV THDVFQYREK Seq ID MO: Mucleic Ac. Coding seq GCAGAAATAG GGTCGCCGGC GGTGCCAGCG CTTCAGGAAA CATGAAGCAG CATGAGGAAG CATGAGGAGA CATGAGGAAG CATGAGGAGAAG CATGAGGAG CATGAGGAG CATGAGGAG CATGAGGAG CATGAGGAG CATGAGGAGAAG CATGAGGAG CATGAGGAG CATGAGGAG CATGAGGAG CATGAGGAG CATGAGGAG CATGAGGAG CATGAGAGCAG CATGAGAGAAG CATGAGAGCAG CATGAGAGCAG CATGAGAGCAG CATGAGAGAAC CATGAGAGAAC CATGAGAGAAC CATGAGAGAAC CATGAGAGAAC CATGAGAGAC CATGAGAGAC CATGAGAGAC CATGAGAGAC CATGAGAC CATGAGCAC CATGACAC CATGAGCAC CATGAGCAC CATGAGCAC CATGACC	LMCATTSNPD LHKDDVNOIR AGPTGPPTAG QOPPLIADKW AQVTGALRSG AYPCQDRPYW 127 DNA see dd Accession eence: 32-6' 11 1 CCTAGGGAGA CAGTGGGCT CCTGCCTGCG AAGCAGATTG ACCATTGGGA	SDIKINGPCPD HLYGPRPEPE PSTATTYPLS PALPRILDSV RGKMLLPSGR RVSSRSELNQ Quence 1 H: NM_0041 70 1 1 TCAACCCCGA TCGTGGAGGT CGCTGCTGCT AAGAGCTGAA ATTCCTGTGG	GGYSLFLVAA PRPPTTTPQ PVDDACNVNI PEEPLSKKLF RUMRPDVKAQ VDQVGYVTYD 81 31 GATGCTGAAC GCTGGGGCTG GCTGTTTCCC GGGACAGGAA CACATCGGA	HEFGRACALD PTAPPTVCF PDAIAEIGNQ PFSGRQVWVY MVDPRSASEV ILQCPED 41 AAAGTGCTGT GAAGAGGAGT CTCACGGCCC GTTAGTCCTA	HSSVPRALMY GPPTVHPSER LYLPHOGKYW TGASVLGPRR DRMFPGVPLD 51 CCCGGCTGGG CTCTGGGCTC AGCATGAGAA AAGTGTACTT CAGTGGCCAA	360 420 480 540 660 660 120 180 240 300
60 65	CTSEGRGUS PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP RFSEGRGSRP LOKUGLGADV THDVFQYREK Seq ID NO: Nucleic Ac. Coding seq 1 	LWCATTSNED LHKDDVNOIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG AYPCQDRFYW 127 DNA med id Accession corner: 32-6 11 CCTAGGGAGA CAGTGGCCT CCTCCTGCG AAGCAGATTG ACCATTGGGA	SDIKINGFCCPB HLYGPREPE PSTATTVPLS PALPRILDSV RVSSRSELNQ RUENCE 1 1 NM_0041 70 21 TCAACOCCGA TCGTGGAGGT CGCTGCTGGT AAGAGCTGAA ATTCCTGTGG ATTGAGGATGG	GGYSLFUVAA PRPPTTTPQ PVDDACNVNI PSEPLSKKLF RUMRPDVKAQ VDQVGYVTVD 81 31 GATGCTGAAC GCTGGGCTG GCGGACAACAA CACAATCGGA ATCAGTTCTO	HEFGRALGLD PTAPPTVCTF FDAIAEIGNO PFSGRQVWVY MVDPRSASEV ILQCPED 41 AAAGTGCTGT GAAGAGGAGT CTCACGGCCC CTTATTCCAC GTTAGTCCTA AAACRGTTTC	ESSYPEALMY GPPTVHPSER LYLFKDGKYW TGASVILGPRE DRMFPGVPLD 51 } CCCGGGCTGGG CTCTGGCCTC AGCATGAGAA AAGTGTACTT CAGTGGCCAA TTTCTGGAAAC	360 420 480 540 600 660 120 180 240 300
60 65 70	CTSEGREGGS PMYRFTEGPP PTAGPTGPPS PASEGRGSRP LDKLGIGADV THDVPQYREK Seq ID NO. Nucleic Ac. Coding seq 1 GCAGRANATAG GGTCGCCGGC GGTGCCAGGG GTTCAGGAA CATGRAGAA CATGRAGAA AGGAGAAAATAG AGGCAATGAT	LWCATTSNFD LHKDDVNOIR AGPTGPTAG QOPFLIADKW AQVTGALRSG AYFCQDRFYW 127 DNA see td Accession sence: 32-6' CTAGGGAGA CAGTGGGGCT CCTGCCTGGG AGCAGATTG ACCATTGGGA TCCCTGAGG CCCTGAGG CCCTGAGG CCCTGAGG CCCTGAGG CCCTGAGG CCCTGAG	SDIKINGFCPBP EHLYGPREPEP FSTATTVPLS PALPRIKDSV RGWALLFSCR RVSSRSELNQ JULICE A #! NM_0041 TCAACCCCGA TCGTGGACGT CGCTGCTGGT AAGACTGGTA ATTCCTGTGG ACGAGCAAA ATTCAGGGCCA AGGAGGACAA AGGAGGCCCA	GGYSLFLVMA PRPFITTIPQ PVDDACNVNI PEEPLSKKLP RLMRFDVKAQ VDQVGYVTYD 81 31 GATGCTGAAC GCTGGGGCTG GCTGTTTCAC GGGACAAGAA CACAATCGGA ATCAGTTTGAAC ATCAGTTTGAA ATCAGTGGGTA	HEFGHALGU FTAPFTVCPT FDATAEIGNO FPSGRQWWY MVDPRSASEV ILQCPED 41 ANAGTGCTGT GANGAGGAGT CTCACGGCCC GTTAGTCCTA CTTATTCACG ANACAGTTC ANACAGTTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAG	HSSVPEALMY GPPTVHPSER LYLPKDGKYM TGASVLGPR DRMFPGVPLD 51 } CCCGGCTGGG CTCTGGGCTC AGCATGAGAA AGTGTACTT CAGTGGCCAA TTTCTGAAAC CCATACAGGC TGAATTTCCA	360 420 480 540 660 660 120 180 240 300
60 65	CTSEGREGGS PMYRFTEGPP PTAGPTGPPS PASEGRGSRP LDKLGIGADV THDVPQYREK Seq ID NO. Nucleic Ac. Coding seq 1 GCAGRANATAG GGTCGCCGGC GGTGCCAGGG GTTCAGGAA CATGRAGAA CATGRAGAA AGGAGAAAATAG AGGCAATGAT	LWCATTSNFD LHKDDVNOIR AGPTGPTAG QOPFLIADKW AQVTGALRSG AYFCQDRFYW 127 DNA see td Accession sence: 32-6' CTAGGGAGA CAGTGGGGCT CCTGCCTGGG AGCAGATTG ACCATTGGGA TCCCTGAGG CCCTGAGG CCCTGAGG CCCTGAGG CCCTGAGG CCCTGAGG CCCTGAG	SDIKINGFCPBP EHLYGPREPEP FSTATTVPLS PALPRIKDSV RGWALLFSCR RVSSRSELNQ JULICE A #! NM_0041 TCAACCCCGA TCGTGGACGT CGCTGCTGGT AAGACTGGTA ATTCCTGTGG ACGAGCAAA ATTCAGGGCCA AGGAGGACAA AGGAGGCCCA	GGYSLFLVMA PRPFITTIPQ PVDDACNVNI PEEPLSKKLP RLMRFDVKAQ VDQVGYVTYD 81 31 GATGCTGAAC GCTGGGGCTG GCTGTTTCAC GGGACAAGAA CACAATCGGA ATCAGTTTGAAC ATCAGTTTGAA ATCAGTGGGTA	HEFGHALGU FTAPFTVCPT FDATAEIGNO FPSGRQWWY MVDPRSASEV ILQCPED 41 ANAGTGCTGT GANGAGGAGT CTCACGGCCC GTTAGTCCTA CTTATTCACG ANACAGTTC ANACAGTTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAGTC ANACAG	HSSVPEALMY GPPTVHPSER LYLPKDGKYM TGASVLGPR DRMFPGVPLD 51 } CCCGGCTGGG CTCTGGGCTC AGCATGAGAA AGTGTACTT CAGTGGCCAA TTTCTGAAAC CCATACAGGC TGAATTTCCA	60 120 600 600 600 120 180 240 420 420 480
60 65 70	CTSEGRGUSE PMYRFTEGPP PTAGPTGPPS FYSEGRGSRP LDKLGIGADV THDVPDYREK Seq ID NO: Nucleic Ac. Coding seq GCAGAAATAG GGTCGCCGGC GGTGCCAGGG GGTGCCAGGG GGTGCCAGGA CTTCAGGAAA CATGAAGAA AGAGAAATAT AGCCCATGAT TTTTATTCTG TCCGGTGAAC	LMCATTSNPI LMKDDVNDIR AGPTGPFTAG GGPFLIADKW AQVTGALRSG AYPCODRFYW 127 DNA see id Accession sence: 32-6' CTTAGGGAGA CAGTAGGGCT CCTCCTGAGG AAGCAGATTG ACCATTGGGA TCCCTGAAG GCCTGGAG TTTAACAACG CATGGGCAC	SDIKINGFCPBP EHLYGPREPEP FSTATTVPLS PALPRIKDSV RGWHLFSGR RVSSRSELNQ PURICE 1 H 1 NM_0041 70 21 1 TCAACCCCGA TCGTGGACGT CGCTGCTGCT AGAGCCTGAA ATTCCTGTGG ACGAGCAAA ATTCCTGTGG ACGAGCAAA AGGAGGCCA TGGATGGCCG TGGATGGCCG TGGATGGCCG TGGATGGCCG TGGATGGCCA TGGATGGCAG TGGAGGCAA	GGYSLFLVMA PRPFITTIPQ PVDDACNVII PEEPLSKKLP RLNRFDVKAQ VDQVGYVTYD 81 31 GATGCTGAAC GCTGGGGCTG GCGACAAGAA CACAATCGGA ATCAGTTTCA ATGCTTTGAA ATGCTGTAAC ATGCTTTGAAC CACCTGGTA CACCTGGTA	### HEFGHALGLU PTAPPTVCPT FDATAEIGNO PPSGRGWWY MVDPRSASEV ILQCPED ###################################	HSSVPEALMY GPPTVHPSER LYLFKDGKYM TGASVLGPR DRMFPGVPLD 51 { CCCGGCTGGG CTCTGGGCTC AGCATGAGAA AGTGTACT CAGTUGCCAA TTTTCTGAAAC CCATACAGGC GAATGCCTT TGAATTCCA GAATGCCTT CCAAGGTGTG CCAAGGTGTG CCAAGGTGTG CCAAGGTGTG CCAAGGTGTG	360 420 480 540 600 660 120 240 300 240 360 420 480 540
60 65 70	CTSEGREGGS PMYRETEGPP PTAGFTGPPS PTAGFTGPPS PTAGFTGPS PTSEGRGSR LDKLGLGADV THDVFQYREK Seq ID MO: Nucleic Ac. Coding seq 1 GCAGAAATAG GGTGCCGGC GTTCEGGAAA GGTGCCAGC GTTCEGGAAA AGACAAACAC AGAGAAATT TTTTATTCTG TCCGGTGAAC CAGAGAATT CTCCGTGAAA CAGAGAATT CTCGGTGAAC CAGAGAATT CTCCGGTGAAC CAGAGAATT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAATT CGTGTGAAC CAGAGAAT CGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGAAC CAGAGAAT CGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CA	LMCATTSNED LMKDDVNOIR AGPTGPTAG QUPFLIADKW AQVTGALRSG AYPCQDRPYW 127 DNA see Ld Accession 11 CTAGGAGA CAGTGGGCA AAGAGA AAACTGGGA TCCCTGCTGCG AAGAGA CCCTGAGA GCCTGGAG CCTGCGAGA CCCTGAGA CCTAGAGACA TTAACAACG CATGGGCA ACCAGACCTG	SDKINGECPD EDKINGECPD EDKINGECPD EDKINGD EDK	GGYSLFUVAA PRPFITTPQ PVDDACNVNI PSEPLSKKLP PSEPLSKKLP RLMRPDVKAQ VDQVGYVYD 31 31 ATGCTGAAC GCTGGGGCTG GCACAACAA ACTGCGGAA ATGCTTTCCC ATGCTTTCCAA ATGCTGTAAA ATGTTGGTAA ATGTTGTAA ATGTTGTAAA ATGTTGTAAA CCTCTATGAA CCTCTATGAA CACCTGTCT AGTCCGCTTC AGTCCGCTTC AGTCCGCTTC	EFGRACAU PTAPPT/CPT PTAPT/CPT PDATAEIGNG PFSGRGWNY MVDPRSASEV IIQCPED 41 AAAGTGCTST GAAGAGGGT CTGATGCAGG GATGACAAGG GTTGATGCAG	HSSVPRALMY GPPTVHPSER LYLPHODKYM TGASVLGPRE DRMPPGVPLD \$1 CCOGCTSGG CTCTSGGCTC AGGTTANACA AGGTGGCCAA AGGTGGCCAA AGGTGGCCAA AGGTGGCCAA CCATACAGGC CGAATACAGGC GAATGCCTT CCAAGGTGT CCAAGGTGT CCCAAGGTGT CCCAAGGTGT CTCAACAGGC	360 420 480 540 600 660 120 180 240 300 420 420 420 600 650
60 65 70 75	CTSEGREGGS PMYRETEGPP PTAGFTGPPS PTAGFTGPPS PTAGFTGPS PTSEGRGSR LDKLGLGADV THDVFQYREK Seq ID MO: Nucleic Ac. Coding seq 1 GCAGAAATAG GGTGCCGGC GTTCEGGAAA GGTGCCAGC GTTCEGGAAA AGACAAACAC AGAGAAATT TTTTATTCTG TCCGGTGAAC CAGAGAATT CTCCGTGAAA CAGAGAATT CTCGGTGAAC CAGAGAATT CTCCGGTGAAC CAGAGAATT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAATT CGTGTGAAC CAGAGAAT CGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGAAC CAGAGAAT CGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CGTGTGAAC CAGAGAAT CA	LMCATTSNED LMKDDVNOIR AGPTGPTAG QUPFLIADKW AQVTGALRSG AYPCQDRPYW 127 DNA see Ld Accession 11 CTAGGAGA CAGTGGGCA AAGAGA AAACTGGGA TCCCTGCTGCG AAGAGA CCCTGAGA GCCTGGAG CCTGCGAGA CCCTGAGA CCTAGAGACA TTAACAACG CATGGGCA ACCAGACCTG	SDKINGECPD EDKINGECPD EDKINGECPD EDKINGD EDK	GGYSLFUVAA PRPFITTPQ PVDDACNVNI PSEPLSKKLP PSEPLSKKLP RLMRPDVKAQ VDQVGYVYD 31 31 ATGCTGAAC GCTGGGGCTG GCACAACAA ACTGCGGAA ATGCTTTCCC ATGCTTTCCAA ATGCTGTAAA ATGTTGGTAA ATGTTGTAA ATGTTGTAAA ATGTTGTAAA CCTCTATGAA CCTCTATGAA CACCTGTCT AGTCCGCTTC AGTCCGCTTC AGTCCGCTTC	### ALTERNACION OF THE PROPERTY OF THE PROPERT	HSSVPRALMY GPPTVHPSER LYLPHODKYM TGASVLGPRE DRMPPGVPLD \$1 CCOGCTSGG CTCTSGGCTC AGGTTANACA AGGTGGCCAA AGGTGGCCAA AGGTGGCCAA AGGTGGCCAA CCATACAGGC CGAATACAGGC GAATGCCTT CCAAGGTGT CCAAGGTGT CCCAAGGTGT CCCAAGGTGT CTCAACAGGC	600 540 600 660 120 180 300 300 480 540 660 720 780
60 65 70	CTSEGREGER PHYRETESIP PHAGETOPS PHYRETESIP PHAGETOPS PHAGETOPS SESSIORASE LOKICICADAY LOKICICADAY COCINICADAY COCINICADAY COCINICADAY COCINICADAY COCINICADAY COCINICADAY CARROLLARIA CATGARACAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAAA CATGARACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	LMCATTENED LMCATTENED LMCATTENED LMCATTENED LMCADE APPOALARS APPOA	SUKMIGPCIP HIT/ORPREPS PETATTYPIS PALPRILIDS PALPRILIDS RESSESSION TO THE STATE OF THE STATE TO THE STATE TO THE STATE ARGACCICA AR	QGYSLEVANA PREPTITED PREPTITED PREPLENCE PREPLENCE RIMREDVENQ VOQUGYVTYD 81 31 31 GATGCTGGAC GCTGGTGGCC GCTGGTTCCC GGGGACAGGAC ATGCGCTTCCA ATGCCGTTGAA ATGCCGTTGAA ATGCCGTTGAA ATGCCGTTGAA ATGCCGGTC ATGCCTTGAA ATGCCGCTCCCC CCCCCCCCCC	HEPGRAJGLD PTAPPTYCET FPARTAGE FPSGRQWWY MVDPRSASSV ILQCPED 41 ANAGECTET GANGAGGAG CTTAGECTA ANAGAGTAG GATAGTAGAG GATGAGAGG CTTAGTCAG ANAGAGTAG CTTAGTCAG ANAGAGTAG CTTAGTCAG CTTAGTC	STI LICENSTRUCTOR OF THE STANDARD OF THE STANDARD DEMPHOYPED DEMPHOYPED DEMPHOYPED DEMPHOYPED DEMPHOYPED OF THE STANDARD OF TH	360 420 480 540 600 660 120 180 240 300 420 420 420 600 650
60 65 70 75	CTSEGREGER PHYRETESIP PHAGETOPS PHYRETESIP PHAGETOPS PHAGETOPS SESSIORASE LOKICICADAY LOKICICADAY COCINICADAY COCINICADAY COCINICADAY COCINICADAY COCINICADAY COCINICADAY CARROLLARIA CATGARACAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAAA CATGARACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	LMCATTENED LMCATTENED LMCATTENED LMCATTENED LMCADE APPOALARS APPOA	SUKMIGPCIP HIT/ORPREPS PETATTYPIS PALPRILIDS PALPRILIDS RESSESSION TO THE STATE OF THE STATE TO THE STATE TO THE STATE ARGACCICA AR	QGYSLEVANA PREPTITED PREPTITED PREPLENCE PREPLENCE RIMREDVENQ VOQUGYVTYD 81 31 31 GATGCTGGAC GCTGGTGGCC GCTGGTTCCC GGGGACAGGAC ATGCGCTTCCA ATGCCGTTGAA ATGCCGTTGAA ATGCCGTTGAA ATGCCGTTGAA ATGCCGGTC ATGCCTTGAA ATGCCGCTCCCC CCCCCCCCCC	HEPGRAJGLD PTAPPTYCET FPARTAGE FPSGRQWWY MVDPRSASSV ILQCPED 41 ANAGECTET GANGAGGAG CTTAGECTA ANAGAGTAG GATAGTAGAG GATGAGAGG CTTAGTCAG ANAGAGTAG CTTAGTCAG ANAGAGTAG CTTAGTCAG CTTAGTC	STI LICENSTRUCTOR OF THE STANDARD OF THE STANDARD DEMPHOYPED DEMPHOYPED DEMPHOYPED DEMPHOYPED DEMPHOYPED OF THE STANDARD OF TH	60 120 360 600 600 120 300 420 420 420 420 720 780 720 780
60 65 70 75	CTSEGREGER PHYRETESIP PHAGETOPS PHYRETESIP PHAGETOPS PHAGETOPS SESSIORASE LOKICICADAY LOKICICADAY COCINICADAY COCINICADAY COCINICADAY COCINICADAY COCINICADAY COCINICADAY CARROLLARIA CATGARACAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAA CATGARACAAAA CATGARACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	LIMCATTSNEP LIMCATTSNEP LIMCATTSNEP LIMCATSNEP LIMCATSNEP LIMCATSNEP LATE DIA see LA Accession L	SUKMIGPCIP HIT/ORPREPS PETATTYPIS PALPRILIDS PALPRILIDS RESSESSION TO THE STATE OF THE STATE TO THE STATE TO THE STATE ARGACCICA AR	QGYSLEVANA PREPTITED PREPTITED PREPLENCE PREPLENCE RIMREDVENQ VOQUGYVTYD 81 31 31 GATGCTGGAC GCTGGTGGCC GCTGGTTCCC GGGGACAGGAC ATGCGCTTCCA ATGCCGTTGAA ATGCCGTTGAA ATGCCGTTGAA ATGCCGTTGAA ATGCCGGTC ATGCCTTGAA ATGCCGCTCCCC CCCCCCCCCC	HEPGRAJGLD PTAPPTYCET FPARTAGE FPSGRQWWY MVDPRSASSV ILQCPED 41 ANAGECTET GANGAGGAG CTTAGECTA ANAGAGTAG GATAGTAGAG GATGAGAGG CTTAGTCAG ANAGAGTAG CTTAGTCAG ANAGAGTAG CTTAGTCAG CTTAGTC	STI LICENSTRUCTOR OF THE STANDARD OF THE STANDARD DEMPHOYPED DEMPHOYPED DEMPHOYPED DEMPHOYPED DEMPHOYPED OF THE STANDARD OF TH	600 660 660 660 660 660 660 660 660 660

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	MLNKVLSRLG	VAGQWRFVDV	LGLEESLGS	VPAPACALLL	LPPLTAQHEN	FRKKQIBELK	
5	GQEVSPKVYP	MKQTIGNSCG	TIGLIHAVAN	NODKLGPEDG	SVLKQFLSET	EKMSPEDRAK	120
3	CFEKNEAIQA	AHDAVAQEGQ	CRVDDKVNFH	FILFNNVDGH	LYBLDGRMPF	PVNHGASSED	180
	TLLKDAAKVC	REFTEREQGE	VRFSAVALCK	AA			
10	Seq ID NO:	129 DNA sec	Tuence				
10	Nucleic Act	ld Accession	1 #: NM_0002	13			
	Coding sequ	ence: 127-5	385				
	1	11	21	31	41	51	
15	1	1	1	1	1	1	60
13	CGCCCGCGCG	CTGCAGCCCC	ATCTCCTAGC	GGCAGCCCAG	GCGCGGAGGG	AGCGAGTCCG	120
	CCCCGAGGTA	GGTCCAGGAC	GGGCGCACAG	CAGCAGCCGA	GGCTGGCCGG	*COOMICS NO	180
	AAGAGGATGG	CAGGGCCACG	CCCCAGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	240
	AGCGTCAGCC	TCTCTGGGAC	CTTGGCAAAC	CGCTGCAAGA GCCTACTGCA	AGGCCCCAGT	GRAGAGCIGC	300
20	ACGGAGTGTG	TCCGTGTGGA	TAAGGACTGC	GCCTACTGCA	CHUNCUMUNI	GITCAGGGAC	360
20	CGGCGCTGCA	ACACCCAGGC	GUAGCIGCIG	GAGACCCAGA	WOOD CO COLO	GRUCKICGIG	420
	GICATGGAGA	GCAGCTTCCA	ANTCACAGAG	CGTCTGCGGC	TIGACACCAC	CCIGCOGCGC	480
	AGCCAGATGT	CCCCCCAAGG	CCTGCGGGTC	CCCGTGGACC	CCGG1GMGGM	CARCCACTEC	540
	GAGCIGGAGG	TGTTTGAGCC	MCTGGAGAGC	CTCAAGAAGA	TOTACATCCT	CATGGACTIC	600
25	TOURCTOOK	TOTCCGATGA	CONCENCIAC	ATTGGATTTG	CCAACTETOT	CCIGGCICGG	660
23	ACCOMPOSOCO	ACCT CACCAG	CACCOCTICACI	ALIGORITIC	ACCOUNTAGE CO.	CARCAGTGAC	720
	ACCOLUTECT.	CCTTCAAGAA	CATCATCAGC	AAGCTGAAGG CTGACAGAAG	ATGTGGATGA	CTTCCGGAAT	780
	PARCOCCACC	CACACOCCAT	CTCACCCAAC	CTGGATGCTC	CTGAGGGGGG	CTTCGATGCC	840
	ATTOCTTOCAGA	CACCTOTOTO	CACCAGCGAC	ATTRICCTORC	GCCCCGACAG	CACCCACCTG	900
30	CTCCTCCTCT	CCACCGAGTC	AGCCTTCCAC	TATGAGGCTG	ATGGCGCCAA	COTGCTGGCT	960
50	GGCATCATGA	GCCGCAACGA	TGARCGGTGC	CACCTGGACA	CCACGGGCAC	CTACACCCAG	
	TACAGGACAC	AGGACTACCC	GTCGGTGCCC	ACCUTGGTGC	GCCTGCTCGC	CAAGCACAAC	1080
	ATCATCCCCA	TCTTTGCTGT	CACCAACTAC	TCCTATAGCT	ACTACGAGAA	GCTTCACACC	1140
	TATTTCCCTC	TOTOCTCACT	GOGGGTGCTG	CAGGAGGACT	CCTCCAACAT	CGTGGAGCTG	1200
35	CTGGAGGAGG	CCTTCAATCG	GÁTCCGCTCC	AACCTGGACA	TCCGGGCCCT	AGACAGCCCC	1260
-	CGAGGCCTTC	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGACGAGGAC	TGGGTCCTTT	1320
	CACATOOGGC	GGGGGGAAGT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGTG	1380
	GATGGGACGC	ACCITGIGGGA	GCTGCCGGAG	GACCAGAAGG	GCAACATCCA	TCTGAAACCT	1440
	TCCTTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
40	CTGCAAAAAG	ACCTGCGGTC	AGCTCGCTGC	AGCTTCAACG	GAGACTTCGT	GTGCGGACAG	1560
	TGTGTGTGCA	GCGAGGGCTG	GAGTGGCCAG	ACCTGCAACT	GCTCCACCGG	CTCTCTGAGT TGGGGAGTGC	1620
	GACATTCAGC	CCTGCCTGCG	GGAGGGCGAG	GACAAGCCGT	GCTCCGGCCG	TGGGGAGTGC	1680
	CAGTGCGGGC	ACTGTGTGTG	CTACGGCGAA	GGCCGCTACG	AGGGTCAGTT	CTGCGAGTAT	1740
4.5	GACAACTTCC	AGTGTCCCCG	CACTTCCGGG	TTCCTCTGCA	ATGACCGAGG	ACCICTCC	1800
45	ATGGGCCAGT	GTGTGTGTGA	GCCTGGTTGG	ACAGGCCCAA	GCTGTGACTG	TCCCCTCAGC	1860
	AATGCCACCT	GCATCGACAG	CAATGGGGGC	ATCTGTAATG	GACGTGGCCA	CTGTGAGTGT	1920
	GGCCGCTGCC	ACTGCCACCA	GCAGTCGCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC	1980
	TCGGCGATCC	ACCCGGGCCT	CTGCGAGGAC	CTACGCTCCT	GCGTGCAGTG	CCAGGCGTGG	2040
50	GGCACCGGCG	AGAAGAAGGG	GCGCACGTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGGTG	2100
50	GACGAGCTTA	AGAGAGCCGA	GGAGGTGGTG	GTGCGCTGCT	CCTTCCGGGGA	CGAGGATGAC	2160
	GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCAA	CAGCACTGTC	2220
	CTGGTGCACA	AGAAGAAGGA	CTGCCCTCCG	GGCTCCTTCT	GGTGGCTCAT	CCCCCTGCTC	2280 2340
	CTCCTCCTCC	TGCCGCTCCT	GGCCCTGCTA	CIGCIGCIAT	GCTGGAAGTA	COCCOMMENTS	2400
55	TGCAAGGCCT	GCCTGGCACT	TCTCCCGTGC	TOCAACCOAG	GICACATOGI	CTGTGCCTGC GGGCTTTAAG CACGCCCATG	2460
22	GAAGACCACT	ACATGCTGCG	GGAGAACCIG	AIGGCCICIG	CCALCITOON	CAACAACATG	2520
	CIGOGGGGGG	COMMUNICATION	#CM#CCCCCC	ACCATCAACC	CCACAGAGCT	GGTGCCCTAC	2580
	GGGCTGTCC	TROCCOCC	COCCETTIVE	ACCGAGAACC	TGCTGAAGCC	TGACACTCGG	2640
	GAGTGGGGG	AGCTGCGCCA	CCACCTTTOC	GAGAACCTGA	ACGAGGTCTA	CAGGCAGATC	2700
60	TOCCOTOTAC	ACARGUECCA	GCAGACCAAG	TTCCGGCAGC	AGCYCAATGC	CGGGAAAAAG	2760
00	CARCACCACA	CCATTOTOGA	CACACTGCTG	ATTGGGGGGGGG	GCTCGGCCAA	GCCGGCCCTG	2820
	CTCAACCTTA	CAGAGAAGCA	GGTGGAACAG	AGGGCCTTCC	ACGACCTCAA	GGTGGCCCCC	2880
	GGCTACTACA	COCTCACTGC	AGACCAGGAC	GCCCGGGGCA	TOGTGGAGTT	CCAGGAGGGC	2940
	GTGGAGCTGG	TGGACGTACG	GGTGCCCCTC	TTTATCCGGC	CTGAGGATGA	CGACGAGAAG	3000
65	CAGCTGCTGG	TGGAGGCCAT	CGACGTGCCC	GCAGGCACTG	CCACCCTCGG	CCGCCGCCTG	3060
	GTAAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGTCCTTTGA	GCAGCCTGAG	3120
	TTCTCGGTCA	GCCGCGGGGA	CCAGGTGGCC	CCCATCCCTG	TCATCCGGCG	TGTCCTGGAC	3180
	GGCGGGAAGT	CCCAGGTCTC	CTACCCCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
	TACATCCCCC	TGGAGGGTGA	GCTGCTGTTC	CAGCCTGGGG	AGGCCTGGAA	AGAGCTGCAG GGTCCGCCGT	3300
70	GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCCTGC	GGGGCCGCCA	GGTCCGCCGT	3360
	TTCCACGTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCCACC	TGGGCCAGCC	CCACTCCACC	3420
	ACCATCATCA	TCAGGGACCC	AGATGAACTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
	TCACAGCCAC	CCCCTCACGG	CGACCTGGGC	GCCCCGCAGA	ACCCCAATGC	TAAGGCCGCT	3540
	GGGTCCAGGA	AGATCCATTT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
75	GTAAAGTACT	GGATTCAGGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTG	3660
	CCCTCAGTGG	AGCTCACCAA	CCTGTACCCG	TATTGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
	TACGGGGGCTC	AGGGCGAGGG	ACCCTACAGC	TCCCTGGTGT	CCTGCCGCAC	CCACCAGGAA	3780
	GTGCCCAGCG	AGCCAGGGCG	TCTGGCCTTC	AATGTCGTCT	CCTCCACGGT	GACCCAGCTG	3840
	AGCTGGGCTG	AGCCGGCTGA	GACCAACGGT	GAGATCACAG	CCTACGAGGT	CTGCTATGGC	3900

GCCACCCAGA GGCCAGGGT CTCCGATGAC ACTGAGCACC TGGTGAATGG CCGGATGGAC 4260
TTTGCCTTCC CGGGAGCACAC CAACTCCCTG CAACGGATGA CAACACCCC ACCGGGTGC TAAGGACACC TGCTACCCC 4220
TATGGCACCC ACCTGAGCCC ACACGGCGTGC TAAGGACACTC CTCCACCCC 4320

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	ACACGGGACT	ACAACTCACT	GACCOGCTCA CGTCTCCTCC	CACCACTCAC	ACTOGACCAC	TECTETECC	4440 4500
	GACTACTCCA	CCCGCCTGGT	GTTCTCTGCC	CTGGGGGCCCA	CATCTCTCAG	AGTGAGCTGG	4560
_	CAGGAGCCGC	GGTGCGAGCG	GTTCTCTGCC GCCGCTGCAG	GGCTACAGTG	TGGAGTACCA	GCTGCTGAAC	4620
5							4680
	GACCTCCTGC	CCAACCACTC	CTACGTGTTC CATCACCATT CTTCACTTTG	CGCGTGCGGG	CCCAGAGCCA	GGAAGGCTGG	4740
	GGCCGAGAGC	GTGAGGGTGT	CATCACCATT	GAATCCCAGG	TGCACCCGCA	GAGCCCACTG	4800
	TGTCCCCTGC	CAGGCTCCGC	CTTCACTTTG	AGCACTCCCA	GTGCCCCAGG	CCCGCTGGTG	4860 4920
10	TTCACTGCCC	TGAGCCCAGA	CTCGCTGCAG	CTGAGCTGGG	AGCGGCCACG	CCCACCCACC	4980
10	GCATTCCCCCC	TOGGETACCI	GGTGACCTGT CAGCCCCGAG	ACCCCCCCCC	CCGTCCCGGG	CCTCAGCGAG	5040
							5100
	GAGGGCATCA	TCACCATAGA	GTCCCAGGAT GCTGCAAAGC	GGAGGACCCT	TCCCGCAGCT	GGGCAGCCGT	5160
	GCCGGGCTCT	TCCAGCACCC	GCTGCAAAGC	GAGTACAGCA	GCATCACCAC	CACCCACACC	5220
15	AGCGCCACCG	AGCCCTTCCT	AGTGGATGGG	CCGACCCTGG	GGGCCCAGCA	CCTGGAGGCA	5280
	GGCGGCTCCC	TCACCCGGCA	TGTGACCCAG GGACCAACAG	GAGTTTGTGA	GCCGGACACT	GACCACCAGC	5340
	GGAACCCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400 5460
	CCCCCGCCAT	GTCCCACTAG	GCGTCCTCCC	GACTCCTCTC	CACACCACCA	CTUAGCTACT	5520
20	CCATCCTTGC	CARCANGEGE	GCCCAGCCCA GCAAGGTCCG AGGACCCAGC	TOTAL TOTAL	CCCCAAACCT	ATTTOTALCC	5580
20	ABBUNGCTGG	CATGARGGGG	AGGACCAGC	CTTTGTTCTG	CACTTAATAA	ATGGTTTTGC	5640
	ACTG	grochochor	Mancechae		010117011701	A100111100	2010
	ALIO						
~ -							
25		130 Protein					
	Protein Ac	cession #: 1	NP_000204				
						51	
	1	11	21	31	41	51	
30	W Grananana	1	SLEGTLANEC	WAY WILLOWS	dimmoray.	CTURMBAND	60
50	CHITCAPILLAA	COORDINATION	ESSFQITEET	OTDITTLERSO	MSPOGLBARI.	PPGERRHEEL	120
							180
	POTDMRPEKL	KEPWPNSDPP	PSFKNVISLT PSTESAPHYE	EDVDEPRNKL	QGERISGNLD	APEGGPDAIL	240
~-	QTAVCTRDIG	WRPDSTHLLV	FSTESAPHYE	ADGANVLAGI	MSRNDERCHL	DITGTYTOYR	300
35							360
	EAPNRIRSNL	DIRALDSPRG	PIPAVTNYSY LRTEVTSKMP SDGLKMDAGI QPCLREGEDK QCVCEPGWTG IHPGLCEDLR TYSYTMEGDG	QKTRTGSFHI	RRGEVGIYQV	QLRALEHVDG	420
	THVCQLPEDQ	KGNIHLKPSF	SDGLKMDAGI	ICDVCTCELQ	KEVRSARCSF	NGDFVCGQCV	480 540
	CSEGWSGOTC	NCSTGSLSDI	ONCINERARY	POSTROBECUC	CACVCIGEGR	HODGECEIDA	600
40	CUCHOCOLVE	CNDRGRCSMG	TUDGI.CEDI.D	SCACOCOPRISMA	CERRCEACER	CALECTER	660
70	T.VOAPPUUUD	DITCHIMION	TYSYTMECTIC	APRIPHETULU	HKKKDCPPGS	PWWI-TPI-LI-L	720
							780
	SGNLKGRDVV	RWKYTNINNOR	PGFATHAASI	NPTELVPYGL	SLRLARLCTE	NLLKPDTREC	840
	AQLIQUEEN	LNEVYRQISG	PGFATHAASI VHKLQQTKFR	QQPNAGKKQD	HTIVDTVLMA	PRSAKPALLK	900
45							960
	LVEAIDVPAG	TATLGRRLVN	ITIIKEQARD PVEGELLFQP	VVSPEQPEFS	VSRGDQVARI	PVIRRVLDGG	1020
	KSQVSYRTQD	GTAQGNRDYI	PVEGELLFQP	GEAWKELQVK	LLELQEVDSL	LRGRQVRRPH	1080
	VQLSNPKFGA	HLCOPHSTTI	11RDPDELDR YWIQGDSESE SEPGRLAFNV	SPTSQMLSSQ	PPPHGDLGAP	QNPNAKAAGS	1140 1200
50	RKIHPNWLPP	SGKPMGYRVK	OWNERS A PARK	TROPUSATION	APPAPPARET	TAVEUCVCIU	1260
50	MUGEGPISSE	ARAL NUMBER	RMLLIENLRE	SOPVEYTURA	PHICAGWICPER	EATTNLATOP	1320
	KEDMOTETTE	DIPIUDAOSG	POVDSPLMYS	DOVLESPEGS	ORPSVSDDTR	HLVNGRMDFA	1380
	PPGSTNSLHR	MTTTSAAAYG	EDYDSFLMYS THLSPHVPHR	VLSTSSTLTR	DYNSLTRSEH	SHSTTLPRDY	1440
_	STLTSVSSHD	SRLTAGVPDT	PTRLVFSALG	PTSLRVSWQE	PRCERPLQGY	SVEYQLLNGG	1500
55	ETHIDI MY DND	ACTRUVVEDI.	T-PNHCYVPRV	RAGSORGWOR	ERECVITIES	OVHPOSPLCP	1560
	LPGSAFTLST	PSAPGPLVFT	ALSPDSLQLS PYKFKVQART	WERPRRPNGD	IVGYLVTCEM	AQGGGPATAP	1620
	RVDGDSPBSR	LTVPGLSENV	PYKFKVQART	TEGFGPEREG	IITIESQDGG	PFPQLGSRAG	1680
			TEPFLVDGPT	LGAQHLBAGG	BUTRHVTQEF	VERTLTTEGT	1740
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00	Sen ID NO:	131 DNA sec	mence				
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	Coding sequ	mence: 132.	.2231				
65				31 .	41	51	
03	1	11	21	1 .	14	1	
	COMPONENCE COM	COCACCOCAC	CCTCTGCCAG	GTTCGGTCCG	CCATCCTCGT	CCCCCCCCCCC	60
	GCCGGCCCCT	GCCCCGGGGCC	CAGGGATCCT	CCAGCTCCTT	TOGCCCGCGC	CCTCCCTTCG	120
	CTCCGGACAC	CATGGACAAG	TTTTGGTGGC	ACGCAGCCTG	GGGACTCTGC	CTCGTGCCGC	180
70	TGAGCCTGGC	GCAGATCGAT	TTTTGGTGGC TTGAATATAA	CCTGCCGCTT	TGCAGGTGTA	TTCCACGTGG	240
	AGAAAAATGG	TOGCTACAGO	ATCTCTCGGA	CGGAGGCCGC	TGACCTCTGC	AAGGCTTTCA	300
	ATAGCACCTT	GCCCACAATG	GCCCAGATGG	AGAAAGCTCT	GAGCATCGGA	TTTGAGACCT	360
	GCAGGTATGG	GTTCATAGAA	GGGCATGTGG	TGATTCCCCCG	GATCCACCCC	AACTCCATCT	420
75	GTGCAGCAAA	CAACACAGGG	GTGTACATCC	TCACATCCAA	CACCTCCCAG	TATGACACAT	480
75	ATTGCTTCAA	TGCTTCAGCT	CCACCTGAAG	AAGATTGTAC	ATCAGTCACA	GACUTGCCCA	540 600
	ATGCCTTTGA	1 GACCAATT	ACCATAACTA AATCCTGAAG	ACATCTACCO	CAGCAACCC	ACTGATGATG	660
	ACCTGAGCAG	COCCUCACO	ACTGAAAGGA	GCAGCACTTC	AGGAGGTTAC	ATCTTTTACA	720
	CCTTTTCTAC	TGTACACCCC	ATCCCAGACG	AAGACAGTCC	CTGGATCACC	GACAGCACAG	780
80	ACAGAATCCC	TGCTACCAGT	ATCCCAGACG ACGTCTTCAA	ATACCATCTC	AGCAGGCTGG	GAGCCAAATG	840
	AAGAAAATGA	AGATGAAAGA	GACAGACACC	TCAGTTTTTC	TGGATCAGGC	ATTGATGATG	900
	ATGAAGATTT	TATCTCCAGC	ACCATTTCAA	CCACACCACG	GGCTTTTGAC	CACACAAAAC	960
	AGAACCAGGA	CTGGACCCAG	TGGAACCCAA	GCCATTCAAA	TCCGGAAGTG	CTACTTCAGA	1020
0.5	CAACCACAAG	GATGACTGAT	GTAGACAGAA	ATGGCACCAC	TGCTTATGAA	GGAAACTGGA	1080
85							1140
	ATTCTACAAG	CACAATCCAG	GCAACTCCTA AGATGGCATG	GIAGTACAAC	GGAAGAAACA	GCTACCCAGA	1200
	AGGAACAGTG	GTTTGGCAAC	AGATOGCATG	AGGGATATCG	COMMICACCC	MUMUMAGACT	1260

	WO 02/ CCCATTCGAC GGACAACACC CCATGGGACG	AACAGGGACA	GCTGCAGCCT GACAGTTCCT	CAGCTCATAC GGACTGATTT	CAGCCATCCA CTTCAACCCA	ATGCAAGGAA ATCTCACACC	1320 1380 1440
5	CGCTTCAGCC CTCTTTCAAT TGGAAGAAGA	TACTGCAAAT GACAACGCAG TAAAGACCAT	CCAACACAC CAGAGTAATT CCAACAACTT CCAACAACTT	GTTTGGTGGA CTCAGAGCTT CTACTCTGAC	AGATTTGGAC CTCTACATCA ATCAAGCAAT	AGGACAGGAC CATGAAGGCT AGGAATGATG	1500 1560 1620 1680
10	ATACCTCTCA AGACTGGGTC GTTCCTTATC	TTACCCACAC CTTTGGAGTT AGGAGACCAA	AGGDAGGDA	GCAGGACCTT CTGTTGGAGA ACCCCAGTGG	CATCCCAGTG TTCCAACTCT GGGGTCCCAT	ACCTCAGCTA AATGTCAATC ACCACTCATG	1740 1800 1860 1920
15	GTCCTATAAG TGGCTTTGAT	GACACCCCAA TCTTGCAGTT	ATTCCAGAAT TGCATTGCAG	GGCTGATCAT TCAACAGTCG	CTTGGCATCC AAGAAGGTGT CAGAAAGCCA	CTCTTGGCCT GGGCAGAAGA AGTGGACTCA	1980 2040 2100 2160
	TTGGGGTGTA TACAGGGAGC	ACACCTACAC TGGGACACTT	CAGGAAATGG GCTGATGAGA CATTATCTTG AACAGATGCA ACTCTTAAAA	ATGTGCTACT	GATTGTTTCA	ACATAACCAT	2220 2280 2340
20	Seq ID NO: Protein Acc	132 Protein	sequence:				
25	Process Acc	CABION W. P	ouno 4372				
	PTMAOMBKAL	SIGFETCRYG	21 QIDLNITCRF PIEGHVVIPR	IHPNSICAAN	NTGVYILTSN	TSQYDTYCFN	60 120
30	GSSSERSSTS DERDRHLSFS	GGYIFYTFST GSGIDDDEDF AVEYENWNDEA	GPITITIVNR VHPIPDEDSP ISSTISTTPR HPPLIHHEHH TGTAAASAHT	WITDSTDRIP AFDHTKQNQD REERTPHSTS	ATSTSSNTIS WTQWNPSHSN TIOATPSSTT	AGWEPNEENE PEVLLQTTTR RETATOKEOW	180 240 300 360 420
35	GHQAGRRADM KDHPTTSTLT FGVTAVTVGD TPQIPEWLII	DSSHSTTLQP SSNRNDVTGG SNSNVNRSLS LASLLALALI	TANPNTGLVE RRDPNHSEGS GDQDTFHPSG LAVCIAVNSR	DLDRTGPLSM TTLLEGYTSH GSHTTHGSES RRCGQKKKLV	TTQQSNSQSF	STSHEGLEED	480 540 600 660
40	SKSQEMVHLV	NKESSETPDQ	PMTADETKNL	ONADWKICA			
	Nucleic Act	133 DNA sec Ld Accession Lence: 150-7	# : NM_0028	182			
45	,	11	21	31	41	51	
	CENCETTORS	1	GGAGGGAAGA	1	GGGAGGCGCC	GGCGCCAGAC	60
50	GCGGAGGGAA AGCCGAGCCG ATGATACTTC TTTCTCTTCC TGCGGGCAAA	GGAGCTACGA COGCCGCCGC CACTGAGAAT TGAGCAAGAA ACTGTTCCGA	GTAGCCGCCG CGCGCCCCA ACAGACGAGT ATTAAAACAC TTTGCCTCTG	AGAGGCCGCG TGGCGGCCGC CCAACCATGA TGGAAGAAGA AGAACGATCT	GAGCCAGCGA CAAGGACACT CCCTCAGTTT TGAAGAGGAA CCCAGAATGG	CGACCGACCC CATGAGGACC GAGCCAATAG CTTTTTAAAA AAGGAGCGAG	120 180 240 300 360
55	AGCCCAACGC AGTGCCCAA	GACCCTGAAG AGGTAGCGAC GCCAGAGCTG	CTGAAGCACA ATCTGTGCCA CGTGCCTGGG CTGGCCATCC	ACCACTACAT TCTGGAACAC GCTTCCTGAA	CACGCCGATG CCACGCTGAC TGCTGAGAAT	TTCGCCGACG GCACAGAAAT	420 480 540 600 660
60	AGGAGACCAA	GGAGGATGCT	TGCAGGAAAG GAAAAAGTGG GAGGAGAAGC TAAAAAATTT GACGTTATAT	TACCCTGCCC	CTCTTTTTCG	TTTCTTTTCC	720 780 840
65	Seq ID NO: Protein Ac	134 Protein cession #: 1	NP_002873				
70	ENDLPEWKER VWNTHADFAD	GTGDVKLLKH	21 SNHDFQFBPI KEKGAIRLLM RFLNAENAQK Q	RRDKTLKICA	NHYITPMMEL	KPNAGSDRAW	60 120 180
75	Nucleic Ac.	135 DNA sed id Accession uence: 277-	#: NM_000	1077.2			
80	1 CCCAACCTGG	11 GGCGACTTCA	21 GGTGTGCCAC	31 ATTCGCTAAG	GATACCGCCG	TOTOTOCAGA	60 120
	TCCTCCGAGC	ACTOGCTCAC	GAGGGGGCTC	mmoorage an	10000100	arraga	180

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	WO 02	GACCCCGCCA	CTCTCACCCG TGCACCGGGC	ACCCGTGCAC CGGGGCGCGG	GACGCTGCCC CTGGACGTGC	GGGAGGGCTT GCGATGCCTG	540 600
5	GCGCGCGGCT TCCCTCAGAC GATCATCAGT TTTCGTAGTT	CCCGTGGACC GCGGGGGGCA ATCCCCGATT CACCGAAGGT TTCATTTAGA CCCCACTACC	CCAGAGGCAG GAAAGAACCA CCTACAGGGC AAATAGAGCT GTAAATGTCC	TAACCATGCC GAGAGGCTCT CACAACTGCC TTTAAAAATG ATTTATATCA	CGCATAGATG GAGAAACCTC CCCGCCACAA TCCTGCCTTT TTTTTTATAT	CCGCGGAAGG GGGAAACTTA CCCACCCCGC TAACGTAGAT ATTCTTATAA	660 720 780 840 900 960
10	AAATGTAAAA AGCACTCACG	AAGAAAACA CCCTAAGCGC ACTTCATGAC GTCACACTGC	CCGCTTCTGC ACATTCATGT AAGCATTTTG	CTTTTCACTG GGGCATTTCT TGAACTAGGG	TGTTGGAGTT TGCGAGCCTC AAGCTCAGGG	GCAGCCTCCG GGGTTACTGG	1020 1080 1140 1200
15	Seq ID NO: Protein Acc	136 Protein	sequence:				
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20	ELLLHGAEP	PSADWLATAA NCADPATLTR RAAAGGTRGS	PVHDAAREGF	LDTLVVLHRA	PNSYGRRPIQ GARLDVRDAW	VMMMGSARVA GRLFVDLAEB	60 120
25	Nucleic Ac:	137 DNA sec id Accession lence: 104-	1 #: NM_058	196.1			
30	GCCCCCACCC	11 TCTGCTTGGC TGGCTCTGAC GAGCTGCTGC	CATTCTGTTC	TCTCTGGCAG	GTCATGATGA	TGGGCAGCGC	60 120 180
35	TCTCACCCGA GCACCGGGCC GGCTGAGGAG	CCCGTGCACG GGGGCGCGC CTGGGCCATC AACCATGCCC AGAGGCTCTG	ACGCTGCCCG TGGACGTGCG GCGATGTCGC GCATAGATGC	GGAGGGCTTC CGATGCCTGG ACGGTACCTG CGCGGAAGGT	CTGGACACGC GGCCGTCTGC CGCGCGGCTG CCCTCAGACA	TGGTGGTGCT CCGTGGACCT CGGGGGGCAC TCCCCGATTG	240 300 360 420 480
40	CTACAGGGCC AATAGAGCTT TAAATGTCCA CGCTTCTGCC	ACAACTGCCC TTAAAAATGT TTTATATCAT TTTTCACTGT	CCGCCACAAC CCTGCCTTTT TTTTTATATA GTTGGAGTTT	ACCTAGATA TTCTTATAAA TCTGGAGTGA	TTOGTAGTTT TAAGCCTTCC AATGTAAAAA GCACTCACGC	CCCACTACOG AGAAAAACAC CCTAAGCGCA	540 600 660 720
45	AGCATTTTGT	GGCATTTCTT GAACTAGGGA AGAACCAAAG	AGCTCAGGGG	GGTTACTGGC	TTCTCTTGAG	TCACACTGCT	840
50	Seq ID NO: Protein Ac	138 Protei: cession #: 1	n sequence: NP_478103.1				
	1	11	21	31	41	51	
55	MMMGSARVAE RLPVDLAEEL	LLLLHGAEPN GHRDVARYLR	CADPATLTRP AAAGGTRGSN	VHDAAREGFL HARIDAAEGP	DTLVVLHRAG SDIPD	ARLDVRDAWG	60
	Nucleic Ac	139 DNA se id Accessio uence: 272-	n.#: NM_058	1197.1			
60	couring seq						
	1	11	21 	31 1	41	51 1	
	CCCAACCTGG	GGCGACTTCA	GGTGTGCCAC	ATTCGCTAAG	TGCTCGGAGT	TAATAGCACC	120
65	GGATTTGAGG GGGCTGGCTG GGAGAGCAGG GCCGGCGGCG	GGGAGCAGCA	GAGGGGGCTC GGTGGGGGGG CGGGGAGCAG TGGAGCCTTC	ACCGCGTGCG CATGGAGCCG GGCTGACTGG	ACCGGAGGAA CTCGGCGGGCT GCGGCGGGGA CTGGCCACGG	GARAGAGGAG GCGGAGAGGG GCAGCATGGA CCGCGGCCCG	180 240 300 360
70	GGGTOGGGTA TAGTTACGGT CGGGCGACTC	GAGGAGGCCGA TGGAGGACGA GGGAGGCTTC	GGGCGCTGCT TCCAGGTGGG AGTTTGCAGG CTGGGGAGTT	GGAGGCGGGG TAGAAGGTCT GGAATTGGAA TTCAGAAGGG	GCGCTGCCCA GCAGCGGGAG TCAGGTAGCG GTTTGTAATC	CAGGGGGATGG	420 480 540 600 660
75	ACAGATCTCT TCATGATGAT ACTGOGCCGA	CGAATGCTGA GGGCAGCGCC CCCCGCCACT	GAAGATCTGA CGAGTGGCGG CTCACCGGAC	AGGGGGGAAC AGCTGCTGCT CCGTGCACGA GGGCGCGGGCT	GCTCCACGGC CGCTGCCCGG GGACGTGCGG	TAGATGGAAG GCGGAGCCCA GAGGGCTTCC GATGCCTGGG	720 780 840 900
80	GCGCGGCTGC CCTCAGACAT CATCAGTCAC	GGGGGGCACC CCCCGATTGA CGAAGGTCCT	AGAGGCAGTA AGAACCAGA ACAGGGCCAC TAGAGCTTTT	GAGGCTCTGA AACTGCCCCC AAAAATGTCC	GATAGATGOO GAAACCTOGG GCCACAACCC TGCCTTTAA	CGGTACCTGC GCGGAAGGTC GAACTTAGAT ACCCCGCTTT CGTAGATATA	960 1020 1080 1140 1200
85	TGCCTTCCCC TGTAAAAAA ACTCACGCCC	CACTACOGTA AAAAACACOG TAAGCGCACA	AATGTCCATT CTTCTGCCTT TTCATGTGGG	TATATCATTI TTCACTGTGT CATTTCTTGC	TOTATATATT TOGAGTITTO GAGCCTCGCA	CTTATAAAA TGGAGTGAGC GCCTCCGGAA TTACTGGCTT TAAAATAATT	1260 1320 1380 1440 1500

Cog ID NO. 140 Protein seguence: Protein Accession #: NP 478104.1

1	11	21	31	41	51	
1	1	1	1	1	1	
MEPAAGSSME	PAAGSSMEPS	ADWLATAAAR	GRVEEVRALL	EAGALPNAPN	SYCRRPIQUE	60
DRAFFARADA	ORI STREET	PER PROCES OFF.	BAAGUT DUDG	CENTRATEDED	DODAL CAMET	120

KEER

Seq ID NO: 141 DNA sequence

Nucleic Acid Accession #: NM_058195.1

15	coorng sed	deuce: 163-6					
1.5	1	11	21	31	41	51	
	1	1	1	1	1	1	
		GGCGCCTCCG					60
20		GTCCGGGTGG					120
20		AGGGAAGGCG					180
	GTGGGTCCCA	GTCTGCAGTT	AAGGGGGCAG	GAGTGGCGCT	GCTCACCTCT	GGTGCCAAAG	240
	GGCGGCGCAG	CGGCTGCCGA	GCTCGGCCCT	GGAGGGGGGG	AGAACATGGT	GCGCAGGTTC	300
		TCCGGATTCG					360
		GGCTCACGGG					420
25		TACTGAGGAG					480
	CATGATGATG	GGCAGCGCCC	GAGTGGCGGA	CCTCCTCCTC	CTCCACGGCG	CGGAGCCCAA	540
		CCCGCCACTC					600
		GTGGTGCTGC					660
		GTGGACCTGG					720
30		GGGGGCACCA					780
		CCCGATTGAA					840
		CGAAGGTCCT					900
		ATTTAGAAAA					960
~ ~		CACTACCGTA					1020
35		AAAAACACCG					1080
		TAAGCGCACA					1140
		TCATGACAAG					1200
	CTCTTGAGTC	ACACTGCTAG	CAAATGGCAG	AACCAAAGCT	CAAATAAAAA	TTAAAAAT	1260
40	TTCATTCATT	CACTC					

Seq ID NO: 142 Protein sequence: Protein Accession #: NP_478102.1

MGGGCVGPS LQLEGGEWRC SPLVPKGGAA ÄAELGPGGGE NMVRRPLVTL RIRRACGPPR VRVFVVHIPF LITGENARGA PAAVALVILMI LEGGELGGD LPREPGHDDG QRPSGGAAAA PREMAGLERP RHSHPTPARR CPGGLGGHAG GARGGGAGA RAKZLGPSAR GE

Seq ID NO: 143 DNA sequence Nucleic Acid Accession #: NM_018131 Coding sequence: 412..1107

GARATTGCAC ACTIAAAGAC ATCAGTGGAT GAAATCACAA GTGGGAAAGG AAAGCTGACT GATAAAGAGA GACAGAGACT TITGGAGAAA ATTCGAGTCC TIGAGGCTGA GAAGCAGAAA ОКТИМИДИЯ (ВСАДВДИЕТ ТІТОВДИМА АТТСЕЙТСЕ ТІТОВОСТІЙ ОВМОЯГАВМА АТТСЕЙТСЕ ТІТОВОСТІЙ ОВМОЯГАВМА АТТСЕЙТСЕ ОКТИМОВ СОСТАВТИТЬ ОСТАВОСТІЙ ОВМОЯГАВМА ВАЛСЕМОВІ ОКТОРОВІ ОКТИМОВ ОСТАВОТНІКО CHANCEATH TEORETON TETTINETCO ATTENDED THANAGATT CARACTOTA TITLETOTTA GETHURUGE ATTITIKANT AHARTITES CATTITICAT ANACCECCE ATCACCTT GEACCTCUG CATCONGRIGHE ANACCECCE ATCACCTT GEACCTCUG CATCONGRIGHE TOTACATCA COCCECANG ACAGANITO GERAGCAGG TETACTGAGA TACHACATT TETCACTGAG TACATGAGA TACHACATT TETCACTGAG ANAATACTTG GERAGGAAGA GATRACCTCAG GITATTGCTA ATGGGTTAAT CALCAGCAA GCARAGTATI TRANSTITICS GOGGITTIGA ARANTCHAMS ATRATRACC ARGGITCITA ACTOTOTICS CATICITATA GARGACCTA AGRARACCIA CARICCHAM TITURATUS ATTOTICARGA GOTOGIGATA GARACTATIT TITUTATUSA TOTICATA GARACTATA GARACTARA GAR

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	AAGTTGGGGA TCCCCAACTC	TGTTCTGCGC	ACGAAACAGT	ATCTGTTTGA	GGCATAATCT	TAAGTGGCCA	1860 1920
	CACACAATGT	TTTCTCTTAT	GTTATCTGGC	AGTAACTGTA	ACTTGAATTA	CATTAGCACA	1980
5	ATTGACAGTA	TITTAGTTAT	TTTTGGCATT	CTTAAAGCTG	GGCAATGTAA	TGATCAGATC	2100
		TGAACAGGTA TTCTAACATG					2160
	ATTTAATGTT	TT					
10				•			
	Seq ID NO:	144 Protein	sequence:				
	Protein Acc	ession #: 1	45 ⁷ 09090T				
15	1	11	21	31	41	51	
	Ĩ	1	1	ī	Ī	1	
	MEIQLKDALE	KNOOWLVYDO	QREVYVKGLL VEROTITOLS	FELSEFRRKY	ETTAKEVENL	NOLLYSORRA	60 120
20	DVQHLEDDRH	KTEKIQKLRE	ENDIARGKLE	EEKKRSEELL	SQVQSLYTSL	LKQQEEQTRV	180
20		TLDFENEKLD		IUKEUKKAKK	NNIAGIDELY	8	
	Seq ID NO:	145 DNA sec	Tuence	GR.			
25		ence: 50					
23							
	1	11	21	31	41	51	
20	CCGCCAGATT	TGAATCGCGG	GACCCGTTGG	CAGAGGTGGC	GGGGGGGGCA	TGGGTGCCCC	60
30	GACGTTGCCC	CCTGCCTGGC	AGCCCTTTCT	CAAGGACCAC	ATGGCCGAGG	CATTCAAGAA	120 180
	CCACTGCCCC	ACTGAGAACG	AGCCAGACTT	GGCCCAGTGT	TTCTTCTGCT	TCAAGGAGCT	240 300
	CCCTTTCCTT	GAGCCAGATG TCTGTCAAGA	AGCAGTTTGA	AGAATTAACC	CTTGGTGAAT	TTTTGAAACT	360
35							420 480 .
	CCTCTGGCCG	GCGAAGAAAG GAGCTGCCTG	GTCCCAGAGT	GGCTGCACCA	CTTCCAGGGT	TTATTCCCTG	540
		CCTTCCTGTG GTTTCAACTG					600 660
40	TGCCTGTGCA	GCGGGTGCTG	CTGGTAACAG	TGGCTGCTTC	TCTCTCTCTC	TCTCTTTTTT	720 780
	AAGGCAGTGT	CCCTTTTGCT	AGAGCTGACA	GCTTTGTTCG	CGTGGGCAGA	GCCTTCCACA	840
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45	ACAGTTTTTT	TGTTGTTGTG	TTTTTTTTTTT	TTTTTTTTT	GGTAGATGCA	TGACTTGTGT	1020
	TATTTTGTTT	AATGGAGACA GAATTGTTAA	TTCACAGAAT	AGCACAAACT	ACAATTAAAA	CTAAGCACAA	1080 1140
	AGCCATTCTA	AGTCATTGGG AGCGTCTGGC	GAAACGGGGT	GAACTTCAGG	TGGATGAGGA	GACAGAATAG	1200 1260
50	AGTGAGCCGC	GGGGCACATG	CTGGCCGCTC	CTCCCTCAGA	AAAAGGCAGT	GGCCTAAATC	1320
	CTTTTTAAAT	GACTTGGCTC	GATGCTGTGG	GGGACTGGCT	GGGGGAGAGA	AGGCCGTGTG	1380 1440
	CCAGGTCCCC	GCTTTCTTTG	GAGGCAGCAG	CTCCCGCAGG	GCTGAAGTCT	GGCGTAAGAT	1500
55	GCTGGAAACC	ATTOGCCCTC TCTGGAGGTC	ATCTCGGCTG	TAGAGCIGCA	ATAAAAAGCC	TGTCATTTC	1560
	Con In No.	146 Protein					
	Protein Ace	cession #: 1	NP_001159				
60							
	1	11	21	31	41	51 1	
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65		DDPIEEHKKH VRRAIBQLAA		KQFEELTLGE	FLKLDRERAK	NKIAKEINNK	120
	Nucleic Ac:	147 DNA sec	a#: NM_014	176.1			
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75	AGTGCATCCC	AGGCAGCTCT AGAGAGCTTC	TAGTGTGGAG	CAGTGAACTG	TGTGTGGTTC	CITCTACTIG	120 180
15	CCCCCAGGCA	TCACATGTTG	GCAAGATAAA	GACCAAATGG	ATGACCTGCG	AGCTCAAATA	240
	TTAGGTGGAG	CATTTGAACC	TCCTCAGATC	CGATTTCTCA	CTCCAATTTA	TCATCCAAAC	300 360
80	ATTGATTCTG	CTGGAAGGAT	TTGTCTGGAT	GTTCTCAAAT	TGCCACCAAA	AGGTGCTTGG	420 480
٥٠ .	AACCCTGATG	TCAACATCGC ACCCGCTCAT	GGCTGACATA	TCCTCAGAAT	TTAAATATAA	TANGCCAGCC	540
	TTCCTCAAGA	ATGCCAGACA TGCTTGATAA	GTGGACAGAG	AAGCATGCAA	GACAGAAACA	AAAGGCTGAT	600 660
85	CAGAAAAGGA	AGGCCAGTCA	GCTAGTAGGC	ATAGAAAAGA	AATTTCATCC	TGATGTTTAG	720
83	ACCTIVATANT	CTGGTTCATC	TATATTTCAT	GACATAATTT	TTGTGTAGTT	TATTTATCTT	780 840
	GTACATATGT	ATTTTGAAAT	CTTTTAAACC	TGAAAAATAA	ATAGTCATTT	AATGTTGAAA	900

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Seq ID NO: 148 Protein sequence: Protein Accession #: NP_054895.1 _

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	1	11	21	31	41	51	
	1	I	1	1	1	1	
			GITCWQDKDQ				60
	YPPEPPQIRF	LTPIYHPNID	SAGRICLDVL	KLPPKGAWRP	SLNIATVLTS	IQLLMSEPNP	120
10	DDPLMADISS	EFKYNKPAFL	KNARQWTEKH	ARQKQKADEE	EMLDNLPEAG	DSRVHNSTQK	180

DDPLMADISS RFKYNKP. RKASOLVGIE KKFHPDV

Seq ID NO: 149 DNA sequence Nucleic Acid Accession #: NM_003812 15

15	Coding sequ	uence: 224-2	722				
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20			CCCCGTGCCC				120
	CCATGCGCGC	CGAGCCGGCG	TGACCGGCTC	CGCCCGCGGC	CGCCCCGCAG	CTAGCCCGGC	180
	GCTCTCGCCG	GCCACACGGA	GCGGCGCCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGGCAG	240
	CAGCTCGCGG	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GGCGCTTCCT	GCGGCCCCCA	300
	ACCIGGGGGGG	CONGCTOGG	TGCCTGCCAG	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CGCACGCCGC	CCTGCCGCCT	360
25	GCTTCTCGTC	CTTCTCCTGC	TGCCTCCGCT	CGCCGCCTCG	TCCCGGCCCC	GCGCCTGGGG	420
	GCCTGCTGCG	CCCAGCGCTC	CGCATTGGAA	TGAAACTGCA	GAAAAAAATT	TGGGAGTCCT	480
			TGCAACAGAA				540
			TGCCTTCAAG				600
	ARCCCCTTAT	CACCITICITY	ACACANAGGC	ARGACACCAG	CABABACATA	ATABGGCTGT	660
30			TCCAGATTGA				720
50			TGTCTTCTGA				780
	ACCA CACAMAC	WALGOLLIGI	GAGAGCACTG	TTACTACCAT	CCAACCATCA	GAGGGGTCAA	840
			CAACCTGCAA				900
			CACTAGAGCT				960
35			TGGCAGGACA				1020
	CCLARCACCE	CHOCHETCCI	CCTTTCTCTC	TORATTACAG	TOOTTONANA	GARGGARGAG	1080
			GTATATTTGA				1140
	TA A MODERN	AAAACCTATA	AGAAGCATCG	CTCTTCTCAT	CCACATACCA	ACAACTTTCC	1200
	AAACTCCCCTC	CTCBACCTTG	TGGATTCTAT	TTACAAGGAG	CAGCTCAACA	CCAGGGTTGT	1260
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	CCIGGIGGCI	CATCACTTCT	CAAAATACCG	CCACCCCATT	AACCACCATC	CTCATCCTCT	1380
			CATTTCACTA				1440
			GAGTTGGTGT				1500
			TGGCTCAAAA				1560
45			CAGAATCCTG				1620
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			TCAACAGGCC				1740
			GGGAGGAGTG				1800
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55			AACTTCAGGG				2280
	TOGAGCTCCA	CGTATTOGTC	GTGGTGCCCA	TORGATCATT	CCAMCTICCI	TCTACCATCA	2340
			CATGTGGCCC				2400
							2460
60			TGAGCAGCTG				2520
oo			ATGAAGCCAC				2520
							2640
			TCATAATAGG				2700
							2760
65			GAATCAGCTG				2820
03			GCAGCAGTGT				2820
	CFFIGGGTGG	TAATUACTAC	GGAGCTAAAG	TIGGGGTGAC	AMOUNTGGGG	AAAAAGAAAA	
	CIGICICITY	TGGAAATAAT	GTCAAAGAAC	ACCITICACC	ACCIGTCAGT	AMALUGGGGA	2940
			TAAAAAGAAC				3000
70	ACGAAGGAAC	AACACACACA	CAAAAATTAA	ATGCAATAAA	GUAATCATTA	AAAA	

Seq ID NO: 150 Protein sequence: Protein Accession #: NP_003803

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			_				
75	1	11	21	31	41	51	
	1	1	1	I	ı	1	
	MKPPGSSSRQ	PPLAGCSLAG	ASCGPORGPA	GSVPASAPAR	TPPCRLLLVL	LLLPPLAASS	- 60
	RPRAWGAAAP	SAPHWNETAE	KNLGVLADED	NTLOQUESSN	ISYSNAMQKE	ITLPSRLIYY	120
	INQDSESPYH	VLDTKARHOO	KHNKAVHLAQ	ASFQIEAFGS	KFILDLILNN	GLLSSDYVEI	180
80	HYENGKPOYS	KGGEHCYYHG	SIRGVKDSKV	ALSTONGLIG	MFEDDTFVYM	IEPLELVHDE	240
	KSTGRPHIIO	KTLAGOYSKO	MKNLTMERGD	OWPFLSBLQW	LKRRKRAVNP	SRGIFEEMKY	300
	LELMIVNDHK	TYKKHRSSHA	HTNNFAKSVV	NLVDSIYKEQ	LINTRVVLVAV	ETWTEKDQID	360
	ITTNPVOMLH	EFSKYRORIK	QHADAVRLIS	RVTFHYKRSS	LSYFGGVCSR	TRGVGVNEYG	420
			WEPSSRKPKC				480
85	RDFLORGGGA	CLENRPTKLE	EPTECGNGYV	EAGEECDOGF	HVECYGLCCK	KCSLSNGAHC	540
			RDAVNECDIT				600
	NGRCKTRONO	COVINGTERA	GSDKFCYEKL	NTEGTEKGNC	GKDGDRWIOC	SKHDVFCGFL	660

	LCTNLTBAPR	IGOLOGELIP	TSFYHOGRVI	DCSGAHVVLD	DDTDVGYVED	GTPCGPSMMC	720
	LDRKCLQIQA	LNMSSCPLDS TNLIIGSIAG	KGKVCSGHGV	CSNEATCICD	FTWAGTDCSI	RDPVRNLHPP	780
5	Nucleic Aci	151 DNA sec d Accession lence: 250-1	1 #: NM_0239	15			
10	1	11	21	31	41	51	
10	GCACGAGGG	TTTCGTTTTC	ATGCTTTACC	AGAAAATCCA	CTTCCCTGCC	GACCTTAGTT	60
	TOABAGOTTA	TTCTTAATTA	GAGACAAGAA	ACCTGTTTCA	ACTTGAAGAC	ACCGTATGAG	120 180
	CCACGCCTC	AGCCAGCCAC	AAGTGTTTCC	TGACACGCAT	CTTTGCTTAC	ACTGCATCAC	240
15	AACTGAAGAA	AATOGTCCCC TGGGGTTCAA	CTTGACGCTT	GCAAAATTAC	CAAATAACGA	GCTGCACGGC	300
	CAAGAGAGTC	ACAATTCAGG	CAACAGGAGC	GACGGGCCAG	GAAAGAACAC	GGCAAGCATC	360 420
	TTGCTGAATG	ACACAATTGT GTTTAGCAGT	GTGGATCTTC	TTCCACATTA	GGAATAAAC	CAGCTTCATA	480
20	TTCTATCTCA ATACTCCATC	AAAACATAGT ATGCAGGATT TTTATGCAAA	GGTTGCAGAC	TACTTCAAGT	CGCTGACATT	CAGATACACT	540 600
20	TCAGTTTTGT	TTTATGCAAA	CATGTATACT	TOCATOGTGT	TCCTTGGGCT	GATAAGCATT	660
							720 780
~-	ATCCTGACAA	TATCTGTTTG ATGGTCAGCC	AACAGAGGAC	AATATCCATG	ACTGCTCAAA	ACTTAAAAGT	840
25							900 960
	AGGCAATTCA	TTCTGATCGG TAAGTCAGTC	AAGCCGAAAG	CGAAAACATA	ACCAGAGCAT	CAGGGTTGTT	1020
	GTGGCTGTGT	TTTTTACCTG	CTTTCTACCA	CACABABA	GCAGAATTCC	TTTTACTTT CTGCAAAGAA CTTTTTCATG GAGTGAAAGC TTACACTGAT	1080
30	ATTACACTTT	TCTTGTCTGC	GTGTAATGTT	TGCCTGGATC	CAATAATTTA	CTTTTTCATG	1200
	TGTAGGTCAT	TTTCAAGAAG TGCAAAGTGT	GCTGTTCAAA	AAATCAAATA	TCAGAACCAG	GAGTGAAAGC	1260 1320
	GTGTAGGCCT	TTTATTGTTT	GTTGGAATCG	ATATGTACAA	AGTGTAAATA	AATGTTTCTT	1380
35	TTCATTATCC	TTARAAAAAA	AA				
55							
	Seq ID NO: Protein Ac	152 Protein cession #: 1	n sequence: NP_076404				
40	1	11	21	31 	41	51	
	MGFNLTLAKL	PMNELHGQES	HNSGNRSDGP	GKNTTLHNEF	DTIVLPVLYL	IIFVASILLN FILCRYTSVL	60
	GLAVWIFFHI	RNKTSPIPYL	KNIVVADLIM	TLTFPFRIVH	DAGFGPWYFK	FILCRYTSVL	120 180
45	NGOPTEDNIH	DCSKLKSPLG	VKWHTAVTYV	NSCLEVAVLV	ILIGCYIAIS	VLSLPNIILT RYIHKSSRQF	240
45	NGQPTEDNIH ISOSSRKRKH	DCSKLKSPLG NQSIRVVVAV PIIYFPMCRS	VKWHTAVTYV PPTCPLPYHL	NSCLEVAVLV CRIPFTPSHL	ILIGCYIAIS DRLLDESAQK	RYIHKSSROF	240 300
45 50	NGQPTEDNIH ISQSSRKKH PLSACNVCLD Seq ID NO: Nucleic Ac	DCSKLKSPLG NOSIRVVVAV	VKWHTAVTYV PFTCFLPYHL PSRRLFKKSN Quence	NSCLFVAVLV CRIPFTPSHL IRTRSESIRS	ILIGCYIAIS DRLLDESAQK	RYIHKSSROF	240
	NGQPTEDNIH ISQSSRKKH PLSACNVCLD Seq ID NO: Nucleic Ac	DCSKLKSPLG NQSIRVVVAV PIIYFFMCRS 153 DNA see id Accessio	VKWHTAVTYV PFTCFLPYHL PSRRLFKKSN Quence	NSCLFVAVLV CRIPFTPSHL IRTRSESIRS	ILIGCYIAIS DRLLDESAQK	RYIHKSSROF	240
50	NGQPTEDNIH ISQSSRKRKH PLSACNVCLD Seq ID NO: Nucleic Ac Coding sequ	DCSKLKSPLG NQSIRVVVAV PIIYFFMCRS 153 DNA sei id Accession uence: 149-	VKWHTAVTYV PPTCPLPYHL FSRRLFKKSN Quence n #: D80008 739	NSCLFVAVLV CRIPFTPSHL IRTRSESIRS	ILIGCYIAIS DRLLDESAQK LQSVRRSEVR	RYIHKSSRQF ILYYCKEITL IYYDYTDV	240 300
	NGQPTEDNIH ISQSSRKRKH PLSACHVCLD Seq ID NO: Nucleic Ac Coding seq 1 GTTCGGCGCC	DCSKLKSPLG NOSIRVVVAV PIIYFFMCRS 153 DNA seid Accessio uence: 149- 11 AAAGCGCGGA	VKWHTAVTYV PFTCPLPYHL PSRRLFKKSN Quence n #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT	NSCLFVAVLV CRIPFTPSHL IRTRSESIRS .1 31 AGGCQAGAGC	ILIGCYIAIS DRLLDESAQK LQSVRRSEVR 41 CTGGCGCTGT CGTGAGAGCT	PYIHKSSROP ILYYCKEITL IYYDYTDV 51 AGGACTAGAA GGRGGTTGGC	240 300
50	NGQPTEDNIH ISQSSRKRKH PLSACHVCLD Seq ID NO: Nucleic Ac Coding seq 1 GTTCGGCGCC	DCSKLKSPLG NOSIRVVVAV PIIYFFMCRS 153 DNA seid Accessio uence: 149- 11 AAAGCGCGGA	VKWHTAVTYV PFTCPLPYHL PSRRLFKKSN Quence n #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT	NSCLFVAVLV CRIPFTPSHL IRTRSESIRS .1 31 AGGCQAGAGC	ILIGCYIAIS DRLLDESAQK LQSVRRSEVR 41 CTGGCGCTGT CGTGAGAGCT	PYIHKSSROP ILYYCKEITL IYYDYTDV 51 AGGACTAGAA GGRGGTTGGC	60 120 180
50 55	NGOPTEDNIH ISQSSRKRKH PLSACNVCLD Seq ID NO: Nucleic Ac. Coding sequ 1 GTTCGGCGCC CGAAAGGAGT AAGGCCGCG CGAGCTGCAT	DCSKLKSPLG NQSIRVVAV PIIYFFMCRS 153 DNA seid Accession uence: 149- 11	VKMHTAVTYV PPTCPLPYHL PFTCPLPYHL Quence n #: D80008 739 21 GCGGAGGCCG GAGCCAGAT CGTCGGCCAT AAGGGCAACT	NSCLEVAULV CRIPFTPSHL IRTRSESIRS 1.1 31 AGGCOAGAGC ACCATTITGG GTTCTGCGAA GCTTGCCGAA	ILIGCYIAIS DRLLDESAQK LQSVRRSEVR 41. CTGGGGGTGT GGTGAGAGGT AAAGCCATGG AACAGGATG	PYIHKSSROP ILYYCKEITL IYYDYTDV 51 AGGACTAGAA GOTGGTTGGC AACTGATCCG GACTCAGACA AATGAGCAA	60 120 180 240 300
50	NGOPTEDNIH ISQSSRKRKH PLSACNVCLD Seq ID NO: Nucleic Ac. Coding sequ 1 GTTCGGCGCC CGAAAGGAGT AAGGCCGCG CGAGCTGCAT	DCSKLKSPLG NQSIRVVAV PIIYFFMCRS 153 DNA seid Accession uence: 149- 11	VKMHTAVTYV PPTCPLPYHL PFTCPLPYHL Quence n #: D80008 739 21 GCGGAGGCCG GAGCCAGAT CGTCGGCCAT AAGGGCAACT	NSCLEVAULV CRIPFTPSHL IRTRSESIRS 1.1 31 AGGCOAGAGC ACCATTITGG GTTCTGCGAA GCTTGCCGAA	ILIGCYIAIS DRLLDESAQK LQSVRRSEVR 41. CTGGGGGTGT GGTGAGAGGT AAAGCCATGG AACAGGATG	PYIHKSSROP ILYYCKEITL IYYDYTDV 51 AGGACTAGAA GOTGGTTGGC AACTGATCCG GACTCAGACA AATGAGCAA	60 120 180 240
50 55	NOOPTENNIH I SOSSEKERH PLSACHVCLD Seq ID NO: Nucleic Ac. Coding sequence The sequence of the s	DCSKLKSPLG MOSIRVVAV PILYFFMCRS 153 DNA seid Accessio: uence: 149- 11. AAAGCSCGGA GAGTGGAAG GOGGGCCG GAGTTGGAAG CCAACTGATT TGCACTGTAG	VKMHTAVTTV PTTCELPYHL PSTRLFKKSN Quence n H: D80008 739 21 GCGGAGGCCG GAGCCCAGAT GGTCGGCCAT TGTTATATA TGATACCAAC CATACCATTA	NSCLEVAULV CRIPFTPSHL IRTRSESIRS .1 31 AGGCOAGAGC ACCATTTIGG GTTCTGCGAA GCCTGCCTTC ACAAACCAG TATCAAATT TGACCGCTTG TATCACTTT	ALI CTOGGCTGT CGCGCTGT CGTCAGAGCT AAAGCACTGT AAAGCATGT ACAGGATG CGACACTGT CTCGGATAGTGT CGACACTGT CTCGGATAGTGT CACAGGATG CACAGGATG CACAGGATGT CTCGGATAGTGT CTCGGATAGTGT CTCGGATAGTGT CTCGGATAGT CACAGGATGT CTCGGATAGT CACAGGATGT	S1 S1 S1 S1 S1 S1 S1 S1	60 120 180 300 360 420 480
50 55 60	NOOPTENNIH I SOSSEKERH PLSACHVCLD Seq ID NO: Nucleic Ac. Coding sequence The sequence of the s	DCSKLKSPLG MOSIRVVAV PILYFFMCRS 153 DNA seid Accessio: uence: 149- 11. AAAGCSCGGA GAGTGGAAG GOGGGCCG GAGTTGGAAG CCAACTGATT TGCACTGTAG	VKMHTAVTTV PTTCELPYHL PSTRLFKKSN Quence n H: D80008 739 21 GCGGAGGCCG GAGCCCAGAT GGTCGGCCAT TGTTATATA TGATACCAAC CATACCATTA	NSCLEVAULV CRIPFTPSHL IRTRSESIRS 1.1 31 AGGCOAGAGC ACCATTTIGG GTTCTGCGAA GCCTGCCTTC ACAAACCAG TATCAAATT TGACCGCTTG TATCACATTT TGACCGCTTG ATTACCATTT	ALI CTGGCGCTGT CGTGGGGCTGT CGTGAGAGCTGT AAAGCACTGTGAGAGTGTCTGAGAGTGTGTGAGAGTGTGAGAGTGTGTGAGAGTGTGA	S1 S1 S1 S1 S1 S1 S1 S1	60 120 180 240 300
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50 55 60	NOOPTENNIH I SQSSRKRKH PLSACNVCLD Seq ID NO: Nucleic Ac Coding seq i GTTCGGCGCC CGAAAGGAGT AAGGCGCGCG GGAGCTGCAT AGTTCTGGAG GTAAGGTTGAA AAATCGACG ATGGGAATAT TGAAGGTTTT	DCSKLKSPLG MOSIRVVAV PIIYFPMCRS 153 DNA se- id Accessio- id Accessio- anagegedga Gangegedga Gangegedga Gangagaaa angagaaa	VKMETAVITY PTCTLPYHL PSRRLFKKSN Quence d #: D80006 21 [GCGGAGGCCG GAGCCCAGAT CGTCGCCAT AAGGGCAACT CATACCTGTA TGATACCAAC CATACCTGTA TGCAAATCC AAGGATATGAA AAGATCTCT AGGATATGAA	NSCLEVAULU RTRSESIRS 1.1 31 AGGCOAGAGC ACCATTTIGG GTTCTGCGAA GCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTA ATTACGATTT TGACACTTA ACCACCAAAA	ALIGCYIAIS DRLLDESAQK LQSVRRSEVR 41 CONTROL	S1 INTERNATION OF THE STATE O	60 120 180 240 300 420 480 540 600
50 55 60	NOOPTEINIIM I SQSSRKRKH PLSACNVCLD Seq ID NO: Nucleic Ac Coding sequ free Coding sequ coding sequ free Coding sequ cod	DCSKLKSPLG MOSIRVVVAV PIIYFFMCRS 153 DNA sei- did Accession uence: 149- 11 ANAGCSCGGA GAGTGGGAAG GAGTGGGAAG GGGGCCCG GAGATGAAG GGTAGCGCCG GGAATGAAT GGAATGATT AATAATTATA GACATTAGAG GACATTAGAG GACATTTTAC CCGTCATGAC CCTCATGCC CTCATGCAC CCTCATCACC CTCATCACC CTCATC	VKMETAVTTV PFTCFLPYHL PSTRILFKKSN quence a #: D8000f 739 21 i GCGGAGGCCG GAGCCCAGAT GGTCGCCAT TGTGTATA TAGGCCAAC TGTTGTATAA TGGCAAATSC AAAGATCTA TGGCAAATSC AAAGATCTA TGGGAAATGA AATTTGAAA AATTTGAAA AATTTGAAA AATTTGAAG CATGGGAA CATGGCCCAA CATGGCCCAA CATGGCCCAA CATGGCCCAA CACACCTCC CCACACTCC CC	NSCLEVAULU. CRIPPTSHL IRTRSESIRS 1.1 31 AGGCOMBAGC ACCATITIOG GTTCTGCGAA GCCTICCTTC ACAAAACCAG TATCAAATT TGACCGCTTT TGACACTATA TGATGATTATGGC ATGATGATTATGGC ATGATGATGGC ATGTGACTATA TGATGATGGC ATGTGACTATA TGATGATGGC GGCACTTCCAC GGCACTTCCAC GTCACCTCC	A1 CONTROL OF CONTR	S1 ILYYCKEITL IYYDYTDV 51 AGGACTAGAA GGGTGGTTGGC AACTGATCGGCA ATGAAGCAAA TGGAGAGAAAT TGGAGAGAAAT TGGAGAGAAAT TGGAGAGAAAT TGGAGAGAAAT TGGAAGAAAT TGAAGAGTCCG TATTAAAAAAA AAGGAGTCCC TAACTCATTGGA	60 120 240 300 420 420 480 540 600 720 780 840
50 55 60 65	NOOPTENNIN I SQSSRKRKH PLSACHVCLD Seq ID NO: Nucleic Ac. Coding seq i GTTCGGCGCC CGAAAGGAGT AAGGCCCGGA GGAGCTGGAT AGGTCGATGGAT AGGTCGATGGAT AGGTCGATGGAT AGGTCGATGGAT AGGTCGATGGAT AGGTCGATGGAT AGGTCGATGGAT AGGAGGAGGATGGT	DCSKLKSPLG MOSIRVVVAV PIIYPPMCRS 153 DNA se- 164 Accessio- uence: 149- 11 AAAGCSGCGGA GAGGGCCGG GAGGTGGGAAG GGGGGCCG GAGATGAAG GCAACTGATA GCAATTACAC GACTATCAC CCACCCCTC TTAAGGTAAC CCACCCCTCT TTAAGGTAACAC CCACCCCTCT TTAAGGTAACAC CCACCCCCTC TTAAGGTAAGAC CCACCCCCTC TTAAGGTAAGAC CCCACCCCTC TTAAGGTAAGAC CCCACCCCTCT TTAAGGTAAGAC CCCACCCCTCT TTAAGGTAAGAC CCCACCCCTCT TTAAGGTAAGAC CCCACCCCCTCT TTAAGGTAAGAC CCCACCCCTCT TTAAGGTAAGAC CCCACCCCTCT TTAAGGTAAGAC CCCACCCCTCT TTAAGGTAAGC CCCACCCCTCT TTAAGGTAACC CCCACCCCTCT TTAAGGTAAGC CCCACCCCTCT TTAAGGTAACC CCCACCCCTCT TTAAGGTAACC CCCACCCCTCT TTAAGGTAACC CCCACCCCCTCT TTAAGGTAACC CCCACCCCCTCT TTAAGGTAACC CCCACCCCCTCT TTAAGGTAACC CCCACCCCCTCT TTAAGGTAACC CCCACCCCCTCT TTAAGGTAACC CCCACCCCCTCT TTAAGGTAACC CCCACCCCTCT TTAAGGTAACC CCCACCCCTCT TTAAGGTAACC CCCACCCCCTC CCCCCCCCCC	VKMETAVITY PFTCPLPYHL PFTCPLPYHL PFTCPLPYHL PFTCPLPYHL PFTCPLPYHL PFTCPLPYHL PFTCPLPYHL PFTCPLPYHL GUGAGGCG GAGCCAGAT GAGCCAGAT CGTCGCCAT TUTATACA AAGGCAACT CTTTATACAA AAGGCAACT CTTTATACAA AAGGCAACT CTTATACAA AAGGCAACT CTTATACAA AATTIGAAT AATTIGAAT CTCGATGGAA CCACCACTCC CTAAGAATACT CTAAGAATACT CTCGATGGAA CCACCACTCC CTAAGAATACT C	NSCLEVAULU CRIPTESHL IRTRSESIRS 1.1 31 AGGCOAGAGG ACCALTITIGG GTTCTGCGAA ACCALTITIGG GTTCTGCGAA ACCALTITIGG ACAAAACCALT ACAAAACCALT ATTACCALTIT ACCACCALAA CACCALAA ACCACAAA ACCACAAA ACCACAAA ACCACAAAA CACCAC	41 TOGGGGTOT COTTONION ACCARGANT TOTOLOGIA ACCARGANT TOTOLOGIA ACCARGANT TOTOLOGIA ACCARGANT A	S1 GGACTAGAA GGTGGTTGGG GGACATAGA GTGAGAAA TGAGAGAAA TTGAGAGAAA TTGAGAGAAA AGGAGTGT TATTAAAAA AAGGAGTCT TTAACATTAGAGCTTA	60 120 240 300 420 480 660 660 6720 780 840 900
50 55 60	NGOPTEMNIH ISOSSERIENI FLEACHVCLD Seq ID No NUCleic & C COding seq I GTTCGGGGGC CGMAAGGAGT AAGGCGGGA AATGCAATA AATTCTGGAG AATGCAATA AATTCTGGAG AATGCAATA AATTCTGGAG AATGCAATA AATTCTGGAGT CTCCTCCTCTTA AAATTCTGGAGT TGGAGTTGG	DCSKLISPIG MSSIRVVVM PSITYPMCRS MSSIRVVMM PSITYPMCRS 10 11 12 AAAGCSCCGA GAGGGCCCGA GAGGGCACCA GAGGGCCCGA GAGGGCCCGA GAGGGCCCCA GAGGGCCCCA GAGGGCCCCA GAGGGCCCCA GAGGGCCCCCA CTGCACAGGC CCCACCCCCA CTGCACAGGC CTCACCCTCCA CTGCACAGGC CTCACCCCCA CTTACAGGAGC CTCACCCCCC CTCACCCCCA CTTACAGGAGC CTCACCCCCC CTCACCCCCC CTCACCCCC TCACCCC CTCACCC CTCA	VINHTAUTY PEPTCELPHIL PERRELPKKSN perceptual perceptua	NSCLEVAVIA CELIPTESHIL IRTRSBSIRS .1 31 AGGCUNDAGAC ACCAPITTICG GTTCTGCGAA GCCANACCAG TATCAAATTT TAGCACCTAT ACCACAAAA TATCACACCAAA TATCACACCACC TAGCACCACC TAGCACCC TAGCACCACC TAGCACCACC TAGCACCACC TAGCACCACC TAGCACCACC TAGCACCC TAGCACCACC TAGCACCC AGCACCC AGCACCC AGCACCC TAGCA	41 TOTAL CONTROL OF THE PROPERTY OF THE PROP	51 1 AGGACTAGAA AGGACTAGAA AGGACTAGAA ACTAGAGAA ACTAGAGAA ACTAGAGAAA TGGAGAAA TGGAGAAAA TGGAGAAAA TGGAGAAA TGGAGAAAA TGGAGAAAA TGGAGAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAAA TGGAGAAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAA TGGAGAAAAA TGGAGAAAAA TGGAGAAAA TGGAGAAAAA TGGAGAAAAA TGGAGAAAAAA TGGAGAAAAA TGGAGAAAA	60 120 180 300 300 360 420 480 660 6720 780 840 960 960
50 55 60 65	NGOPTEMNIH ISGSSRIREN FLSACHVCID Seq ID NO: NUCleic Ac Coding seq TTOGGGGCC GUANGGNAT ANGCCAGG GAGGGATGAT TGAGGATGAT TGAGGATGAT AAATGAGCCAG GGGGGCCAC TGGGAATAT TGAGGATTAT TGAAGGTTTA GGGAGTGAT AGGAGTTTAT AGGAGTTTAT AGGAGTTTAT AGGAGTTTAT AGGAGTTTAT AGGAGTTTAT AGGAGTTTT GGAGTTT AGGAGTT GGAGTT	DCSKLISPIG MSSIRVVVAV PIIYEPHCRS ISJ DNA se- did Accessio. ISJ DNA se- did Accessio. ISJ DNA se- did Accessio. ISJ DNA se- did Accessio. ANAGCGCCCG GAGTIGARA GAGTIGATA GAGTIGATA GAGTIGATA GAGTIGATA GACTATCAG GACTATAGA GACTATCAG GACTATAGA TTAGACTTA TTAGACTTA TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TTAGACTTAC TAGACTTAC TTAGACT	VINHERATTY PEPTCELPHIL PERELPHKSN Quence I I	NSCLEVAVILV CILIPTESILI IRTRSESIES 1.1 31 AGGCAMAGAC ACCATITIOS GTTCTGGGAA GCCTTCTGGAA GCCTTCTGGAATTT ATTACACTT ATTACACTT ATTACACTT ATTACACATT ATTACACATT TGGTACTTAT ACCACCAMA ATTGTAGTAGT ATTGTACTAT TGGTACTTAT TGGTATTAT TGGTACTTAT TGGTATTATAT TGGTACTTAT TGGTATTATATACAC TGGCTATTCTTAT TGGTATTATATATATATATATATATATATATATAT	41 CONSIGNATION OF THE PROPERTY OF THE PROPE	RYTHKSSROP ILIYYCKETT IYYDYTDV 51 AGGACTAGAA GUTGGTTGGC GACTGGACA ACTGATCG GACTGGACA ACTGATCG GACCACCAG TTGGAGGAAA TTGGAGGAAA TTGGAGGAGA TTGAAGGATT TTGGAGGAGA TTGAAGGATT TTGGAGGAGA TTGAAGGATT TTGGAGGAGA TTGAAGGATT TTGGAGGAGA TTGAAGGATT TTGGAGGAGA TTGAAGGATT TTGGAGGAGA TTGAAGGATT TTGGAGGAGA TTGAAGGATT TTGGAGGAGA TTGAAGGATT TTGGAGGAGA TTGAAGGATT TTGGAGGAGA	60 120 180 240 360 420 660 720 660 780 900 960 1020
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50 55 60 65 70	NGOPTEMIN I I SQSSBRERS I SQSS	DCSKLISPION MOSIBAVVANA PIIIPPROCES 113 INA see 1149- 1151 INA see 1149- 1151 INA see 1149- 1170 INA 1	VINHERATTY PEPCOLPHIA PROPERTY PARTY PROPERTY PARTY PA	NSCLPYAVLV CILIPTERILI IRTHSESIES 1.1 3.1 3.1 AGGCARGAGA AGGCARGAGA AGGCARGAGA AGGCARGAGA TATCARAMTT TRANCAGATT TRANCAGATT TRANCAGATT ATTARACGATT TRANCAGATT TRAN	41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RYTHERSROP INTEGER TO STATE OF THE PROPERTY OF	600 1200 1800 1800 1800 1800 1800 1800 18
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	TTTTACCATG	TTGGCCAGGC TGGGATTACA TATGGTGCAA	TGGTTTCAAA	CTCCTGACCT	CAAGTGACCC	ACCTTGGCCT	2040
	CCCAAAGTTT	TGGGATTACA	AGTGTGGGCC	ACCGCGGCCA	GCCTATGATC	CATTTTGAAT	2100
	GAATTTTTTA	TATGGTGCAA	GGTGTCAATC	CACCTTCACT	TTTTCTTGGG	AATATAGATA	2160
5	TCCAGCTGTT	TCACTACCAT	TTTTTGAAAG	GACTGCCCTT	TGCTCTATCA	CCTTTGCATT	2220 2280
,	ATTCACCTOT	AGTAGTTGTC	TGARTGCCAA	TACCATATT	CTATCTACTC	TATGTAATTT	2340
	TCTABTABTT	TTTTCTCTCC CTTGAAACAG	ATAGTATTAA	TGTGTCATAT	TTTTGCTGTT	GTTTGTATTT	2400
	TTTGTAGAGA	TGGGGTTTCA	CCGTGTTGGC	CAGGCTGTGT	TGAACTCCTG	AGCTAAAGCA	2460
	ATACACTTGC	CTCGTCCTCC	CCATGTGCTG	GGATTACAGG	CGTGAGCCTT	GGTGCTGGCC	2520
10	CAGTGTACCA	CATTTCTTTT	TGAGATTTGT	TTTGGCTATG	TTAAGTCCTT	TGCTTTTGAT	2580
	GTGAAATTTG	GGAACAGGCA	GGGTGTGGTG	GCTTATGCCT	GTAATCCTAG	AACTTTGGGA	2640
	GCCTAGATG	GGTGGATCAC CTACAAAAA	TTGAGCTCAG	GAGTTCCAGA	CCAGCCCGGG	CCTATGGCAA	2700
	AACTCCGTCT	CGGCAGGCTG	TAGAAAAAAT	PAGCCAGGIG	CCCCACACCC	CARCACTOCA	2820
15	GTGAGCTGAG	ATCACACCAC	TGTACTCCAG	CTTGGGTGAC	AAAGTGAGAC	TCTATCTCAA	2880
13	AAAGAAATTA	ATCACACCAC GGATCAATTT	GTCAATTTCT	ACAACAACAA	CAACAAAAAC	CCCTGTTGGG	2940
	CACCTTGATT	GAGATTGCAT	TGAATTTATA	TAAAACTGTT	GGGAGAATTG	ACATCTTAAT	3000
	AATATTGAGT	CTTCTGGCCT	ATAAACAAGG	TCTGTCTTCC	TAGGTATTAA	TGTTTTGTCT	3060
20	TOTATTTCTC	TTAATAATCT	TTTGTACTTT	TCAGTGTACA	GGTCTACCAT	GTCAGCATTT	3120
20	CATAGTTTTG	ATGCTAAATG	GTATTTTAAA	ATTTCAAATT	CTAACCACTT	GTTGCTAGTA	3180
	AATAGAAATA	CAATTGATGT	TGAACTTGTA	TCCTTCAGCC	TTGCTAAACT	GTGAGTTCTC	3240
		TGTAAATTAC	ATCAACAGTC	ATGTGTTCTA	TGAATAAAGA	GTTTTACTCC	3300
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	TIKPRHCSLL	RNRRCTVAYL	YDRLLRIRAL	RMETGRATEN	ALREMANES	WEWENNIKKS	180
	KCEQLIRQGV	T.DUTT.C	KPPKSDIIEV	KCLKDIGEFE	ADDGIBANTE	MALITHYCE	100
	ACEQUEE GOV	DUNTES					
35	Seq ID NO:	155 DNA sec	ruence				
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	CGAAAGGAGT	GAGGCGCCGA	GAGCCCAGAT	ACCATTTTGG	CGTGAGAGCT	GGTGGTTGGC	120
	AAGGCCCCCCCG	CACTGGGAAG	CGTCCGCCAT	GTTCTGCGAA	ARAGCCATGG	AACTGATCCG	180
	CGAGCTGCAT	CGCGCGCCCG GAGATGAAAG	AAGGGCAACT	GCCTGCCTTC	AACGAGGATG	GACTCAGACA	240
45	AGTTCTGGAG	GAGATGAAAG	CTTTGTATGA	ACAAAACCAG	TCTGATGTGA	ATGAAGCAAA	300
	GTCAGGTGGA	CGAAGTGATT	TGATACCAAC	TATCAAATTT	CGACACTGTT	CTCTGTTAAG	360
	AAATCGACGC	TGCACTGTAG GGTAGCGTCT	CATACCTGTA	TGACCGCTTG	CTTCGGATCA	GAGCACTCAG	420 480
	ATGGGAATAT	AATAATTATA	PARCATOC	ATTACGATTT	PACKEGGGGG	TOGGROOM	540
50	TCAACCTTTC	GACATTACAC	AGGATATGAA	ACCACCAAAA	AGCCTATATA	TTGAAGCTGG	600
	ATGCAGTGGC	GACATTACAC GCGATCTCGG	CTCAACCTGC	AACCTCCACC	TCCCAGGTTC	ACCTCAACTG	660
	CARCCTCCAC	CTCCCAGGTC	CCCTCTCTAA	AAGACTATGG	AGAATTTGAA	GTTGATGATG	720
	GCACTTCAGT	CCTATTAAAA ACAAGGAGTC	AAAAATAGCC	AGCACTTTTT	ACCTCGATGG	AAATGTGAGC	780
	AGCTGATCAG	ACAAGGAGTC	CTGGAGCACA	TCCTGTCATG	ACCATGCGCC	GAGGCACTTC	840
55	CAGGCTTCAC	TCAACTCATG	GACTCCTCTG	TACTCACTCT	CTCCACCACT	CCCTTCACCT	900 960
	CCCTCTTTGA	TTTTAGAAGC	TATAGACATT	GTTTAAGATA	ACTAAGAATA	CTTGGCTAAG	1020
	AAGTATAATT	TGCTAACTAT	TANGGACTTI	CITITITIAN	CACTATICAC	COCKACCTICCI	1080
	TOTCHARCTO	CTGGCCTCAA	CACTOCTO	CACCETAGCE	TCTCAAAGTG	TTGAGATCAC	1140
60	AGGCGTGAGC	CACTGCACCC	GGCCCCTACT	CCTTTTTCTA	ATAAGCTGTA	TCTGTAATCA	1200
	CAGCATTCCT	CACTGCACCC ACAGTTGTTA	CAGTGTGTTT	TTTAAATGAA	AGTAAACATG	GTTACATTTG	1260
	AATCTCTTAA	ATAAGCAGTC	ACTTGGCTGG	ACAGGAAGAA	GGTAGATCCT	GIGIGICITG	1320
	TTTTCTGGTC	ATGTGTATTG	TACAAGCTAG	AGAGCTGAAT	TTCTGAGATA	CACATTTTCA	1380
65	AATCACATGC	AAGTGAAGAT	GATGGTCTGT	AGAAATTTTC	AGTATATATA	ATGTTTAATG	1440 1500
03	ACATACTAAT	TTATCATCTG	GCTATTTGGG	AAGGAAGGAC	ACACATGGAT	TTTGCACATT	1500 1560
	CALCATEG	TGGCTGGTGT GTGAAATTGG	COCTACACAA	CONNCETTOR	ACAGEMETET	CTGAGATTCA	1620
	GATTGACTGA	AAAGTCACAT	GRACACTTCA	TTGTCTTTTA	ATGGTATGTT	TTAAACAGCT	1680
	CACATTTTAA	AAAGTCACAT ATTTTGATGA	AATCCAGTTT	ATTOGTTTGT	TCTTTTATGC	TTTGGGTGTT	1740
70	GCATCCGAGA	AATCTTTTCC	CATCCCAAGA	TCACAATTTT	TTTTCCTTTT	TACTTCTAGA	1800
	AGTGTTATAA	TTTTAAGCTT	TATACTTTGG	TCTATGACCC	GTTTTTTTT	TIGITTIGIT	1860
	TIGITITITC	GTTTGTTTCT	TTGTTTTGAG	ATGGAGTCTT	GTTCTGTCAC	CCAGGCTGGG	1920
	GTGCAGTGGC	GTGATCTTGG	CTCACTGCAA	TCTCTATCCC	CTGGGTTCAA	GTGATTCTCT	1980
75	TGTCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGCACAGGC	CGCCACGCCT	GGCTAATTTT	2040
13	TGTATTTTTA	GTAGAGACAG CCACCTTGGC	AGTTTTACCA	TGTTGGCCAG	GLTGGTTTCA	AACTCCTGAC	2100
	CAGCOTATOR	TCCATTTTGA	ATTANT	TATATOGUATTA	AAGGTGTCAA	TOTACCTTON	2220
	CTTTTTCTTC	GGARTATAGA	TATCCAGCTO	TTTCACTACC	ATTTTTTTTAA	AGGACTGCCC	2280
	TTTGCTCTAT	GGAATATAGA CACCTTTGCA	TTTTTGTTAA	AAAGTAGTTG	TCAATGTATA	TGTGGGTTTA	2340
80	TTTCAGGACT	CTGTTTTGTT	CCATTGACCT	GTTTTTCTCT	CCTGAATGCC	AATACCATAT	2400
	TTGTATGTAG	TAATESTATEST	TTTCTAATAA	TTCTTGAAAC	AGATAGTATT	AATGTGTCAT	2460
	ATTTTTGCTG	TTGTTTGTAT TGAGCTAAAG	TTTTTGTAGA	GATGGGGTTT	CACCGTGTTG	GCCAGGCTGT	2520
	GTTGAACTCC	TGAGCTAAAG	CAATACACTT	GCCTCGTCCT	CCCCATGTGC	TGGGATTACA	2580
85	COCCETARCE	TYPICATION	CCCAGTGTAC	CACATTTCTT	TTTGAGATTT	GTTTTGGCTA	2640
92	TGTTAAGTCC	TTTGCTTTTG AGAACTTTGG	ATGTGAAATT	TUGGAACAGG	CAGGGTGTGG	TOGCTTATGC	2700 2760
	CAGTAATCCT	AGAACTTTGG GGCCTATGGC	BARROTCO T	CTCTACAL	AUTHORNOTO	ATTACCCACC	2820
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	WO 02	/086443 CATGCCTGTA	GTCACAGTTA	CACGGCAGGC	TGAGGTGGGA	GGATCACTTG	2880
	AACCCCAGAG	GTCAAGACTG	CAGTGAGCTG	AGATCACACC	ACTGTACTCC	AGCCTGGGTG	2940
	ACAAAGTGAG	ACTCTATCTC	AAAAAGAAAT	TAGGATCAAT	TTGTCAATTT	CTACAACAAC	3000
5	TYGGGAGAAT	ACCCCTGTTG TGACATCTTA	ATAATATTGA	GTCTTCTGGC	CTATABACAA	GGTCTGTCTT	3060 3120
-	CCTAGGTATT	AATGTTTTGT	CTTCTATTTC	TCTTAATAAT	CTTTTGTAGT	TTTCAGTGTA	3180
	CAGGTCTACC	ATGTCAGCAT	TTCATAGTTT	TGATGCTAAA	TGGTATTTTA	AAATTTCAAA	3240 3300
	CCTTGCTAAA	CTGTGAGTTC	TCATGGTGTT	TTTGTAAATT	ACATCAACAG	TCATGTGTTC	3360
10		GAGTTTTACT					
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	MPCEKAMELI	RELHRAPEGO	LPAFNEDGLR	OVLEEMKALY	EQNOSDVNEA	KSGGRSDLIP	60
	LATYMPELCC	RNRRCTVAYL DEGLDITODM	YDRLLRIRAL KDDKCLYTPA	RWEYGSVLPN	ALREHMAARE	ONT-HT-DGDVS	120 180
20	KRLWRI						
	Sea ID NO:	157 DNA sec	mience				
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25	Coding seq	uence: 148-	621				
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	1	1		1	1	GGACTAGAAC	60
	GAAAGGAGTG	AGGCGCCGAG	AGCCCAGATA	CCATTTTGGC	GTGAGAGCTG	GTGGTTGGCA	120
30	AGGCCGCGGG	AGTGGGAAGC	GTCCGCCATG	TTCTGCGAAA	AAGCCATGGA	ACTGATCCGC	180
		GCGCGCCCGA AGATGAAAGC					240 300
	TCAGGTGGAC	GAAGTGATTT	GATACCAACT	ATCAAATTTC	GACACIGITC	TCTGTTAAGA	360
35		GCACTGTAGC					420
33	CGGTGTCTAR	GTAGCGTCTT AAGACTATGG	GCCAAATGCA AGAATTTGAA	GTTGATGATG	GCACTTCAGT	CCTATTAAAA	480 540
	AAAAATAGCC	AGCACTTTTT	ACCTCGATGG	AAATGTGAGC	AGCTGATCAG	ACAAGGAGTC	600
	CTGGAGCACA	TCCTGTCATG	ACCATGCGCC	GAGGCACTTC	CAGGCTTCAC	TCAACTCATG	660 720
40	TATAGACATT	GTTTAAGATA	ACTAGGAATA	CTTGGCTAAG	AAGTATAATT	TGCTAACTAT	780
	TAAGGACTTT	CTTTTTTTAA GAGACTGTCT	TGTTGTACAC	TATTCTTCCT	ACTCTTTTTT	GGTTTTGGTT	840
	GCAGTCCTCC	GAGACTGTCT	CACTATGTTG	CCCAAGCTGG	AGGCGTGAGC	CACTGCACCC	900 960
45	GGCCCCTACT	CCTTTTTCTA	ATAAGCTGTA	TCTGTAATCA	CAGCATTCCT	ACAGTTGTTA	1020
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	TACAAGCTAG	AGAGCTGAAT	TTCTGAGATA	CACATTTTCA	AATCACATGC	AAGTGAAGAT	1200
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50	GCTTGTGGC	TATGGGGTGA	TCACCAGTAT	CACCACTITG	GAAGGGGACA	GTGAAATTGG	1380
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	AATCCAGTTT	TTGTCTTTTA ATTCGTTTGT	TCTTTTATGC	TTTGGGTGTT	GCATCCGAGA	AATCTTTTCC	1500 1560
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	CCCAGTGTAC	CACATTTCTT	TTTGAGATTT	GTTTTGGCTA	TGTTAAGTCC	TTTGCTTTTG	2460
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	1	11	21 	31	41	51	
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	TIKFRHCSLL	RELHRAPEGQ RNRRCTVAYL KKNSQHFLPR	YDRLLRIRAL	RWEYGSVLPN			120
5	Nucleic Ac	159 DNA sec id Accession uence: 149-2	#: Eos se	quence			
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10	GTTCGGCGCC	AAAGCGCGGA	GCGGAGGCCG	AGGCGAGAGC	CTGGCGCTGT	AGGACTAGAA	60
	CGAAAGGAGT	GAGGCGCCGA	GAGCCCAGAT	ACCATTTTGG	CGTGAGAGCT	GGTGGTTGGC	120
		GAGTGGGAAG					180
15	CGAGCTGCAT	CGCGCGCCCG TGTAGTCCCA	AAGGGCAACT	AGGCTGAAGT	GAGAGGATTG	CATGGCTCCA	240 300
	GGAAGTTGAA	ACTGCAGTGA	ACTGTGGTCA	CGCTATTACA	CTCCAGCCTG	GGTGACAGAC	360
	TGAATCCCTG	TCTCAAAAAG	GAAAAGGAGG	ATGGACTCAG	ACAAGTTCTG	GAGGAGATGA	420 480
	GTAGCATACC	TGAACAAAAC TGTATGACCG	CTTGCTTCGG	ATCAGAGCAC	TCAGATGG	ACGCTGCACT	480
20							
		160 Protein cession #: E		3			
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	CTGCCTGCCT	TCAACAATTA	G				
30	Seq ID NO:	161 DNA sec id Accession	quence				
50		uence: 1333					
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35	CONTROCOCC	 GGATCTCAGG	CACCATGAGGA	(The state of the	NG NG GGTGTGTG	TOTOGRADA	60
55	ACAGGGAGGC	CONCRETOR	ACAGACACAG	TOGTCCCAGG	ATTGGAGAGC	AGTCCAGGTG	120
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50	CHARLES CHARLES	CCTAAGGGCC	TORGOTOGOR	CACCACACCA	GROCCEGGG A	GTGTCAGCAG	900 960
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ου	CCTCCCCAGA	GTCCTCAGGG ATGAGGGCTC	AGGOGCTTCC	CARCACCATTT	ACCORDANCE OF	CACTTTATGG	1560 1620
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	TTCTACGGGG	AGCCCAGGAA	GCTGCTCACC	CAAGATTGGG	TGCAGGAAAA	CTACCTGGAG	2100
70	TACCGGCAGG	TGCCCCGCCAG	TGATCCTGCG	CACTACGAGT	TCCTGTGGGG	TTCCAAGGCC	2160
	CACGCTGAAA	CCAGCTATGA	GAAGGTCATA	AATTATTTGG	TCATGCTCAA	TGCAAGAGAG GGGAGTCTGA	2220 2280
	GCACCAGCCG	CAGCOGGGGC	CAAAGTTTGT	GGGGTCAGGG	CCCCATCCAG	CAGCTGCCCT	2340
75	COCCUMENTAL PROPERTY	B CROCK CCCC	OR MINORING COLO	WATER PROPERTY.	AAGAGAGGAA	TOROTOTTOT	2400
13	CAGTGGCAGT	GGGTGGAAGT GATTTATCCT ACTTCACCAT	GAGCACACTG	TATGTCATCT	CIGGGTTCCT	TOTCTATTGG	2460 2520
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85							
	PAGE TO MO.	162 Proteir	n gemience.				

Seq ID NO: 162 Protein sequence: Protein Accession #: AAA68877.1

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5	POGGASSSIS	VYYTLWSOFD	EGSSSOEERE	PSSSVDPAOL	EFMPOEALKL	KVAELVHFLL	120
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	LGLSCDSMLG	DGHSMPKAAL	LIIVLGVILT	KDNCAPEEVI	WEALSVMGVY	VGKEHMFYGE	240
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10	PODILECTOR						
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	Nucleic Act	ld Accession Lence: 30-80	1 #: AF29210	0			
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20	ATATACGAGA	GAGTGTAAAA CCCTCAAGAT	GGATCATTGG	ACAGGAAGAA	GTTAGAACAG	CIGTACAATA	240 300
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	CAGCAACACA	GTGCGAGTTC	TCCAAACAGG	AGTTCATGGA	TGGCATGACA	GAATTAGGAT	420
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						ATATTAACAA	2400
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60	TTTGAAAATT	TCTATTCAGG	CTACTGGAAT	TGGTTATTAA	AAGAAAAAGG	AAAAAGAAGA	2640 2700
	GAAAAATTTT	TTTCAGTATT	ATATATOTAT	ATATCTATAT	ATATGTACTG	TTTTGTTTCC	2760
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0.5	EFMIXIMTELG VWNLVI MCDP	CDSIEQLKAQ KPLDLWNFPI.	TERHKRS DX	DIMNITIDES	THIADDMENY	KGLDLEMAIA DEBGAWPVLI	180 240
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10	CACCCCCCCC	GCTGCCGCCC	CCACCAACTG	COOCCOCC	TOCOGOGOGO	TCCCCGCTTC TCCATGCTGC AGAGGAGGCT	240
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	ACTOTOTOCA	TGGTTTGATC	CTTTATTAGT	TOGCTCTAAT	ATTTTTCTGT	AGATCCTTTT	4560
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	WO 02/	006443					
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	CTCTACTGAA	AATACAAAGC	AAAATTAGCC	AGGTGTGGTG	GCGGGCGCCT	GTGGTCCCAG	5520
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	GCCTATGAGA	GGCATTTATG	ATTTTTGTGC	CTACAATAAG	TCAGCCTGTC	TEGTCTGAGT	6420
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	NSKKONSNPT	CLVALGRIQP YEYPHODDHN	YIVPQNSGEI	NVKPTEFITR	PAVNGKFVYV	DORATAILGY	360 420
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	ces to Mo.	167 DNA Be					
55	Nucleic Ac:	id Accession	2 #: NM_0144	100			
	Coding sequ	uence: 86-1	126				
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	CTGCAACGCC	AAGCTCAACC	TCACCTCGCG	GGCGCTCGAC	COGGCAGGTA	ATGAGAGTGC	480
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	CACATCTGTC	ACCACTTCTA	CCTCGGCCCC	AGTGAGACCC	ACATCCACCA	CCAAACCCCAT	900
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	TCCTGCAAAA	GGGGGGCCCC	AGCAGCCCCA	TANTANAGGC	TGTGTGGCTC	CCACAGCTGG	1080
	ATTGGCAGCC	CTTCTCTTTGG	CCGTGGCTGC	TGGTGTCCTA	CTGTGAGCTT	CTCCACCTGG	1140
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-0	CITCIGCIGC	GCTGGTTTGC	GGCTTTGGGA	AATAAAATAC	CGTTGTATAT	ATTCTGGCAG	1320
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	AGGATGCTAA	CCTTCCTACT	CACTTTCTCC	TAGCCAGCCT	GGACTTTGGA	GCGTGGGGTG	1500
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WO 02/086443 TIGTATAGIG AAAAAAA

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	TTGTCCATCG	TGACATCAAG	GATGAGAACA	TCCTGATAGA	CCTACGCCGT	TCCCGTGGAG GGCTGTGCCA GACTTTGATG	720					
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	AGAGGGACCA	GGAGATTCTG AATCCGCCGG	GAAGCTGAGC	TCCACTTCCC	AGCCCATGTC	TCCCCAGACT	960 1020					
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40	AAAAAAAAAACC	CHACACACACAC	GGCCTCGTCC	THEFT	ABGCCTGGCC	TGGCCTGGCC	1140					
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	DQRILEAELH RPCPFGLVLA	FPARVSPDCC TLSLAWPGLA	ALTRRCLAPK PNGQKSHPMA	PSSRPSLERI MSQG	LLDPWMQTPA	MVCGDIPFER EDVTPQPLQR	300					
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05	GCACCACTGG	GTACACAGAC	GACGCCAGGA	CGGCAAGTGT	CGGCACTGTG	GGAAGGGATT	660					
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	GLQHLAPPPP MLKSVSRRKC DGKCRHCGKG PPTWILRARR NPKSGGNQGA LSTLDQLRLK LHAEPNPEAG KMPYAGTAPS GUBGPHEDPP	TPGAPCSESE AACKIVVHTP FQQKFTPHSK PQNTLKASKK KIIQSFLWYL PPPFVAILPL PEDRDEGATD DFLMGSSKOL PORNDIGYLE	RQIRSTVDWS CIEQLBKINF EIVAISCSWC KKRASPKRKS NPRQVFDLSQ GTGNDLARTL RLPLDVFNNY AKHIRVVCDG	ESATYGEHIW RCKPSFRESG KQAYHSKVSC SKKGPEBGRW GGPKEALEMY NWGGGYTDEP PSLGFDAHVT MDLTPKLGDE ALOVGHGDE	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAM KPQCVVFLNI LTOCREVULT	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVFV CGGDGTVGWI GNVVQLDRWD PEKFNSRFRN PRYCAGTMPW TSKAI PVOVD	120 180 240 300 360 420 480 540
	GLQHLAPPPP MLKSVSRRKC DGKCRHCGKG PPTWILRARR NPKSGGNQGA LSTLDQLRLK LHAEPNPEAG KMPYAGTAPS GUBGPHEDPP	TPGAPCSESE AACKIVVHTP FQQKFTPHSK PQNTLKASKK KIIQSFLWYL PPPFVAILPL PEDRDEGATD DFLMGSSKOL POPMDIGYLE	RQIRSTVDWS CIEQLBKINF EIVAISCSWC KKRASPKRKS NPRQVFDLSQ GTGNDLARTL RLPLDVFNNY AKHIRVVCDG	ESATYGEHIW RCKPSFRESG KQAYHSKVSC SKKGPEBGRW GGPKEALEMY NWGGGYTDEP PSLGFDAHVT MDLTPKLGDE ALOVGHGDE	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAM KPQCVVFLNI LTOCREVULT	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVFV CGGDGTVGWI GNVVQLDRWD PEKFNSRFRN PRYCAGTMPW TSKAI PVOVD	120 180 240 300 360 420 480 540 600 660
50	GLQHLAPPPP MLKSVSRRKC DGKCRKCGKG PPTWILRARR NPKSGGNQGA LSTLDQLRLK LHAEPNPEAG KMPYAGTAFS GHPGEHHDFE GEPCKLAASR YDKBQLKEAS	TPGAPCSESE AACKIVVHTP FPGQKFTPHSK PQNTLKASKK KIQSPLMYL PPEPVAILPL PEDRDEGATD DFLMGSSKOL PQRHDDGYLE IRIALRNQAT VPLGTVVVPG	RQIRSTVDWS CIEQLBKINF EIVAISCSWC KKRASFKRKS MERQVFDLSQ GTGNDLARTL RLPLDVFNNY AKHIRVVCDG VIGFTMTSLA MVQKAKRRSA DSDLELCRAK	ESATYGIHIW RCKPSFRESG KQAYHSKVSC SKKGPEEGRW GGPKEALEMY NWGGGYTDEP FSLGFDAHVT MDLTPKIQDL ALQVGGHGER APLHSDQQPV IERLQQBPDG	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESRBAM KPQCVVFLNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQK	YVGEQYCVAR RHHWVHRRQ SLGVHAAVV I PLMKPLLVFV COGDGTVOWI GNVVQLDRWD PEKFNSRFRN PRYCAGTMPW TSKAI PVQVD VSMHDYFALH LSPKWCFLDA	120 180 240 300 360 420 480 540 600 660 720
	GLQHLAPPPP MLKSYSRRKC DGKCRHCGKG PPTHILRARR NPKSGGNQGA LSTLDQLRLK LHAEPNPEAG KMPYAGTAFS GHPGEHHDFE GEPCKLAASR YDKBQLKEAS TTASSPEID	TPGAPCSESE AACKIVVHTP PCQKFTFHSK PQNTLKASKK KIQSPLWYL PPEDRDEGATD DPLMGSSKDL PQRHDDGYLE IRIALRNQAT VPLGTVVVPG BADGRINVVT	RQIRSTVDWS CIEQLBKINF BIVAISCSWC KKRASFKRKS NFRQVFDLSQ GTGNDLARTL RLFLDVFNNY AKHIRVVCDG VIGFTMTSLA MVQKAKRRSA DSDLELCRAM	ESATYGHIW RCKPSFRESG KQAYHSKVSC SKKGPEBGRW GGPKEALEMY NWGGGYTDEP PSLGFDAHVT MDLTPKIQDL ALQVGGHGER APLHSDQQPD IERLQGBPDG DEBLLGASAR	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAN KPQCVVFLNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQE PDLPTPTSPL	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVEV CGGDGTVGWI GNVVQLDRWD PEKPNSRPRN PRYCAGTMPW TSKAI PVQVD VSMHDYEALH LSPKWCFLDA PTSPCSPTPR	120 180 240 300 360 420 480 540 600 660 720 780
50	GLQHLAPPPP MLKSYSRRKC DGKCRHCGKG PPTHILRARR NPKSGGNQGA LSTLDQLRLK LHAEPNPEAG KMPYAGTAFS GHPGEHHDFE GEPCKLAASR YDKBQLKEAS TTASSPEID	TPGAPCSESE AACKIVVHTP PCQKFTFHSK PQNTLKASKK KIQSPLWYL PPEDRDEGATD DPLMGSSKDL PQRHDDGYLE IRIALRNQAT VPLGTVVVPG BADGRINVVT	RQIRSTVDWS CIEQLBKINF BIVAISCSWC KKRASFKRKS NFRQVFDLSQ GTGNDLARTL RLFLDVFNNY AKHIRVVCDG VIGFTMTSLA MVQKAKRRSA DSDLELCRAM	ESATYGHIW RCKPSFRESG KQAYHSKVSC SKKGPEBGRW GGPKEALEMY NWGGGYTDEP PSLGFDAHVT MDLTPKIQDL ALQVGGHGER APLHSDQQPD IERLQGBPDG DEBLLGASAR	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAN KPQCVVFLNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQE PDLPTPTSPL	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVEV CGGDGTVGWI GNVVQLDRWD PEKPNSRPRN PRYCAGTMPW TSKAI PVQVD VSMHDYEALH LSPKWCFLDA PTSPCSPTPR	120 180 240 300 360 420 480 540 600 660 720 780 840
50	GLGRLAPPPP MLKSVSRRKC DGKCRHCGKG PPTWILMARR NPKSGGNQGA LSTLDQLRLK LHAEPNPEAG KMPYAGTAPS GHPGEHHDPE GEPCKLAASR TYDKEQLKEAS TTASRFYRID SLQGDAAPPQ YLLDHAPPEI	TPGAPCSESE AACKIVVHTP FQQKFTFHSK PQNTLKASKK KIIQSPLWYL PPEPVALLPL PEDRDEGATD DPLMGSSKDL PQRHDDGYLE IRIALRNQAT VPLGTVVVPG RAQEHLNYVT GEBLIEAARK LDAVEENGET	ROIRSTVDWS CIEQLEKINF BIVAISCSWC KKRASFKRKS OFTENDLARTL RLPLDVFNNY VIGFTMTSLA MYQKAKRSA BSDLELCRAM BIAQDEIYIL NDPCKLQELM	ESATYGHIW RCKPSFRESG KQAYHSKVSC SKKGPEBGRW GGPKEALEMY NWGGGYTDEP PSLGFDAHVT MDLTPKIQDL ALQVGGHGER APLHSDQQPD IERLQGBPDG DEBLLGASAR	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAN KPQCVVFLNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQE PDLPTPTSPL	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVEV CGGDGTVGWI GNVVQLDRWD PEKPNSRPRN PRYCAGTMPW TSKAI PVQVD VSMHDYEALH LSPKWCFLDA PTSPCSPTPR	120 180 240 300 360 420 480 540 600 660 720 780
50 55	GLGRLAPPPP MLKSVSRRKC DGKCRHCGKG PPTWILMARR NPKSGGNQGA LSTLDQLRLK LHAEPNPEAG KMPYAGTAPS GHPGEHHDPE GEPCKLAASR TYDKEQLKEAS TTASRFYRID SLQGDAAPPQ YLLDHAPPEI	TPGAPCSESE AACKIVVHTP PCQKFTFHSK PQNTLKASKK KIQSPLWYL PPEDRDEGATD DPLMGSSKDL PQRHDDGYLE IRIALRNQAT VPLGTVVVPG BADGRINVVT	ROIRSTVDWS CIEQLEKINF BIVAISCSWC KKRASFKRKS OFTENDLARTL RLPLDVFNNY VIGFTMTSLA MYQKAKRSA BSDLELCRAM BIAQDEIYIL NDPCKLQELM	ESATYGHIW RCKPSFRESG KQAYHSKVSC SKKGPEBGRW GGPKEALEMY NWGGGYTDEP PSLGFDAHVT MDLTPKIQDL ALQVGGHGER APLHSDQQPD IERLQGBPDG DEBLLGASAR	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAN KPQCVVFLNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQE PDLPTPTSPL	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVEV CGGDGTVGWI GNVVQLDRWD PEKPNSRPRN PRYCAGTMPW TSKAI PVQVD VSMHDYEALH LSPKWCFLDA PTSPCSPTPR	120 180 240 300 360 420 480 540 600 660 720 780 840
50	GLGHLAPPPP MLKSVSRRKC DGKCHGOKG PPTWILARAR MPKSGGNQA LSTLDQLRLK LHAEPNPLA GHPGEHEDFE GEPCKLAASR YDKBQLKEAS TAGRPYRJ SLQGDAAPPQ YLLDHAPPEI SLQGDAAPPQ TLDHAPPEI SQDTEAAYL SGG ID NO:	TPGAPCSESE AACKIVVHTP PQOKFTPHSK PQNTIKASKK KIIGSFLWYL PPPPVALIPL PERDROEGAL PGREDOGYLE KILLENQAT VPLGTVVVPG RAGEHLMYVT GEBLIBAAKR LDAVENGET ENRGHYQMIQ 173 DNA 864	RQIRSTUDMS CIEQLBALINF EIVAISCSWC KKRASFERKSS MPRQVFDLSQ GTGRIDLAFTL RLPLDVFNNY AKHIRVVCDG VIGFTMTSLA MVQKAKRRSA DSDLELCRAM BIADDEIVIL NDFCKLQELH CLHQAALIGQ EEQGETAV TUENCE	ESATYGBHIW EKCKPSPRSG KQAYHSKVSC SKKOPEGGW GGPKEALEMY MWGGGYTDEP FSLGPDAIP MDLTPKIQDL ALQVGGHGER APLHSDQOPV IERLQQBPDG DPELLGASAR RAGGDLMRD RTICHYIVEA	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAN KPQCVVFLNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQE PDLPTPTSPL	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVEV CGGDGTVGWI GNVVQLDRWD PEKPNSRPRN PRYCAGTMPW TSKAI PVQVD VSMHDYEALH LSPKWCFLDA PTSPCSPTPR	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	GLGHLAPPPE MLKSYSREKC DGKCRHCCKG PPTWILRARE MPKSGGNGGA LSTLDQUELK LHAEENPEAG KMFYAGTAFS GHPGEHDPE GEPCKLAASE TASRPYRID SLQCDAAPPG YLLDHAPPEI AQDTELAAYL Seq ID NO: Nucleic Aci	TPGAPCSESE AACKIVVHTP FOOKTFRISK PONTIKASKR KITOSFLWYL PPPPVALLPL PEDRDEGATD DFLMGSSKOL RIALRNOAT VPLGTVVVP RAGESLAVVT GEBLIEAAKR LOAVEENGET ENRGHYOMIQ 173 DNA see id Accession	RQIESTUMS CIEQLEKINF EIVAISCSWC KKRASFKEKS MPRQVFDLS GTGRDLARTL RIPLDVFNNY AKHIRVVCDG VIGFINTSLA MVQRAKRSA DSDLELCRAM EIAQDEIYIL UNDFCKLQELH CLHQAAALGQ REDQETAV quence n #: AF23277	ESATYGBHIW EKCKPSPRSG KQAYHSKVSC SKKOPEGGW GGPKEALEMY MWGGGYTDEP FSLGPDAIP MDLTPKIQDL ALQVGGHGER APLHSDQOPV IERLQQBPDG DPELLGASAR RAGGDLMRD RTICHYIVEA	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAN KPQCVVFLNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQE PDLPTPTSPL	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVEV CGGDGTVGWI GNVVQLDRWD PEKPNSRPRN PRYCAGTMPW TSKAI PVQVD VSMHDYEALH LSPKWCFLDA PTSPCSPTPR	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	GLGHLAPPPE MLKSYSREKC DGKCRHCCKG PPTWILRARE MPKSGGNGGA LSTLDQUELK LHAEENPEAG KMFYAGTAFS GHPGEHDPE GEPCKLAASE TASRPYRID SLQCDAAPPG YLLDHAPPEI AQDTELAAYL Seq ID NO: Nucleic Aci	TPGAPCSESE AACKIVVHTP PQOKFTPHSK PQNTIKASKK KIIGSFLWYL PPPPVALLPL PERDROEGAL PGREDOGYLE KILLENQAT VPLGTVVVPG RAGEHLMYVT GEBLIEAAKR LDAVENGET ENRGHYQMIQ 173 DNA 864	RQIESTUMS CIEQLEKINF EIVAISCSWC KKRASFKEKS MPRQVFDLS GTGRDLARTL RIPLDVFNNY AKHIRVVCDG VIGFINTSLA MVQRAKRSA DSDLELCRAM EIAQDEIYIL UNDFCKLQELH CLHQAAALGQ REDQETAV quence n #: AF23277	ESATYGBHIW EKCKPSPRSG KQAYHSKVSC SKKOPEGGW GGPKEALEMY MWGGGYTDEP FSLGPDAIP MDLTPKIQDL ALQVGGHGER APLHSDQOPV IERLQQBPDG DPELLGASAR RAGGDLMRD RTICHYIVEA	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAN KPQCVVFLNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQE PDLPTPTSPL	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVEV CGGDGTVGWI GNVVQLDRWD PEKPNSRPRN PRYCAGTMPW TSKAI PVQVD VSMHDYEALH LSPKWCFLDA PTSPCSPTPR	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	GLGHLAPPPP MLKSYSREKC DGKCERCOKG DGKCERCOKG DFTHILAREN NPKSGGNQGA LSTLDQLRLK LHAEBNPEAG KOFYAGTAFF GEPCKLAASEA TASSFYRID SLOGDAAPPO YLLDHAPPSI AQDTSLAAYL Seq ID NO: Nucleic Aci Coding sequ	TPGAPCSESE AACKIVUHTP FOOKFTPRSK PONTLKASK KIIQSPLNYL PPPPVALDPL PEDRDEGATD DFIMGSSKDL RIALRNQAT RIALRNQAT ROBELINYUT GEBLIEAAKR LDAVEENGET ENROHYQMIQ 173 DNA sec id Accession uence: 1-16	RQIRSTUDMS CIEGLEKINF EIVALISCSWC KKRASPKRKS NFRQVFDLSQ GTGRIDLARTL RLPLDVFRNY AKHIRVVCDG VIGFTMTSLA MVQKAKRSA DSDLELCARSA EIAQDEIYIL CLHQAAALGQ REQGTAV quence n B: AF23277 62	ESATYGBHIW RCKPSPRESG KQAYHSKYSC SKKOPBEGRM GGPKEALEMY MWGGGYTDEP FSLGPDAEV TBLIPPKIGDL ALQYGGHGER APLHSDQOPV LERLQASDA DPELLGASAR RAGGGLMRD RTICHYIVEA	PETNYSGDPC SRNYREPTPY PMLQQIEEPP REPFILEPPE RKVINLRILA VSKILSHVEE LEPHESREAM KPQCVVELNI LTQCREVVINI LTQCREVVINI PEQURIQVSR AGAKSPTCQK PDLPTPTSPL EQSRTLLMA GASLMKTDQQ	YVGBOYCVAR RHIMVIRRRQ SLGVHAAVVI PLMKPLLVPV CGGDGTVGHI GNVVQLDRWD PEKPNSEPRN PRYCAGTMPW TSKAIPVQVD VSMGDYBALH LSPEKCFLDA FISPEKCFLDA VSTGSKOVVR GDTPRQRASK	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	GLGHLAPPPE MLKSYSREKC DGKCRHCCKG PPTWILRARE MPKSGGNGGA LSTLDQUELK LHAEENPEAG KMFYAGTAFS GHPGEHDPE GEPCKLAASE TASRPYRID SLQCDAAPPG YLLDHAPPEI AQDTELAAYL Seq ID NO: Nucleic Aci	TPGAPCSESE AACKIVVHTP FOOKTFRISK PONTIKASKR KITOSFLWYL PPPPVALLPL PEDRDEGATD DFLMGSSKOL RIALRNOAT VPLGTVVVP RAGESLAVVT GEBLIEAAKR LOAVEENGET ENRGHYOMIQ 173 DNA see id Accession	RQIESTUMS CIEQLEKINF EIVAISCSWC KKRASFKEKS MPRQVFDLS GTGRDLARTL RIPLDVFNNY AKHIRVVCDG VIGFINTSLA MVQRAKRSA DSDLELCRAM EIAQDEIYIL UNDFCKLQELH CLHQAAALGQ REDQETAV quence n #: AF23277	ESATYGBHIW EKCKPSPRSG KQAYHSKVSC SKKOPEGGW GGPKEALEMY MWGGGYTDEP FSLGPDAIP MDLTPKIQDL ALQVGGHGER APLHSDQOPV IERLQQBPDG DPELLGASAR RAGGDLMRD RTICHYIVEA	PETNVSGDFC SRNVREPTFV FMLQQIEEPC RPFIIRPTPS RKVHNLRILA VSKILSHVEE LEFHESREAN KPQCVVFLNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQE PDLPTPTSPL	YVGEQYCVAR RHHWVHRRRQ SLGVHAAVVI PLMKPLLVEV CGGDGTVGWI GNVVQLDRWD PEKPNSRPRN PRYCAGTMPW TSKAI PVQVD VSMHDYEALH LSPKWCFLDA PTSPCSPTPR	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	GLGHLAPPPE MLKSYSRRKC DGKCHCOKG PFTWILTARR NPKSGGNQGA LSTLDQLEK LHAEDNPEAG GHPYAGTAFS GHPCGHHDFS GHPCGHASR YDKEQLKEAS TIASRPYEL SLQGDAPPG YLLDHAPPSI AQDTSLAAYL Seq ID NO: Nucleic Ac Coding sequ	TPGAPCSESE AACKIVUHTP FOOKFTPHSK FOOKFTPHSK KIIGSFLMYL POPPVALIDL PDPPVALIDL PDPPVALIDL PDPLMGSSKDL PORHDDGYLE RIALRNOAT VPLGTTVVPPG RAGBEILMYVT GBELIEANKR LDAVESEGE ENRGHYGMIQ 173 DNA see tid Accession ucnce: 1-166	RQIRSTUDMS CIEGLEKINF EIVALISCSWC KKRASPKSWC KKRASPKSWC KKRASPKSWC KKRASPKSWC KRASPKSWC GTGRIDLARTL RIPLDVFRNY AKHIRVVCDG VIGFTMTSLA MVQKAKRSA DSDLELCAN EIAQDEIYIL CLHQAAALGQ REQGTAV quence n #: AF23277 62 21	ESATYGBHIW RCKPSPRESG KQAYHSKYSC SKKOPEBCRW GGPKEALEMY NWGGGYTDEP FSLGFDAEV TBLIFPKIGPL ALQYGGHGER APLHSDQOPY LERLQQEPG DPELLGASAR RAGGGLHRRD RTICHYIVEA	PETNYSGIPE SRNYREPTPY PMLQQIEEPP REPFILEPPS RKVINLRILA VSKILSHVEE LEFHESREAM KPQCVVELNI LTQCREVVLT PEQLRIQVSR AGAKSPTCQK PDLPTPTSPL EQSRILLHA GASLMKTDQQ	YVGBQYCVAR RHHWVHRRQ SLGVHAAVVI PLMKPLLVFV CGGGGTYGHI GNVVQLDRWD PEIKPNSRFRN PRYCAGTMP TSKAI PYQVD VSMIDVFALH LSPKKCFLDA PTSPCSFTPR VSTGSKOVVR GDTPRQRAEK	120 180 240 360 420 540 600 600 720 780 840 900
50 55 60	GLGHLAPPPP MLKSYSREKC DGKCERCOKG PFTWILEARN PRESGENGGA LSTLDOLUKE LHAEBNIPEAG GHPGEHEDPE GEPCKLAASR THASEFYEID SLGGDAAPPQ YLKDLKEAS THASEFYEID SLGGDAAPPQ YLLDHAPPSI SLGGDAAPPQ LOUISIEC ACI COding sequ	TPGAPCSESE AACKIVVHTP POOKTTPHSK PONTIKASKK KIIOSFLMYL PPPVAILPL PPPVAILPL PPPVAILPL PPPVAILPL PORHDDGYLE IRIALROMAT UPLCTVVVPG RAGESLMYVT GEBLIBAAKR LDAVESNGET LTALBROMT 173 DNA sec id Accession uence: 1-16c unce: 1-16c	RQIRSTUDMS CIEGLEKINF EIVAISCSWC KKRASFKSKS NPRQVFDLSQ GTCSDLASKI RLPLDUPRNY AKHIRVVCA VIGFTMTSLA MVQKAKRKSA EIAQDEIYIL LHPLCAAALIQ REDQSTAV Quence n #: AF23277 62 21 AGCCCTGCOT	ESATYGBHIM RCKPSFRESG KQAYHSKYSC SKKOPEBGRM GGPKEALENY MGGGYTDEP PSLGPDAHYOT ALQVGHGER APLHSDQOPY DPELLGRSAR RTICHYIVEA 31 GTGGTGGGGCA	PETNYSGDFC SENVREDTFY FMLQQIEBEC RPFIIRPTPS RKVINLETLA VSKILGHEV LEFHESREAN KPQCVPELI LTQCREVVLT PEQLEIQVER PEQLEIQVER PEQLEIQVER PEQLEIQVER PEQLEIQVER PEGLEIQVER PE	YVGBQYCVAR RHHWVHERRQ SLGVHAAVVI CGGGGTYGHI GHVVGLDHU PEIKPSLFVI TSKALPYQVD VSHEDYBALP TSKALPYQVD VSHEDYBALP TSFACSTPR GDTPRQRAEK 51 TGGCCTGGCA	120 180 240 360 420 480 540 660 720 780 900
50 55 60	GLGHLAPPPE MLKSYSRRKC DGKCHCOKG PFTWILTARR NPKSGGNQGA LSTLDQLGK KUPYAGTAFS GHPCGHHDFS GHPCGHAPS GHPCGHAPS TASSEPPIA SQCDAPPQ TLDHAPPE AGDTSLAAYL Seq ID NO: Nucleic AC Coding seq:	TPGAPCSESE AACKIVUHTP FOOKFTPHSK FOOKFTPHSK KIIGSFLMYL FOOKFTPHSK KIIGSFLMYL FOOKFTPHSK KIIGSFLMYL FOOKFTPHSK KIIGSFLMYL FOOKFTPHSK FOOKFT FOOKFTPHSK FOOKFTPHSK FOOKFTPHSK FOOKFTPHSK FOOKFTPHSK FOOKFT FOOKFTPHSK FOOKFTPHSK FOOKFTPHSK FOOKFTPHSK FOOKFTPHSK FOOKFT FOOKFTPHSK FOOKFT FOOMFT FOOMFT FOOMFT FOOMFT FOOMFT FOOKFT FOOMFT OOMFT FO	RQIRSTUDMS CIEGLENINF EIVALISCSWC KKRASFKSKS NPRQVFDLSQ GTGRDLART RLFLDVFRNYN AKHIRVVCH AKHIRVVCH AKHIRVCH CHQAAAL DSDLELCRAH ELAGDAILL CLHQAAAL CLHQAAAL CLHQAAAL TUH CHQAAAL TUH AFE 21 AGCCTGCOT AGCCCTGCOT AGCCCTGCOT AGCCCTGCTT	ESATYGHIUM RCKPSPRESG KQAYHSKYSC KKAPBEBGK KQAYHSKYSC SKKAPBEBGR GGPKEALEMY MUGGGYTDEP FSLGPDAHVT MULTPKIQDL ALQVGGHGEP ALGVGGHGAFAR RAGGGLHRD RTICHYIVEA 31 GTGGTGGGCA ACGGGCTACC	PETNVSGDPC SENVREDPT SENVREDPT FMLQQIEBPC MCVSILIFITS REVINLETLA VSKILSIVEE LEPHESREAM RPQCVVPLIN LTQCREVULT LTQCREVULT EQGARTICHE GASLMKTDQQ 41 1 CCAGCCTOTT AGTTCATCCA	YVGBQYCVAR RHHWVHRRQ SLGVHAAVVI PLMKPLLVFV CGGGGTYGHI GNVVQLDRWD PEIKPNSEPRN PRYCAGTMPW TSKAIPVQVV USHIDVEALH LSPEKCFLDA PTSPCSFTPR VSTUSKOVVR GDTPRQRAEK	120 180 300 360 480 540 660 720 840 900
50 55 60	GLGHLAPPPE MLKSYSRRKC DGKCHHCUKG DGKCHHCUKG PFTWILRARR MPKSGGNGGA LSTLDQLEK HARPNPEAG GHPCHGHIDFE GHPCHGHIDFE GHPCHGHIDFE GHPCHGHIDFE GHPCHCHASR YDKSQLKEAS TASSEPVEA VLLDHAPPEI AQDTELAAYL Seq ID NO: COding seq LD NO: TASSEPVEA MUCLEIC AC: CODING SEQ AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONT	TPGAPCSESE AACKIVUHTP FQORFTPHSK FQNTIKASKK KIQSFLMYL FQNTIKASKK KIQSFLMYL FQRHODGYLB FQRHODGYLB FQRHODGYLB FQRHODGYLB FQRHODGYLB FANGE FAGESLIANVA GEBLIBANKA LDAVEENGET ENRGHYGHIQ FAGESLIANVA GEBLIBANKA FAGESLIANVA GEBLIBANKA FAGESLIANVA GEBLIBANKA FAGESLIANVA GEBLIBANKA FAGESLIANVA FAGESLIANVA GEBLIBANKA FAGESLIANVA FAGESLIANVA GEBLIBANKA FAGESLIANVA GEBLIBANKA FAGESLIANVA GEBLIBANKA FAGESLIANVA F	RQIRSTUDMS CIEGLENINF EIVAISCSUC KKRASFKEKS NPRQVFDLSQ GTGRDLARIC RLFLDUVFNNY NWQKAKRSA DSDLELCRAM BIADDEIYIL NDPCKLGELB RLHQAAALGQ REQGTAV QUENCE 18: AP23277 52 21 1 AGCCCTGCOT AGCCTATOTG	ESATYGHILM RCKPSPRESG KQAYHSKYSC KKROPEGOM GGFKEALEMY MUGGGYTDEP FSLGPDARVT DILTPKIQDL ALQVGGHGER APLHSDQOPV IERLQQBVDG DPELLGASAR RAGGDLMRD RTICHYIVEA 31 I GTGGTGGGCA ACGGGCTACC	PETMVSGDPC FERMVSEDPT FMLQQIEEPC FMFIIRPTPS RKVINLRILA VSKILGRUEE LEFRESREAM KPQCVVELNI LTQCEVVLT PEQURIQVSR AGAKSPTCQK QASTALKRIA GASLAKTDQQ 41	YVGBQYCVAR RHHWVHRRQ SLGYHAAVVI PLMKPLLYPV CGGGGTYGRI GNVVQLDRWD PEXFNSEFRN FRYCAGTMPW TSKAIPYQVU USMGDYEALH LSPKKCFLDA PTSPCSSTPR VSTQISKOVVR GDTFRQRAKK	120 180 300 360 480 660 720 780 900
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	concern concern	TCCTCTATAT	OTOCA OCCTT	CTGCCGGCCA	AGATCTTTCC	CATTOCTACC	1380
	ATCAACAAAT	CTGGCTGGGG	CACCTCTGGC	COARABACCA	AADTOOTTY	CTTCATTGGC	1440
	CTCATTCCTC	TGTCCATCTG	COTCOCACTT	CTCCTGGAGG	GGCTGGCCTA	CACAGCTTAT	1500
	TCCCTC CCTC	TGTTCAGTGA	CACACACCTA	CCCTTCCTTC	TCTCTGGGGC	TATACTUTAT	1560
5	COMMONACE	GGGTGGCCCT	CTCATGCTA	TATCTGGCCA	TCATOGCCCG	GCGATGTGGG .	1620
,	NACAN COOCC	AGCAGTACAG	CETCOCCETTE	CCTGAGGTGT	GACATGGCCC	CCAAGCAGAG	1680
	CCCCCTAAACT	GCAATGGGTA	AGGGAGGGAA	CCCCAATCCA	ACAGAAAAGA	CAGGGTGGGA	1740
	COOGLAMAGI	AGTGCTGTGT	TTTACTCTCT	TARTOUTCO	AACCACABAT	CTABABATGCA	1800
	B B CR B COCONO	ATGTAGTATG	CCCTCACACC	TOTTOTTAGA	GGAGGCAACA	CTGATCCCCC	1860
10	AAGAACGG1G	CTGCAGGGGA	WECKSTONE CONTROL	TCACACTCCC	TOTOTOTTO	CATCTGCACA	1920
10	MUATUCAGG	CCTCCTCCTG	CCCTCCACAG	GGCACTCAGA	ACTIVITY	AACCAAGTTA	1980
	ACCCCCATTC	AGTGGCAACT	TOTTONTACOT	ACCTICACTICA	CCCAACCTG	CGGAAGGAGG	2040
	AGTCCCATTC	CCATCTGAAC	PCP PCCPCPC	ACCIGNGION.	AATTTCTACT	CAGCCAGGTG	2100
	COCCCCCCCC	TGTATGTCAC	CCCCACCCCA	CCCATAGCTA	GTCATCAATG	CAATAAGATT	2160
15	GGCCGGTTAG	TACAAGGCCC	*COCCACCCCC	TOTTTOOCA	TCAGAAAACA	CCCTCCAGGA	2220
13	***CONTONION	ATGTGAGATA	AGMIGCCIGA	CATCAACATT	CCAGGGATGA	GCCAAACCAG	2280
	AIGGIGCIII	GCACTGAACT	CCCCACICCA	CTCCACATTA	ABARCCARAC	TTTTCCCAGGA	2340
	CAGGGAGTTA	GATTGTGGTG	CTCCTTANACC	ACCCCATARC	CTACACAGAG	CCCTTCCCTG	2400
	GGANCAAAGA	AAACTGCTCA	GIGCIAAAG	TOCCOTTONE	CINCACACACA	CARCECTOCO	2460
20	TTCCACCTGG	AAAGATTAAG	GACGICIAGA	TOGGITCIIA	ANCTORACTO	TTCCCTTATTT	2520
20	GGGGAGATAA	ACTOTTGAAT	CCCCAACATO	TICAGOOOG	AMOTOR COCCE	BACACACACT	2580
	TAACCTGTAT	CTTTCTTCAA	TCCTCTCAAA	TTCAGCTCTG	ATCTGAGGCT	ACCONCENCES	2640
	CCCCACTTCA	CATAGGTAAG	AGCCACATTT	TOTCOAGGIAI	CACIGORGIC	CCCCTCTTA	2700
	CCCTCATCAT	AGCAGGAGGC	GITTICAAGG	TGGCAATTGG	MCCCC A CTAR	CACCACCCTC	2760
25	TAGAAGCTTC	GGCTACAATC	MAGCGTGTTC	TORGUNGATA	TOGGOVACIAI	CCCCCCTTACC	2820
23	TGATCAAATT	TTCAGGCTAC	TIGGAGCIGC	TIGGACGGAT	PARCCIANACC	CCGGGTTAGC	2880
	ATGTGTGACT	AACTCTCAAA	TGTTCTTGAC	AMICATOTOC	ANTOGROUNG	TITICAGIGI	2940
	TCCCAAAGTG	GGGAATTCTT	TCCAAAATGG	TTATCTTTGA	GACCATCCAT	CONCORDOR	3000
	GGCTTCTCCA	AAACTAGGAG	ACAGCCAAGT	TUTCATACATA	CENTRACTECT	TOTAL	3060
30	TCCAGAAACC	CTGAGGCTGT	ATGAAACIGG	TTCCTACATC	CIARGGIICI	CONTROLOGO	3120
30	CTCATGCCTC	TCCAAGTGAC	TTTTGGCTGT	COCCUCIO	ACCOMPANIA	GUANTONGG	3180
	GAAGCCATTT	ACTAAGCCTT	TIGCAATCCA	GGCTGTTCTC	MCCCCTCCAA	ATCTCCTTTC	3240
	TGGGATCCTG	CAACTAACCC	TGACTIANGG	GITGCITGCI	maga chacas	AGGICCITIC	3300
	TCAAAGGGGC	TGTACCAAGT	GIGCAGAACC	NGCACIANGG	CONCROCAG	ALCCACACAC	3360
35	AAGCCTCTAA	TGTACCAAGT	GCTTCCTACA	CA CCA A CTICA	*CCCTTTTTCC	AACTGTAGCT	3420
33	GGGCAAACCC	ACATCACACA	CITCATCICC	CACGAGGTCA	AGGGTTTTCC	ANGIGIAGEI	3480
	AACAGTTGCC	GAAGGCTGGA	ACCITCONGT	CINTEGUANG	CCCACCTCAT	CCACCCAATC	3540
	CCAACCCATT	CCAAGAAGTT	AGGCAGCAGG	CATTIOCIAN	ADDCAGCIGAT	#GOGGGGGGGGGG	3600
	GTTCTGCTGG	GTTCAGACTT	AAACTATTTT	GAGCATTAGA	MIGGROGAAA	CTTCAAGATT	3660
40	CAAGTGCAGA	GACAGGCTCT	CGCTAAGGGC	CONTROL	CONGCATTIA	Chererecte	3720
40	AATGTAGGAT	CTCAAATCAA	LUIGGUIGIC	CTACCATCAG	TCCCCCTC3C3	ACCIDIOGIC	3780
	GTCAACTTTC	TTTCTAAGTT	AMACAGGCAG	TTTTTCACCA	CCABBACCA	ACTICICATION	3840
	CLOCKTGGTT	CCCGTTTCTT	CCNRCCONCA	ACCOUNTANA	CAATTIGGAGG	CATTUTGGTT	3900
	CAUCITIATO	GAGAATTCAA	ATCOTOTOT	CONTROCTOR	TACARTART	TOTABACATA	3960
45	TITCHCHIT	CCTGCTTTTT	marararara	TAATTTTCAG	GTCAAGTTTT	TTATACTGCA	4020
73		ADAATAAAA		innitition	0.0001111		-320
	CITATTIGIC	. ANAMIAMUA	11C.CACAL				

Seq ID NO: 174 Protein sequence: Protein Accession #: AAP36984

50 31 1 1 21 31 41 51

FYPOGITIES WYTESPILLA LOSSILANY CHYPTHYSE WYLSPENAN LIGHTLING WYTESPILLA LOSSILANY CHYPTHYSE WYLSPENAN LIGHTLING WYTESPILLA WYTESPILLA DESIGNALY LANGEMEN LEKTLESER ISPOLAVYM CHYPTHYSE WYLSPENAN LIGHTLING WYLSPENAN LIGHT W 120 180 240 300 360 420 55 60 540

Seq ID NO: 175 DNA sequence Nucleic Acid Accession 8: NM_000691 Coding sequence: 43..1404 65

KKPEQYSLAF ABV

	1	11	21	31	41	51	
70	1	1	1	1	1	1	
	CCAGGAGCCC	CAGTTACCGG	GAGAGGCTGT	GTCAAAGGCG	CCATGAGCAA	GATCAGCGAG	60
	GCCGTGAAGC	GCGCCCGCGC	CGCCTTCAGC	TCGGGCAGGA	CCCGTCCGCT	GCAGTTCCGA	120
	TTCCAGCAGC	TGGAGGCGCT	GCAGCGCCTG	ATCCAGGAGC	AGGAGCAGGA	GCTGGTGGGC	180
	GCGCTGGCCG	CAGACCTGCA	CAAGAATGAA	TGGAACGCCT	ACTATGAGGA	GGTGGTGTAC	240
75		AGATCGAGTA					300
	GTGGAGAAGA	CGCCCCAGAC	TCAGCAGGAC	GAGCTCTACA	TCCACTCGGA	GCCACTGGGC	360
	GTGGTCCTCG	TCATTGGCAC	CTGGAACTAC	CCCTTCAACC	TCACCATCCA	GCCCATGGTG	420
	GGCGCCATCG	CTGCAGGGAA	CGCAGTGGTC	CTCAAGCCCT	CGGAGCTGAG	TGAGAACATG	480
	GCGAGCCTGC	TGGCTACCAT	CATCCCCCAG	TACCTGGACA	AGGATCTGTA	CCCAGTAATC	540
80	AATGGGGGTG	TCCCTGAGAC	CACGGAGCTG	CTCAAGGAGA	GGTTCGACCA	TATCCTGTAC	600
	ACGGGCAGCA	CGGGGGTGGG	GAAGATCATC	ATGACGGCTG	CTGCCAAGCA	CCTGACCCCT	660
	GTCACGCTGG	AGCTGGGAGG	GAAGAGTCCC	TGCTACGTGG	ACAAGAACTG	TGACCTGGAC	720
	GTGGCCTGCC	GACGCATCGC	CTGGGGGAAA	TTCATGAACA	GTGGCCAGAC	CTGCGTGGCC	780
	CCAGACTACA	TCCTCTGTGA	CCCCTCGATC	CAGAACCAAA	TTGTGGAGAA	GCTCAAGAAG	840
85	TCACTGAAAG	AGTTCTACGG	GGAAGATGCT	AAGAAATCCC	GGGACTATGG	AAGAATCATT	900
	AGTGCCCGGC	ACTTCCAGAG	GGTGATGGGC	CTGATTGAGG	GCCAGAAGGT	GGCTTATGGG	960
		ATGCCGCCAC					1020

	CAGTCCCCGG AGCCTGGAGG	TGATGCAAGA	GGAGATCTTC	GCCCCTCTCC	TGCCCATCGT	GTGCGTGCGC	1080
	AGCCTGGAGG	AGGCCATCCA	GTTCATCAAC	CAGCGTGAGA	AGCCCCTGGC	CCTCTACATG	1140
	TTCTCCAGCA	ACGACAAGGT	GATTAAGAAG	ATGATTGCAG	AGACATCCAG	TGGTGGGGTG	1200
-	GCGGCCAACG	ATGTCATCGT	CCACATCACC	TTGCACTCTC	TGCCCTTCGG	GGGCGTGGGG TCACCGCCGC	1260
5	AACAGCGGCA	TGGGATCCTA	CCATGGCAAG	AAGAGCTTCG	AGACTTTCTC	TCACCGCCGC	1320
	TCTTGCCTGG	TGAGGCCTCT	GATGAATGAT	GAAGGCCTGA	AGGTCAGATA	CCCCCCGAGC	1380
							1440
	CCCATCGGAG	TGCGGACCAC	CCTCACTGGC	TCTCCTGGCC	CTGGAGAATC	GCTCCTGCAG	1500
	CCCATCGGAG CCCCAGCCCA	GCCCCACTCC	TCTGCTGACC	TGCTGACCTG	TGCACACCCC	ACTCCCACAT	1560
10	GGGCCCAGGC	CTCACCATTC	CAAGTCTCCA	CCCCTTTCTA	GACCAATAAA	GAGACAAATA	1620
	CAATTTTCTA						
	Seq ID NO:	176 Proteir	semience:				
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13	,	11	21	31	41	51	
	†	1	17	ī	ī	Ĭ.	
	MONTOPAUND	ADAADGGGDT	PRIOFPROOF	BALORLIORO	ROELVGALAA	DLHKNEWNAY	60
	ABBUTANT DE	TOVMTOVILDE	MANDEDVEKT	BOTOODEL'AL	HSEPT GVVI.V	DLHKNEWNAY IGTWNYPFNL	120
20							180
20	TIQUITI VECOE	CHURTIMEAN	AVUI.TRUTT.E	LCCKERCYVD	SOUCDI-DVACE	RIAWGKPMNS FORVMGLIEG	240
	COMMITTED	CONCIONA	WONT AACT AL	BACKDVERCD	DYGRIIGARE	PORUMGI, TRG	300
							360
	DI AT.VMPCCM	DESTRUCTE	TSSGGVAAND	VIVHITLESI	PEGGVGNSGM	GSYHCKKSFE	420
25	macupacet V	RPLMINDEGLK	MANDEDVANA	TOH			
23	I F SHIGHSCEV	KELFEIDEGEN	************				
	Com TD NO.	177 DNA sec	mence				
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	CONTRACTOR OF	OCCUPATION OF	Channacaac	TTTGGTGGGG	GTGGTCTCGT	GGGGTCCTGC	60
	CIMACCOACG	COCCICIONO	TTCTTGAGCC	CCTTCACGAC	CGTCACCATG	GAAGTGTCAC	120
35	CIGITINGIC	TOTAL ACTOR	AATATOCAAG	TCAACAAAAT	TAAGAAAAA	GAAGTGTCAC GAAGATGCTA	180
"	CATTOCAGCC	CTCOCCOCCA A	ACTATOMATO	AAAACAAAAC	ACAATTGGAA	CATATTTTGC	240
	AGAUUUGACT	OR COMP CREEK	COMPONICA	AATTACTOR	CCAGCAAATG	TEGETTTACE	300
	TCCGCCCAGA	CACCIACATI	Thraccon NG	TOTAL CONTRACT	TOCTOCTOC	TACAAAATCT	360
	ATGANGATGT	TOGCATIANC	CCTCCCCACA	ACABACABAG	GGACCCAAAA	ATCTCTTGTA	420
40	TIGATGAGAT	ICIMUI IMMI	CARAGORA	TARTESTA	ATCCARTANT	GCARAGGTA	480
40	TTAGAGTCAC	MATTGATCCG	COMMONIT	TOTATOTOC	ACCTUTCATA	TTTGGACAGC	540
	TTCCTGTTGT	TGAACACAAA	GTTGAMMAGA	BARROTT	CACACCTCCT	COLLARCOC	600
	TCCTAACTIC	TAGTAACTAT	GATGATGATG	COL S SOURCE	manage soos	COCACTAGAG	660
	ATGGAGCCAA	GTCTGTTGAA CACCTACATT TGGCATTAAC TCTAGTTAAT AATTGATCCG TGAACACAAA TAGTAACTAT ATTGTGTAAC	ATATTCAGTA	CCAAATTTAC	TGTGGAAACA	GCCAGTAGAG	660
15	ATGGAGCCAA AATACAAGAA	TAGTAACTAT ATTGTGTAAC AATGTTCAAA	ATATTCAGTA CAGACATGGA	CCAAATTTAC	TGTGGAAACA GGGAAGAGCT	GCCAGTAGAG GGTGAGATGG	660 720
45	ATGGAGCCAA AATACAAGAA AACTCAAGCC	TAGTAACTAT ATTGTGTAAC AATGTTCAAA CTTCAATGGA	GATGATGATG ATATTCAGTA CAGACATGGA GAAGATTATA	CCAAATTTAC TGGATAATAT CATGTATCAC	TGTGGAAACA GGGAAGAGCT CTTTCAGCCT	GCCAGTAGAG GGTGAGATGG GATTTGTCTA	660 720 780
45	AATACAAGAA AACTCAAGCC	AATGTTCAAA CTTCAATGGA	CAGACATGGA GAAGATTATA	TGGATAATAT CATGTATCAC TTGTTGCACT	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA	GGTGAGATGG GATTTGTCTA AGAGCATATG	660 720 780 840
45	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA	CAGACATGGA GAAGATTATA GACAAAGATA GATGTCAAAG	TGGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA	660 720 780 840 900
45	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA	CAGACATGGA GAAGATTATA GACAAAGATA GATGTCAAAG	TGGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA	660 720 780 840 900 960
-	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA	CAGACATGGA GAAGATTATA GACAAAGATA GATGTCAAAG	TGGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA	660 720 780 840 900 960
45 50	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA	CAGACATGGA GAAGATTATA GACAAAGATA GATGTCAAAG	TGGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA	720 780 840 900 960 1020
-	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA	CAGACATGGA GAAGATTATA GACAAAGATA GATGTCAAAG	TGGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA	720 780 840 900 960 1020 1080
-	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA	CAGACATGGA GAAGATTATA GACAAAGATA GATGTCAAAG	TGGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA	660 720 780 840 900 960 1020 1080 1140
-	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG AAGGATTTCG CCTTGAAAGT AAAAAGGCTTA ATGTTGATTA ACAAGGGTGG ATGCCTTAAT	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCAGCAAATT TGTAGCTGAT TGTTGCAGTA TGAAAACCCA	CAGACATGGA GAAGATTATA GACAAAGATA GACATGTATT CAAGTAAAC AGCTTTGTCA AGCATGTATA AAAGCACATC ACCTTTGACA ACCTTTGACA	TGGATAATAT CATGTATCAC TTGTTTGCAC TGAAGGACAA ACAGGTGGGA ACAGCATTGC CTAAACTTGT AGGTGAAAAA CTCAGACAAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA GTTGGATGTA TACATCCAAG TGATGTTTTA TGCATGTGG TGAAAACATG	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGA ATTTTTGTAA ACTTTTACAAC	660 720 780 840 900 960 1020 1080 1140 1200 1260
50	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG AAGGATTTCG CCTTGAAAGT AAAAAGGCTTA ATGTTGATTA ACAAGGGTGG ATGCCTTAAT	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCAGCAAATT TGTAGCTGAT TGTTGCAGTA TGAAAACCCA	CAGACATGGA GAAGATTATA GACAAAGATA GACATGTATT CAAGTAAAC AGCTTTGTCA AGCATGTATA AAAGCACATC ACCTTTGACA ACCTTTGACA	TGGATAATAT CATGTATCAC TTGTTTGCAC TGAAGGACAA ACAGGTGGGA ACAGCATTGC CTAAACTTGT AGGTGAAAAA CTCAGACAAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA GTTGGATGTA TACATCCAAG TGATGTTTTA TGCATGTGG TGAAAACATG	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGA ATTTTTGTAA ACTTTTACAAC	660 720 780 840 900 960 1020 1080 1140
-	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG AAGGATTTCG CCTTGAAAGT AAAAAGGCTTA ATGTTGATTA ACAAGGGTGG ATGCCTTAAT	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCAGCAAATT TGTAGCTGAT TGTTGCAGTA TGAAAACCCA	CAGACATGGA GAAGATTATA GACAAAGATA GACATGTATT CAAGTAAAC AGCTTTGTCA AGCATGTATA AAAGCACATC ACCTTTGACA ACCTTTGACA	TGGATAATAT CATGTATCAC TTGTTTGCAC TGAAGGACAA ACAGGTGGGA ACAGCATTGC CTAAACTTGT AGGTGAAAAA CTCAGACAAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA GTTGGATGTA TACATCCAAG TGATGTTTTA TGCATGTGG TGAAAACATG	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGA ATTTTTGTAA ACTTTTACAAC	660 720 780 840 900 960 1020 1140 1200 1260 1320
50	AATACAAGAA AACTCAAGCC AGTTTAAAAT ATATTGCTGG AAGGATTTCG CCTTGAAAGT AAAAAGGCTTA ATGTTGATTA ACAAGGGTGG ATGCCTTAAT	AATGTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCAGCAAATT TGTAGCTGAT TGTTGCAGTA TGAAAACCCA	CAGACATGGA GAAGATTATA GACAAAGATA GACATGTATT CAAGTAAAC AGCTTTGTCA AGCATGTATA AAAGCACATC ACCTTTGACA ACCTTTGACA ACCTTTGACT	TGGATAATAT CATGTATCAC TTGTTTGCAC TGAAGGACAA ACAGGTGGGA ACAGCATTGC CTAAACTTGT AGGTGAAAAA CTCAGACAAA	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAAATAAA GTTGGATGTA TACATCCAAG TGATGTTTTA TGCATGTGG TGAAAACATG	GGTGAGATGG GATTTGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGA ATTTTTGTAA ACTTTTACAAC	660 720 780 840 900 960 1020 1140 1200 1260 1360 1380 1440
50	ANTACRAGAA AACTCAAGCC AGGTTHAAAT ATATTGCTGG AAGGATTTCG CCTTGAAAGC AAAAAGGCTT ATGTTAATA ACAAGGGTGG ATGCCTTAAT CCAAGAGCTT GTGGTATTGT AGAAGTGTTC ATGATTATT AGAAGTGTTC ATGATTATT AGAAGTGTTC ATGATGCAGG	AATOTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCAGCAAAT TGTAGCTGAT TGTAGCAGTA TGAAAACCCA TGGATCAACA AGCTTAAAA GGCCGAAAC	CAGACATGGA GACAAGATATA GATGTCAAAG GACATGTATT CAAGTGTATC CAGATTGTCA CAGATTGTCA CAGATTGTCA ACCTTTGACT TGCCAATTGA CTAAACTGGG CATAATTGA TCACACTGGC CATAATTGA TCCACTGGAT TCCACTGACT	TGGATAATAT CATGATATCAC TTGTTGCACT TCTTTCTTAA TGAAGGACAA ACAGCATTGC CTAAACTTGT AGGTGAAAAATT TGAAGGACAA TGAAAAATT TGAAGGACAA TGAAGACTAT TCAAGGGAT TCAAGGGAT TCAAGGGAT TCAAGGGAT TCAAGGGAT	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAATAAA GTTGGATGAA AGTGTGTTTTA TACATCCAAG TGAATGTGGA AGAAACATG TATCAAAGCT GGCCCAAGTC CCCCAACTC CCTGACTGAG AGAAACATC	GGTGAGATGG GATTGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGA ATTTTTGTAA ACTTTACAAC GCCATTGGCT CAGTTAAACT GATGATGCCA GAGATTCAG GAGATTCAG GAGATTCAG GAGATTCAC	660 720 780 840 900 960 1020 1140 1200 1260 1320
50	ANTACRAGAA AACTCAAGCC AGGTTHAAAT ATATTGCTGG AAGGATTTCG CCTTGAAAGC AAAAAGGCTT ATGTTAATA ACAAGGGTGG ATGCCTTAAT CCAAGAGCTT GTGGTATTGT AGAAGTGTTC ATGATTATT AGAAGTGTTC ATGATTATT AGAAGTGTTC ATGATGCAGG	AATOTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCAGCAAAT TGTAGCTGAT TGTAGCAGTA TGAAAACCCA TGGATCAACA AGCTTAAAA GGCCGAAAC	CAGACATGGA GACAAGATATA GATGTCAAAG GACATGTATT CAAGTGTATC CAGATTGTCA CAGATTGTCA CAGATTGTCA ACCTTTGACT TGCCAATTGA CTAAACTGGG CATAATTGA TCACACTGGC CATAATTGA TCCACTGGAT TCCACTGACT	TGGATAATAT CATGATATCAC TTGTTGCACT TCTTTCTTAA TGAAGGACAA ACAGCATTGC CTAAACTTGT AGGTGAAAAATT TGAAGGACAA TGAAAAATT TGAAGGACAA TGAAGACTAT TCAAGGGAT TCAAGGGAT TCAAGGGAT TCAAGGGAT TCAAGGGAT	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAATAAA GTTGGATGAA AGTGTGTTTTA TACATCCAAG TGAATGTGGA AGAAACATG TATCAAAGCT GGCCCAAGTC CCCCAACTC CCTGACTGAG AGAAACATC	GGTGAGATGG GATTGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGA ATTTTTGTAA ACTTTACAAC GCCATTGGCT CAGTTAAACT GATGATGCCA GAGATTCAG GAGATTCAG GAGATTCAG GAGATTCAC	720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500
50	ANTACRAGAA AACTCAAGCC AGGTTHAAAT ATATTGCTGG AAGGATTTCG CCTTGAAAGC AAAAAGGCTT ATGTTAATA ACAAGGGTGG ATGCCTTAAT CCAAGAGCTT GTGGTATTGT AGAAGTGTTC ATGATTATT AGAAGTGTTC ATGATTATT AGAAGTGTTC ATGATGCAGG	AATOTTCAAA CTTCAATGGA GCAAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCAGCAAAT TGTAGCTGAT TGTAGCAGTA TGAAAACCCA TGGATCAACA AGCTTAAAA GGCCGAAAC	CAGACATGGA GACAAGATATA GATGTCAAAG GACATGTATT CAAGTGTATC CAGATTGTCA CAGATTGTCA CAGATTGTCA ACCTTTGACT TGCCAATTGA CTAAACTGGG CATAATTGA TCACACTGGC CATAATTGA TCCACTGGAT TCCACTGACT	TGGATAATAT CATGATATCAC TTGTTGCACT TCTTTCTTAA TGAAGGACAA ACAGCATTGC CTAAACTTGT AGGTGAAAAATT TGAAGGACAA TGAAAAATT TGAAGGACAA TGAAGACTAT TCAAGGGAT TCAAGGGAT TCAAGGGAT TCAAGGGAT TCAAGGGAT	GGGAAGAGCT CTTTCAGCCT AATGGTCAGA TGGAATAAA GTTGGATGAA AGTGTGTTTTA TACATCCAAG TGAATGTGGA AGAAACATG TATCAAAGCT GGCCCAAGTC CCCCAACTC CCTGACTGAG AGAAACATC	GGTGAGATGG GATTGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGA ATTTTTGTAA ACTTTACAAC GCCATTGGCT CAGTTAAACT GATGATGCCA GAGATTCAG GAGATTCAG GAGATTCAG GAGATTCAC	720 780 840 900 960 1080 1140 1200 1320 1380 1440 1560 1560
50	AATRCARGAA AACTCARGCC AGTTTAANAT ATATTGCTGG CCTTGAAAGT TAAAAGGCTT AGTTGATTAA ACAAGGCTT AGTGCTTAAT CCAAGAGGTT GTGGTATTGT AGAAGTGTTC AGAAGTGTTC TCTTTAGAGG CCAAACTTT TCTTTTAGAGG CCTAGATTAA	AATOTTCAAA CTTCAATGGA GCAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCMGCAAAT TGTAGCAGTA TGAAAACCCA TGGATCAACCA AGGATCAACCA GGGCGGAAAC GGCTGTTACAA GGTCTTAAAA AAAAATACTC CAATATCACC CAATATCACC CAATATCACC CAATATCACC CAATATCACC	CAGACATGGA GACAAGATTATA GATGTCAAAG GACAAGATAA GATGTCAAAG GACATGTATT CAGAGTTAGTCA AAGCACATC TGCCAATTGAC CTAAACTGGG CATAATGGA TCCACTGGGT GGCCTTGGCG AAGATTGAC GACTTGGCA AAGATTGA AAGATTGA AAGATTGA AAGATTGA AAGATTGAA TCCACTGGGT GGCCTTGGTG AAGATTGAA	TOGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA TGAAGGACTAA ACAGGTTGC CTAAACTTGT AGGTGAAAA CTCAGACAAA CTCAGACAAA TCAAGCATTAC TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGATTTTGGAG AA AGCTTTCTCA TGTTTCAGTA TCTTCAGTA TCTTCAGTA TCTTCAGTA TCTTTCAGTA TCTTTTCAGTA TCTTTTCAGTA TCTTTTCAGTA TCTTTTTTTTTT	GGGANGAGT CTTTCAGCCT ATTGAGCT TGAGATGAA AGTGTGATGAA AGTGTGTTTA TACATCCANG TGAGTTGTT TACATCANG TGACATGTGG AGAAAACAT TCCCAAAGCT CCCCAAGTC CCTGACTGAG AGAAAACA TTAAGCAGAT CAGAAAACA CATGAGAAAACA CAGAAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAAC CAGAAAAC CAGAAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC GGTGAGATGG GATTIGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGAC AAGAAGAAGA ACTTTTOTAA ACTTTACAAC GCCATTGCCT CAGTATAACA GGGAGTTTCC GGGGTTTTCC ATGGAAATC ATGGAGAATC ATGGAGAATC ATGAGAATC ATGGAGAATC	720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500	
50	AATRCARGAA AACTCARGCC AGTTTAANAT ATATTGCTGG CCTTGAAAGT TAAAAGGCTT AGTTGATTAA ACAAGGCTT AGTGCTTAAT CCAAGAGGTT GTGGTATTGT AGAAGTGTTC AGAAGTGTTC TCTTTAGAGG CCAAACTTT TCTTTTAGAGG CCTAGATTAA	AATOTTCAAA CTTCAATGGA GCAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCMGCAAAT TGTAGCAGTA TGAAAACCCA TGGATCAACCA AGGATCAACCA GGGCGGAAAC GGCTGTTACAA GGTCTTAAAA AAAAATACCC AAAAAATACCC CAATATCACC CAATATCACC CAATATCACC CAATATCACC	CAGACATGGA GACAAGATTATA GATGTCAAAG GACAAGATAA GATGTCAAAG GACATGTATT CAGAGTTAGTCA AAGCACATC TGCCAATTGAC CTAAACTGGG CATAATGGA TCCACTGGGT GGCCTTGGCG AAGATTGAC GACTTGGCA AAGATTGA AAGATTGA AAGATTGA AAGATTGA AAGATTGAA TCCACTGGGT GGCCTTGGTG AAGATTGAA	TOGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA TGAAGGACTAA ACAGGTTGC CTAAACTTGT AGGTGAAAA CTCAGACAAA CTCAGACAAA TCAAGCATTAC TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGATTTTGGAG AA AGCTTTCTCA TGTTTCAGTA TCTTCAGTA TCTTCAGTA TCTTCAGTA TCTTTCAGTA TCTTTTCAGTA TCTTTTCAGTA TCTTTTCAGTA TCTTTTTTTTTT	GGGANGAGT CTTTCAGCCT ATTGAGCT TGAGATGAA AGTGTGATGAA AGTGTGTTTA TACATCCANG TGAGTTGTT TACATCANG TGACATGTGG AGAAAACAT TCCCAAAGCT CCCCAAGTC CCTGACTGAG AGAAAACA TTAAGCAGAT CAGAAAACA CATGAGAAAACA CAGAAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAAC CAGAAAAC CAGAAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC GGTGAGATGG GATTIGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGAC AAGAAGAAGA ACTTTTOTAA ACTTTACAAC GCCATTGCCT CAGTATAACA GGGAGTTTCC GGGGTTTTCC ATGGAAATC ATGGAGAATC ATGGAGAATC ATGAGAATC ATGGAGAATC	720 780 840 900 960 1080 1140 1200 1320 1380 1440 1560 1560 1620	
50	AATRCARGAA AACTCARGCC AGTTTAANAT ATATTGCTGG CCTTGAAAGT TAAAAGGCTT AGTTGATTAA ACAAGGCTT AGTGCTTAAT CCAAGAGGTT GTGGTATTGT AGAAGTGTTC AGAAGTGTTC TCTTTAGAGG CCAAACTTT TCTTTTAGAGG CCTAGATTAA	AATOTTCAAA CTTCAATGGA GCAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCMGCAAAT TGTAGCAGTA TGAAAACCCA TGGATCAACCA AGGATCAACCA GGGCGGAAAC GGCTGTTACAA GGTCTTAAAA AAAAATACCC AAAAAATACCC CAATATCACC CAATATCACC CAATATCACC CAATATCACC	CAGACATGGA GACAAGATTATA GATGTCAAAG GACAAGATAA GATGTCAAAG GACATGTATT CAGAGTTAGTCA AAGCACATC TGCCAATTGAC CTAAACTGGG CATAATGGA TCCACTGGGT GGCCTTGGCG AAGATTGAC GACTTGGCA AAGATTGA AAGATTGA AAGATTGA AAGATTGA AAGATTGAA TCCACTGGGT GGCCTTGGTG AAGATTGAA	TOGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA TGAAGGACTAA ACAGGTTGC CTAAACTTGT AGGTGAAAA CTCAGACAAA CTCAGACAAA TCAAGCATTAC TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGATTTTGGAG AA AGCTTTCTCA TGTTTCAGTA TCTTCAGTA TCTTCAGTA TCTTCAGTA TCTTTCAGTA TCTTTTCAGTA TCTTTTCAGTA TCTTTTCAGTA TCTTTTTTTTTT	GGGANGAGT CTTTCAGCCT ATTGAGCT TGAGATGAA AGTGTGATGAA AGTGTGTTTA TACATCCANG TGAGTTGTT TACATCANG TGACATGTGG AGAAAACAT TCCCAAAGCT CCCCAAGTC CCTGACTGAG AGAAAACA TTAAGCAGAT CAGAAAACA CATGAGAAAACA CAGAAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAAC CAGAAAAC CAGAAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC GGTGAGATGG GATTIGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGAC AAGAAGAAGA ACTTTTOTAA ACTTTACAAC GCCATTGCCT CAGTATAACA GGGAGTTTCC GGGGTTTTCC ATGGAAATC ATGGAGAATC ATGGAGAATC ATGAGAATC ATGGAGAATC	660 720 780 840 900 1020 1080 11200 1260 1380 1380 1500 1560 1620 1680 1740 1860	
50	AATRCARGAA AACTCARGCC AGTTTAANAT ATATTGCTGG CCTTGAAAGT TAAAAGGCTT AGTTGATTAA ACAAGGCTT AGTGCTTAAT CCAAGAGGTT GTGGTATTGT AGAAGTGTTC AGAAGTGTTC TCTTTAGAGG CCAAACTTT TCTTTTAGAGG CCTAGATTAA	AATOTTCAAA CTTCAATGGA GCAAGCCTG ATCCACCAAA TAGTTATGTG AATACATGAA TCMGCAAAT TGTAGCAGTA TGAAAACCCA TGGATCAACCA AGGATCAACCA GGGCGGAAAC GGCTGTTACAA GGTCTTAAAA AAAAATACCC AAAAAATACCC CAATATCACC CAATATCACC CAATATCACC CAATATCACC	CAGACATGGA GACAAGATTATA GATGTCAAAG GACAAGATAA GATGTCAAAG GACATGTATT CAGAGTTAGTCA AAGCACATC TGCCAATTGAC CTAAACTGGG CATAATGGA TCCACTGGGT GGCCTTGGCG AAGATTGAC GACTTGGCA AAGATTGA AAGATTGA AAGATTGA AAGATTGA AAGATTGAA TCCACTGGGT GGCCTTGGTG AAGATTGAA	TOGATAATAT CATGTATCAC TTGTTGCACT TCTTTCTTAA TGAAGGACTAA ACAGGTTGC CTAAACTTGT AGGTGAAAA CTCAGACAAA CTCAGACAAA TCAAGCATTAC TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGAACTTTT TGATTTTGGAG AA AGCTTTCTCA TGTTTCAGTA TCTTCAGTA TCTTCAGTA TCTTCAGTA TCTTTCAGTA TCTTTTCAGTA TCTTTTCAGTA TCTTTTCAGTA TCTTTTTTTTTT	GGGANGAGT CTTTCAGCCT ATTGAGCT TGAGATGAA AGTGTGATGAA AGTGTGTTTA TACATCCANG TGAGTTGTT TACATCANG TGACATGTGG AGAAAACAT TCCCAAAGCT CCCCAAGTC CCTGACTGAG AGAAAACA TTAAGCAGAT CAGAAAACA CATGAGAAAACA CAGAAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAAC CAGAAAAC CAGAAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAAC CAGAAAC GGTGAGATGG GATTIGTCTA AGAGCATATG CTGCCAGTAA ACTGGTAACT ACTATGAGTG GGTGGCAGAC AAGAAGAAGA ACTTTTOTAA ACTTTACAAC GCCATTGCCT CAGTATAACA GGGAGTTTCC GGGGTTTTCC ATGGAAATC ATGGAGAATC ATGGAGAATC ATGAGAATC ATGGAGAATC	660 720 780 840 900 1020 1080 11200 1260 1380 1380 1500 1560 1620 1680 1740 1860	
50 55 60	ANTICANGA ANTICANGA ANTICANGA ATATICANG ATATICANG CETTANAN ANGATTIA ANGAGETTA ANGAGETTA ANGAGETTA ANGAGETTA ANGAGETTA COAGGGETGA TOCAGGGETTA TOCAGGGETTA TOCAGGGETTA ANGATTCAGG COAGGATTA ANGATTCAC TOCAGGATTA ANGATTCAC TOCAGGATTA ANGATTCAC TOCAGGATTA ANGATTCAC TOCAGGATTA	ANTOTTCANA CTTCANTOCA CCANAGCTES ATOCACCANA TAGTTATOTA TAGTATATOTA TAGTATATOTA TOTACCANA TOTACCA	CAGACATGGA GAGAGATATATA GATOTCAAAG GACAAGATA GATOTCAAAG GACATGTAT CAAGTATATC CAGATTGTCA AGCTTTGACA ACCTTTGACA TCCACATTGACA TCCACTGAGT TCCACTGAGT GGCCTTGTGA AAGTTGTGA AAGTTGTGA AAGTTTGACA TCCACTGAGT GGCCTTGTGA TCCACTGAGT TCCACTGAGT TCCACTGAGT COTTATGGGA TTGCTGATTA GAATTTATCA GAATTATCAGA TTGCTGATTA GAATTATCAGA TTGCTGATTA GAATTATCACA CTTCCTGATT	TOGATAATAT CATGATATCAC TTGTTGACT TTGTTGACT TGTATGACT TGTATGACAT TGAAGGACAA ACAGGTGGGA ACAGGTTGC CTAAACTTGT AGGTGAAAAA TTGAAGGAAAT TGAAGCAAA TGAAGCAAT TGAAGCAAA TGAAGCATTAC TGAAGCAAA ATTTAACA TGTACGACTTAT TGTAGGCAAA AGGTTTAA TGTAGGCATTAT TGTATTGAAGGAAT ATTTATCACA ATTTATCACAT ATTTATCACAT TTGAAGGAAT TTGAAGGAAT TTGAAGGAAT TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTG	GGGAAGAGT CTTTCAGCT AATGOTCAGA TGGAATAAA AGTGTGTTTAGATCAAA AGTGTGTTTA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TATCAAAGCT CCCAAACTC CCTGACTCAA TCCCAAACTC CAAACAAAAAA TAAAAAAA TAAAAAAAT TAAAACAGAT TCACAACTG GAAAAAAA TAAAAAAAA TAAAAAAAAA AAAAAAAA	GOTGAGATGG GATTIGTCTA AGAGCATATA GAGCATATA CTGGTAACT GGTGGCAGAC AGAAGAAAAAAAAAA	660 720 840 960 1020 1140 1200 1320 1320 1440 1560 1680 1740 1860 1920
50	ANTICANGA ANTICANGA ANTICANGA ATATICANG ATATICANG CETTANAN ANGATTIA ANGAGETTA ANGAGETTA ANGAGETTA ANGAGETTA ANGAGETTA COAGGGETGA TOCAGGGETTA TOCAGGGETTA TOCAGGGETTA ANGATTCAGG COAGGATTA ANGATTCAC TOCAGGATTA ANGATTCAC TOCAGGATTA ANGATTCAC TOCAGGATTA ANGATTCAC TOCAGGATTA	ANTOTTCANA CTTCANTOCA CCANAGCTES ATOCACCANA TAGTTATOTA TAGTATATOTA TAGTATATOTA TOTACCANA TOTACCA	CAGACATGGA GAGAGATATATA GATOTCAAAG GACAAGATA GATOTCAAAG GACATGTAT CAAGTATATC CAGATTGTCA AGCTTTGACA ACCTTTGACA TCCACATTGACA TCCACTGAGT TCCACTGAGT GGCCTTGTGA AAGTTGTGA AAGTTGTGA AAGTTTGACA TCCACTGAGT GGCCTTGTGA TCCACTGAGT TCCACTGAGT TCCACTGAGT COTTATGGGA TTGCTGATTA GAATTTATCA GAATTATCAGA TTGCTGATTA GAATTATCAGA TTGCTGATTA GAATTATCACA CTTCCTGATT	TOGATAATAT CATGATATCAC TTGTTGACT TTGTTGACT TGTATGACT TGTATGACAT TGAAGGACAA ACAGGTGGGA ACAGGTTGC CTAAACTTGT AGGTGAAAAA TTGAAGGAAAT TGAAGCAAA TGAAGCAAT TGAAGCAAA TGAAGCATTAC TGAAGCAAA ATTTAACA TGTACGACTTAT TGTAGGCAAA AGGTTTAA TGTAGGCATTAT TGTATTGAAGGAAT ATTTATCACA ATTTATCACAT ATTTATCACAT TTGAAGGAAT TTGAAGGAAT TTGAAGGAAT TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA	GGGAAGAGT CTTTCAGCT AATGOTCAGA TGGAATAAA AGTGTGTTTAGATCAAA AGTGTGTTTA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TATCAAAGCT CCCAAACTC CCTGACTCAA TCCCAAACTC CAAACAAAAAA TAAAAAAA TAAAAAAAT TAAAACAGAT TCACAACTG GAAAAAAA TAAAAAAAA TAAAAAAAAA AAAAAAAA	GOTGAGATGG GATTIGTCTA AGAGCATATA GAGCATATA CTGGTAACT GGTGGCAGAC AGAAGAAAAAAAAAA	660 720 840 960 1020 1140 1200 1320 1320 1440 1560 1680 1740 1860 1920
50 55 60	ANTICANGA ANTICANGA ANTICANGA ANTICANGA ATATICANGA ANGATITA ANAAGGITA ANGAGGITGA ANGAGGI	ANTOTTCANA CTTCANTOCA CCANAGCTES ATOCACCANA TAGTTATOTA TAGTATATOTA TAGTATATOTA TOTACCANA TOTACCA	CAGACATGGA GAGAGATATATA GATOTCAAAG GACAAGATA GATOTCAAAG GACATGTAT CAAGTATATC CAGATTGTCA AGCTTTGACA ACCTTTGACA TCCACATTGACA TCCACTGAGT TCCACTGAGT GGCCTTGTGA AAGTTGTGA AAGTTGTGA AAGTTTGACA TCCACTGAGT GGCCTTGTGA TCCACTGAGT TCCACTGAGT TCCACTGAGT COTTATGGGA TTGCTGATTA GAATTTATCA GAATTATCAGA TTGCTGATTA GAATTATCAGA TTGCTGATTA GAATTATCACA CTTCCTGATT	TOGATAATAT CATGATATCAC TTGTTGACT TTGTTGACT TGTATGACT TGTATGACAT TGAAGGACAA ACAGGTGGGA ACAGGTTGC CTAAACTTGT AGGTGAAAAA TTGAAGGAAAT TGAAGCAAA TGAAGCAAT TGAAGCAAA TGAAGCATTAC TGAAGCAAA ATTTAACA TGTACGACTTAT TGTAGGCAAA AGGTTTAA TGTAGGCATTAT TGTATTGAAGGAAT ATTTATCACA ATTTATCACAT ATTTATCACAT TTGAAGGAAT TTGAAGGAAT TTGAAGGAAT TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA	GGGAAGAGT CTTTCAGCT AATGOTCAGA TGGAATAAA AGTGTGTTTAGATCAAA AGTGTGTTTA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TATCAAAGCT CCCAAACTC CCTGACTCAA TCCCAAACTC CAAACAAAAAA TAAAAAAAT TAAACAGAT TCACAACTG CAAACAATC CAAACAAAAAA AAAAAAAA TCACAACTGG AAAAGAAAAAA TCACAACTGG AAAAGAAAAAAA TCACAACTGG AAAAAAAAAA	GOTGAGATGG GATTIGTCTA AGAGCATATA AGAGCATATA CTGGTAACT GGTGGCAGAC AGAAGAAAAAAAAAA	660 720 840 960 1020 1140 1200 1320 1320 1440 1560 1680 1740 1860 1920
50 55 60	ANTICANGA ANTICANGA ANTICANGA ANTICANGA ATATICANGA ANGATITA ANAAGGITA ANGAGGITGA ANGAGGI	ANTOTTCANA CTTCANTOCA CCANAGCTES ATOCACCANA TAGTTATOTA TAGTATATOTA TAGTATATOTA TOTACCANA TOTACCA	CAGACATGGA GAGAGATATATA GATOTCAAAG GACAAGATA GATOTCAAAG GACATGTAT CAAGTATATC CAGATTGTCA AGCTTTGACA ACCTTTGACA TCCACATTGACA TCCACTGAGT TCCACTGAGT GGCCTTGTGA AAGTTGTGA AAGTTGTGA AAGTTTGACA TCCACTGAGT GGCCTTGTGA TCCACTGAGT TCCACTGAGT TCCACTGAGT COTTATGGGA TTGCTGATTA GAATTTATCA GAATTATCAGA TTGCTGATTA GAATTATCAGA TTGCTGATTA GAATTATCACA CTTCCTGATT	TOGATAATAT CATGATATCAC TTGTTGACT TTGTTGACT TGTATGACT TGTATGACAT TGAAGGACAA ACAGGTGGGA ACAGGTTGC CTAAACTTGT AGGTGAAAAA TTGAAGGAAAT TGAAGCAAA TGAAGCAAT TGAAGCAAA TGAAGCATTAC TGAAGCAAA ATTTAACA TGTACGACTTAT TGTAGGCAAA AGGTTTAA TGTAGGCATTAT TGTATTGAAGGAAT ATTTATCACA ATTTATCACAT ATTTATCACAT TTGAAGGAAT TTGAAGGAAT TTGAAGGAAT TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA	GGGAAGAGT CTTTCAGCT AATGOTCAGA TGGAATAAA AGTGTGTTTAGATCAAA AGTGTGTTTA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TATCAAAGCT CCCAAACTC CCTGACTCAA TCCCAAACTC CAAACAAAAAA TAAAAAAAT TAAACAGAT TCACAACTG CAAACAATC CAAACAAAAAA AAAAAAAA TCACAACTGG AAAAGAAAAAA TCACAACTGG AAAAGAAAAAAA TCACAACTGG AAAAAAAAAA	GOTGAGATGG GATTIGTCTA AGAGCATATA AGAGCATATA CTGGTAACT GGTGGCAGAC AGAAGAAAAAAAAAA	660 720 840 960 1020 1140 1200 1320 1320 1440 1560 1680 1740 1860 1920
50 55 60	ANTICANGA ANTICANGA ANTICANGA ANTICANGA ATATICANGA ANGATITA ANAAGGITA ANGAGGITGA ANGAGGI	ANTOTTCANA CTTCANTOCA CCANAGCTES ATOCACCANA TAGTTATOTA TAGTATATOTA TAGTATATOTA TOTACCANA TOTACCA	CAGACATGGA GAGAGATATATA GATOTCAAAG GACAAGATA GATOTCAAAG GACATGTAT CAAGTATATC CAGATTGTCA AGCTTTGACA ACCTTTGACA TCCACATTGACA TCCACTGAGT TCCACTGAGT GGCCTTGTGA AAGTTGTGA AAGTTGTGA AAGTTTGACA TCCACTGAGT GGCCTTGTGA TCCACTGAGT TCCACTGAGT TCCACTGAGT COTTATGGGA TTGCTGATTA GAATTTATCA GAATTATCAGA TTGCTGATTA GAATTATCAGA TTGCTGATTA GAATTATCACA CTTCCTGATT	TOGATAATAT CATGATATCAC TTGTTGACT TTGTTGACT TGTATGACT TGTATGACAT TGAAGGACAA ACAGGTGGGA ACAGGTTGC CTAAACTTGT AGGTGAAAAA TTGAAGGAAAT TGAAGCAAA TGAAGCAAT TGAAGCAAA TGAAGCATTAC TGAAGCAAA ATTTAACA TGTACGACTTAT TGTAGGCAAA AGGTTTAA TGTAGGCATTAT TGTATTGAAGGAAT ATTTATCACA ATTTATCACAT ATTTATCACAT TTGAAGGAAT TTGAAGGAAT TTGAAGGAAT TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA	GGGAAGAGT CTTTCAGCT AATGOTCAGA TGGAATAAA AGTGTGTTTAGATCAAA AGTGTGTTTA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TATCAAAGCT CCCAAACTC CCTGACTCAA TCCCAAACTC CAAACAAAAAA TAAAAAAAT TAAACAGAT TCACAACTG CAAACAATC CAAACAAAAAA AAAAAAAA TCACAACTGG AAAAGAAAAAA TCACAACTGG AAAAGAAAAAAA TCACAACTGG AAAAAAAAAA	GOTGAGATGG GATTIGTCTA AGAGCATATA AGAGCATATA CTGGTAACT GGTGGCAGAC AGAAGAAAAAAAAAA	660 720 840 960 1020 1140 1200 1320 1320 1440 1560 1680 1740 1860 1920
50 55 60 65	ANTICANGA ANTICANGA ANTICANGA ANTICANGA ATATICANGA ANGATITA ANAAGGITA ANGAGGITGA ANGAGGI	ANTOTTCANA CTTCANTOCA CCANAGCTES ATOCACCANA TAGTTATOTA TAGTATATOTA TAGTATATOTA TOTACCANA TOTACCA	CAGACATGGA GAGAGATATATA GATOTCAAAG GACAAGATA GATOTCAAAG GACATGTAT CAAGTATATC CAGATTGTCA AGCTTTGACA ACCTTTGACA TCCACATTGACA TCCACTGAGT TCCACTGAGT GGCCTTGTGA AAGTTGTGA AAGTTGTGA AAGTTTGACA TCCACTGAGT GGCCTTGTGA TCCACTGAGT TCCACTGAGT TCCACTGAGT COTTATGGGA TTGCTGATTA GAATTTATCA GAATTATCAGA TTGCTGATTA GAATTATCAGA TTGCTGATTA GAATTATCACA CTTCCTGATT	TOGATAATAT CATGATATCAC TTGTTGACT TTGTTGACT TGTATGACT TGTATGACAT TGAAGGACAA ACAGGTGGGA ACAGGTTGC CTAAACTTGT AGGTGAAAAA TTGAAGGAAAT TGAAGCAAA TGAAGCAAT TGAAGCAAA TGAAGCATTAC TGAAGCAAA ATTTAACA TGTACGACTTAT TGTAGGCAAA AGGTTTAA TGTAGGCATTAT TGTATTGAAGGAAT ATTTATCACA ATTTATCACAT ATTTATCACAT TTGAAGGAAT TTGAAGGAAT TTGAAGGAAT TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA TTGAAGGACA TTGAAGACA	GGGAAGAGT CTTTCAGCT AATGOTCAGA TGGAATAAA AGTGTGTTTAGATCAAA AGTGTGTTTA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TATCAAAGCT CCCAAACTC CCTGACTCAA TCCCAAACTC CAAACAAAAAA TAAAAAAAT TAAACAGAT TCACAACTG CAAACAATC CAAACAAAAAA AAAAAAAA TCACAACTGG AAAAGAAAAAA TCACAACTGG AAAAGAAAAAAA TCACAACTGG AAAAAAAAAA	GOTGAGATGG GATTIGTCTA AGAGCATATA AGAGCATATA CTGGTAACT GGTGGCAGAC AGAAGAAAAAAAAAA	660 720 840 960 1020 1140 1200 1320 1320 1440 1560 1680 1740 1860 1920
50 55 60	ANTICANGA ANTICANGA ANTICANGA ANTICANGA ATATICANGA ANGATITA ANAAGGITA ANGAGGITGA ANGAGGI	ANTOTTCANA CTTCANTOCA CCANAGCTES ATOCACCANA TAGTTATOTA TAGTATATOTA TAGTATATOTA TOTACCANA TOTACCA	CAGACATGGA GACAAGATA GACTACAA GACTACAAGATA GACTACAACACAAC	TOGATAATAT CATGATATCAC TTGTTGACT TTGTTGACT TGTATGACT TGTATGACAT TGAAGGACAA ACAGGTGGGA ACAGGTTGC CTAAACTTGT AGGTGAAAAA TTGAAGGAAAT TGAAGCAAA TGAAGCAAT TGAAGCAAA TGAAGCATTAC TGAAGCAAA ATTTAACA TGTACGACTTAT TGTAGGCAAA AGGTTTAA TGTAGGCATTAT TGTATTGAAGCAAT ATTTATCACA ATTTATCACAT ATTTATCACAT TTGAAGAGGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAC TTGAAGAGAC TTGAAGAC TTGAAGAGAC TTGAAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAC TTGAA	GGGAAGAGT CTTTCAGCT AATGOTCAGA TGGAATAAA AGTGTGTTTAGATCAAA AGTGTGTTTA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TATCAAAGCT CCCAAACTC CCTGACTCAA TCCCAAACTC CAAACAAAAAA TAAAAAAAT TAAACAGAT TCACAACTG CAAACAATC CAAACAAAAAA AAAAAAAA TCACAACTGG AAAAGAAAAAA TCACAACTGG AAAAGAAAAAAA TCACAACTGG AAAAAAAAAA	GOTGAGATGG GATTIGTCTA AGAGCATATA AGAGCATATA CTGGTAACT GGTGGCAGAC AGAAGAAAAAAAAAA	660 720 840 960 1020 1140 1200 1320 1320 1440 1560 1680 1740 1860 1920
50 55 60 65	ANTICANGA ANTICANGA ANTICANGA ANTICANGA ATATICANGA ANGATITA ANAAGGITA ANGAGGITGA ANGAGGI	ANTOTTCANA CTTCANTOCA CCANAGCTES ATOCACCANA TAGTTATOTA TAGTATATOTA TAGTATATOTA TOTACCANA TOTACCA	CAGACATGGA GACAAGATA GACTACAA GACTACAAGATA GACTACAACACAAC	TOGATAATAT CATGATATCAC TTGTTGACT TTGTTGACT TGTATGACT TGTATGACAT TGAAGGACAA ACAGGTGGGA ACAGGTTGC CTAAACTTGT AGGTGAAAAA TTGAAGGAAAT TGAAGCAAA TGAAGCAAT TGAAGCAAA TGAAGCATTAC TGAAGCAAA ATTTAACA TGTACGACTTAT TGTAGGCAAA AGGTTTAA TGTAGGCATTAT TGTATTGAAGCAAT ATTTATCACA ATTTATCACAT ATTTATCACAT TTGAAGAGGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAC TTGAAGAGAC TTGAAGAC TTGAAGAGAC TTGAAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAGAC TTGAAGAC TTGAA	GGGAAGAGT CTTTCAGCT AATGOTCAGA TGGAATAAA AGTGTGTTTAGATCAAA AGTGTGTTTA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TGAATCAAA TATCAAAGCT CCCAAACTC CCTGACTCAA TCCCAAACTC CAAACAAAAAA TAAAAAAAT TAAACAGAT TCACAACTG CAAACAATC CAAACAAAAAA AAAAAAAA TCACAACTGG AAAAGAAAAAA TCACAACTGG AAAAGAAAAAAA TCACAACTGG AAAAAAAAAA	GOTGAGATGG GATTIGTCTA AGAGCATATA AGAGCATATA CTGGTAACT GGTGGCAGAC AGAAGAAAAAAAAAA	660 720 840 960 1020 1140 1200 1320 1320 1440 1560 1680 1740 1860 1920
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50 55 60 65	ANTECNIGIA ANTECNIGIA AGETMANO ANTETICATO ANGENTICATO ANTETICATO ANTETIC	ANTOTTCAMA CTTCAMAGGCTG ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATTTCACCAG ATTTCACCAG ATTTCACCAG ATTTCACCAG ATCACCAGA ACCACAGA ACCACCAGA ACCACCACACAC ACCACCAGA ACCACCACACAC ACCACCACACACA	CHARCATGAR MAGATTATA GACAAAGATA GACAAAGATA GACAAAGATA GACAAAGATA GACAAGTATT CACAATTAACC CAGATTATCA CAGATTATT TOCCAATTATC TOCCAATTAC CACAATTAC CACA	TOGATANATA CATOTATANATA CATOTATANATA CATOTATANATA TOTATATANATA TOTATATANATA ANGATANATA ANGATANATA TOTATATANATA ANGATANATA TOTATANATANATANATANATANATANATANATANATANA	GGGARGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GOTTAMATOI GATTETTATA ARACCATATO ARACCATATO COTOCCATATO ACTOCATATO	660 720 780 840 900 960 1020 1140 1320 1380 1560 1560 1680 1680 1920 1980 1980 2160 2220 2240 2460
50 55 60 65 70	ANTECNIGIA ANTECNIGIA AGETMANO ANTETICATO ANGENTICATO ANTETICATO ANTETIC	ANTOTTCAMA CTTCAMAGGCTG ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATTTCACCAG ATTTCACCAG ATTTCACCAG ATTTCACCAG ATCACCAGA ACCACAGA ACCACCAGA ACCACCACACAC ACCACCAGA ACCACCACACAC ACCACCACACACA	CHARCATGAR MAGATTATA GACAAAGATA GACAAAGATA GACAAAGATA GACAAAGATA GACAAGTATT CACAATTAACC CAGATTATCA CAGATTATT TOCCAATTATC TOCCAATTAC CACAATTAC CA	TOGATANATA CATOTATANATA CATOTATANATA CATOTATANATA TOTATATANATA TOTATATANATA ANGATANATA ANGATANATA TOTATATANATA ANGATANATA TOTATANATA ANGATANATA TOTATANATA ANGATANATA ANGATANATA ANGATANATA ANGATANATA ANGATANATA ANGATANATA ANATANATA ANATANATA ANATANATA ANATANAT	GGGARGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GOTTAMATOI GATTETTATA ARACCATATO ARACCATATO COTOCCATATO ACTOCATATO	660 720 840 960 1020 1140 1200 1320 1320 1440 1560 1680 1740 1860 1920
50 55 60 65	ANTECNIGIA ANTECNIGIA AGETMANO ANTETICATO ANGENTICATO ANTETICATO ANTETIC	ANTOTTCAMA CTTCAMAGGCTG ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACCAGA ATTTCACCAG ATTTCACCAG ATTTCACCAG ATTTCACCAG ATCACCAGA ACCACAGA ACCACCAGA ACCACCACACAC ACCACCAGA ACCACCACACAC ACCACCACACACA	CHARCATGAR MAGATTATA GACAAAGATA GACAAAGATA GACAAAGATA GACAAAGATA GACAAGTATT CACAATTAACC CAGATTATCA CAGATTATT TOCCAATTATC TOCCAATTAC CACAATTAC CA	TOGATANATA CATOTATANATA CATOTATANATA CATOTATANATA TOTATATANATA TOTATATANATA ANGATANATA ANGATANATA TOTATATANATA ANGATANATA TOTATANATA ANGATANATA TOTATANATA ANGATANATA ANGATANATA ANGATANATA ANGATANATA ANGATANATA ANGATANATA ANATANATA ANATANATA ANATANATA ANATANAT	GGGARGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GOTTAMATOI GATTETTATA ARACCATATO ARACCATATO COTOCCATATO ACTOCATATO	660 720 780 840 900 1020 1140 1260 1320 1320 1380 1560 1680 1740 1860 1740 2040 2140 2160 2240 2240 2240 2240 2240 2240 22520
50 55 60 65 70	ANTICONGIAN ANTICONGIA ANTICOTO ANGINATION ANTICOTO ANGINATION ANGIN ANGINATION ANGINATION ANGINATION ANGINATION ANGINATION ANGINATI	ANTOTICAMA COTTANTON TOTTCAMA	GRANTORA GRA	TOGATALATAT CATOTACATA TOTALATAT TOT	GGGAAGAGT TCCAACAGG AANGTTCCAA ATGTTCAAC ATGTTCAAC ATGTTCAAC TCAACAGG AATGTTCAA ATGTTTAA ATGTTTTA ATGTTTTA ATGTTTTA ATGTTTTA ATGTTTTA ATGAACAGA ATGAACAGAC ATCAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAC C C ATGAACACACAC ATGAACACACAC ATGAACACACAC ATGAACACACACAC ATGAACACACACAC ATGAACACACACACACACACACACACACACACACACACAC	GOTTMANTON GATTESTATA GARCATATOT AGACCATATOT AGACCATAT	6660 840 950 950 950 950 950 950 950 950 950 95
50 55 60 65 70	ANTICONGIAN ANTICONGIA ANTICOTO ANGINATION ANTICOTO ANGINATION ANGIN ANGINATION ANGINATION ANGINATION ANGINATION ANGINATION ANGINATI	ANTOTICAMA COTTANTON TOTTCAMA	GRANTORA GRA	TOGATALATAT CATOTACATA TOTALATAT TOT	GGGAAGAGT TCCAACAGG AANGTTCCAA ATGTTCAAC ATGTTCAAC ATGTTCAAC TCAACAGG AATGTTCAA ATGTTTAA ATGTTTTA ATGTTTTA ATGTTTTA ATGTTTTA ATGTTTTA ATGAACAGA ATGAACAGAC ATCAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAC C C ATGAACACACAC ATGAACACACAC ATGAACACACAC ATGAACACACACAC ATGAACACACACAC ATGAACACACACACACACACACACACACACACACACACAC	GOTTMANTON GATTESTATA GARCATATOT AGACCATATOT AGACCATAT	6660 840 950 950 950 950 950 950 950 950 950 95
50 55 60 65 70 75	ANTICONGIAN ANTICONGIA ANTICOTO ANGINATION ANTICOTO ANGINATION ANGIN ANGINATION ANGINATION ANGINATION ANGINATION ANGINATION ANGINATI	ANTOTICAMA COTTANTON TOTTCAMA	GRANTORA GRA	TOGATALATAT CATOTACATA TOTALATAT TOT	GGGAAGAGT TCCAACAGG AANGTTCCAA ATGTTCAAC ATGTTCAAC ATGTTCAAC TCAACAGG AATGTTCAA ATGTTTAA ATGTTTTA ATGTTTTA ATGTTTTA ATGTTTTA ATGTTTTA ATGAACAGA ATGAACAGAC ATCAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAC C C ATGAACACACAC ATGAACACACAC ATGAACACACAC ATGAACACACACAC ATGAACACACACAC ATGAACACACACACACACACACACACACACACACACACAC	GOTTMANTON GATTESTATA GARCATATOT AGACCATATOT AGACCATAT	6660 840 950 950 950 950 950 950 950 950 950 95
50 55 60 65 70 75	ANTICONGIAN ANTICONGIA ANTICOTO ANGINATION ANTICOTO ANGINATION ANGIN ANGINATION ANGINATION ANGINATION ANGINATION ANGINATION ANGINATI	ANTOTICAMA COTTANTON TOTTCAMA	GRANTORA GRA	TOGATALATAT CATOTACATA TOTALATAT TOT	GGGAAGAGT TCCAACAGG AANGTTCCAA ATGTTCAAC ATGTTCAAC ATGTTCAAC TCAACAGG AATGTTCAA ATGTTTAA ATGTTTTA ATGTTTTA ATGTTTTA ATGTTTTA ATGTTTTA ATGAACAGA ATGAACAGAC ATCAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAGAC ATGAACAC ATGAACAGAC ATGAACAC C C ATGAACACACAC ATGAACACACAC ATGAACACACAC ATGAACACACACAC ATGAACACACACAC ATGAACACACACACACACACACACACACACACACACACAC	GOTTMANTON GATTESTATA GARCATATOT AGACCATATOT AGACCATAT	6660 840 950 950 950 950 950 950 950 950 950 95
50 55 60 65 70	ARTICAGIAA ARCTCHAGC AGTTTMANT ARTICACTO ACTOM ANAMOGETA ACTOM ANAMOGETA ACTOM	ANTOTICAMA CONTRACTOR	GRAGATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA CARAGTATORA CARAGTAT	TOGATANATA TOGATANATA TOGATANATA TOGATOGAT TOGAT TOGATOGAT TOGAT TOGATOGAT TOGAT TOGATOGAT TOGAT	GGGAAGAGC TCACAGAGAGAGC TCACAGAGAGC C TCACAGAGAGC C TCACAGAGAGAGC TCACAGAGAGAGC TCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GOTTANATO GATTOTTOTA AGRICATOR	6660 840 950 950 950 950 950 950 950 950 950 95
50 55 60 65 70 75	ARTICAGIAA ARCTCHAGC AGTTTMANT ARTICACTO ACTOM ANAMOGETA ACTOM ANAMOGETA ACTOM	ANTOTICAMA CONTRACTOR	GRAGATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA CARAGTATORA CARAGTAT	TOGATANATA TOGATANATA TOGATANATA TOGATOGAT TOGAT TOGATOGAT TOGAT TOGATOGAT TOGAT TOGATOGAT TOGAT	GGGAAGAGC TCACAGAGAGAGC TCACAGAGAGC C TCACAGAGAGC C TCACAGAGAGAGC TCACAGAGAGAGC TCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GOTTANATO GATTOTTOTA AGRICATOR	6650 780 900 1020 1140 1260 1320 1380 1500 1680 1740 1500 1680 1740 1860 1920 2040 2160 2280 2280 2280 2280 2280 2280 282
50 55 60 65 70 75	ARTICAGIAA ARCTCHAGC AGTTTMANT ARTICACTO ACTOM ANAMOGETA ACTOM ANAMOGETA ACTOM	ANTOTICAMA CONTRACTOR	GRAGATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA GARAGTATORA CARAGTATORA CARAGTAT	TOGATANATA TOGATANATA TOGATANATA TOGATOGAT TOGAT TOGATOGAT TOGAT TOGATOGAT TOGAT TOGATOGAT TOGAT	GGGAAGAGC TCACAGAGAGAGC TCACAGAGAGC C TCACAGAGAGC C TCACAGAGAGAGC TCACAGAGAGAGC TCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GOTTANATO GATTOTTOTA AGRICATOR	6660 400 400 400 400 400 400 400 400 400
50 55 60 65 70 75	ARTICONGIA ARCTENAGO ARCTETAMAN ARCTENAGO ARGENTAMAN ARCTENAGO ARGENTAMAN ARCTENAGO ARCTETAMAN ARCTENAGO ARCTETAMAN ARCTE	ANTOTICANA CONTRACTOR TOMANCA	GRANTIANA GRANTI	TOGATANATA TOGATANATA TOGATANATA TOGATANATA TOGATOGAT TO	GGRANGAGE CTTTCAACGA ANTOTCAGA ANTOTCAGA ANTOTCAGA ANTOTCAGA ANTOTTCAGA ANTOTCAGA ANT	GOTTAMATOR GATTOSTATA AGRICANTA 6650 780 900 1020 1140 1260 1320 1380 1500 1680 1740 1500 1680 1740 1860 1920 2040 2160 2280 2280 2280 2280 2280 2280 282	
50 55 60 65 70 75	ARTICONGIA ARCTENAGO ARCTETAMAN ARCTENAGO ARGENTAMAN ARCTENAGO ARGENTAMAN ARCTENAGO ARCTETAMAN ARCTENAGO ARCTETAMAN ARCTE	ANTOTICANA CONTRACTOR TOMANCA	GRANTIANA GRANTI	TOGATANATA TOGATANATA TOGATANATA TOGATANATA TOGATOGAT TO	GGRANGAGE CTTTCAACGA ANTOTCAGA ANTOTCAGA ANTOTCAGA ANTOTCAGA ANTOTTCAGA ANTOTCAGA ANT	GOTTAMATOR GATTOSTATA AGRICANTA 6660	
50 55 60 65 70 75	ARTICONGIA ARCTENAGO ARCTETAMAN ARCTENAGO ARGENTAMAN ARCTENAGO ARGENTAMAN ARCTENAGO ARCTETAMAN ARCTENAGO ARCTETAMAN ARCTE	ANTOTICANA CONTRACTOR TOMANCA	GRANTIANA GRANTI	TOGATANATA TOGATANATA TOGATANATA TOGATANATA TOGATOGAT TO	GGRANGAGE CTTTCAACGA ANTOTCAGA ANTOTCAGA ANTOTCAGA ANTOTCAGA ANTOTTCAGA ANTOTCAGA ANT	GOTTAMATOR GATTOSTATA AGRICANTA 6660 400 400 400 400 400 400 400 400 400	
50 55 60 65 70 75	ARTICAGAMA ARCTEMAGE ARTETHAMA ARCTEMAGE ARGETTHAMA ARGANICA ARGAN	ANTOTYCHAA COCAMACATA ACCATACACA ACCATACACACA ACCATACACACA ACCATACACACAC	GRANTANA GRA	TOGATANATA TOGATANATA TOGATANATA TOGATANATA TOGATOGAT TO	GGRANGAGE CTTTCAACGA ANTOTTCAGA	GOTTANATO GATTOTTOTA AGRICATOR	6660

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		GCCTAAGAAA					3360
		GGCCTGGAAA					3420
	AGAGTGACAA	CGAAAAGGAA	ACTGAAAAGA	GTGACTCCGT	AACAGATTCT	GGACCAACCT	3480
_		TCTTGATATG					3540
5		AAATGAAAAA					3600
		AGAAGACTTG					3660
		TGAACAAGTC					3720
		TGAAGTTTTG					3780
• •		AGCAGAGGCA					3840
10		TCAAGAAGAT					3900
		AGAACCAGGT					3960
		AAAGAAGAGA					4020
		TGATGTCCCT					4080
		GGATTTGGAT					4140
15		TGTCCCATCA					4200
	GTAACAAAGA	ACTGAAACCA	CAGAAAAGTG	TCGTGTCAGA	CCTTGAAGCT	GATGATGTTA	4260
		ACCACTGTCT					4320
		AGTTCCTAAA					4380
00		CACTACOGGT					4440
20		TTCTGGTGTC					4500
		ATCCACTTCT					4560
		CAAGAAATCC					4620
		TCGGGCAAAA					4680
~~		TGATCTGTTT					4740
25		GGTTTTAAAG					4800
		GTTTTTAGTA					4860
		ACTGTCTAAA					4920
		GAGTCTGCTT					4980
20		GCTATCTGAT					5040
30		AGAGCAGTTT					5100
	AGATATGAGA	TAGAGCATAA	TTATCTGTTT	TATCTTAGTT	TTATACATAA	TTTACCATCA	5160
	GATAGAACTT	TATGGTTCTA	GTACAGATAC	TCTACTACAC	TCAGCCTCTT	ATGTGCCAAG	5220
		AGCAATGAGA					5280
25		ACTITGGCTG					5340
35		GTGATTATTT					5400
		GAGAGAAACC					5460
		AAGATCTTAA					5520
	TTCATTTTGG	GAAATCTCCA	TAATTTCAAT	TTGTAAACTT	TGTTAAGACC	TGTCTACATT	5580
40		TGTGACTTGA					5640
40	TCTATTAGCT	AAATTCCAAC	AATTTTGTAC	TTTAATAAAA	TGTTCTAAAC	ATTGC	

Seq ID NO: 178 Protein sequence: Protein Accession #: NP_001058.1

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	MEVSPLOPVN	ENMOVNKIKK	NEDAKKRLSV	ERIYOKKTOL	BHILLRPDTY	IGSVELVTQQ	6
		NYREVTFVPG					12
	NGKGIPVVEH	KVEKMYVPAL	IFGOLLTSSN	YDDDEKKVTG	GRNGYGAKLC	NIFSTKFTVE	18
50	TASREYKKMF	KOTWMDNMGR	AGEMELKPFN	GEDYTCITFQ	PDLSKFKMQS	LDKDIVALMV	24
	RRAYDLAGST	KDVKVFLNGN	KLPVKGFRSY	VDMYLKDKLD	ETGNSLKVIH	EQVNHRWEVC	300
	LIMSEKGPOO	ISPVNSIATS	KGGRHVDYVA	DQIVTKLVDV	VKKKNKGGVA	VKAHQVKNHM	360
		PTFDSQTKEN					42
		KHNRIKGIPK					48
55		LNVREASHKQ					54
		GLLINFIHHN					60
		KYYKGLGTST					66
	RKEWLTNFMB	DRRORKLLGL	PEDYLYGOTT	TYLTYNDFIN	KELILFENSD	NERSIPSMVD	72
		PTCFKRNDKR					78
60		GTRLHGGKDS					84
		NGABGIGTGW					90
		GEVAILNSTT					96
		KMTEEKLAEA					102
	DFFELRLKYY	GLRKEWLLGM	LGAESAKLNN	QARFILBKID	GKII IENKPK	KELIKVLIQR	108
65		KEAQQKVPDE					114
	KDELCRLRNE	REQUILDTLKR	KSPSDLWKED	LATFIEELEA	VEAKEKQDBQ	VGLPGKGGKA	120
		LPSPRGQRVI					126
		GTKTKKQTTL					132
		DSDEDFSDFD					138
70		SSSPPATHFP					144
		VSQKPDPAKT			IVSKAVTSKK	SKGESDDFHM	150
	DFDSAVAPRA	KSVRAKKPIK	YLEESDEDDL	P			

75 Seq ID NO: 179 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 148-7095

80	1	11	21	31	41	51 1	
-	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAAC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
		CCGCAGACCG					180
~ -		GTGTTTGCCG					240
85 .	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CANCORDANTO	TCAATCTTAA	CARACTTARA	THECAGGGTT	CCCATABAAC	ATCATTGGAA	420

	A A CIA CA TECCA	mmCaThaCaC	TOGGGAAAACA	CTYCCAAATTA	ATCTCACTAA	TGACTACCCT	480
	AACACATTCA GTCAGCGGAG	CACCAMACACA	AATCOTOTOT	AAAGCAAGCA	PGATAACTTT	TCACTGGGGA	
	GICAGCGGAG	GAGILLOAGA	MAIGGIGIII	ANNOCANOCA	*********	TOTO CONT	600
	AAATGCAATA	TOTCATCIGA	TGGATCAGAG	CATAGTTTAG	ANGGACAAAA	MITICACTI	660
-	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC	660
5	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	GCAGGCTGCT TTACATTTAC TTTATAAGAT AATGCACAA AAGGCACTAGT TCTGTTACA TCTGTTACA TCTGTTACA TCTAGTACAG AGCAGTTTGT TCAAGACTT AGTAGCCAT AGTAGCCAT AGTAGCCAT AGTAGCCAT AGTAGCCAT AGTAGCCAT AGTAGCCAT AGTAGCCAT CAGGGTACA TCAGGAGGAG ATTTCTCTGGA TAAATTAGCC TCACACTGTG TCACACTGTG TCACACTGTG TCACACTGTG TCACACTGTG TCAGAGGGAG CCCAATATG TGAGGAGGAG CCCAATATG	840
	AATOCCTCAT	TORCATOTOC	TOCCTOCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ARIGOCICAL	TOTOTICE CO	CONCERNOCCE	CTTTTTTCTC	ANGTTOTTAC	AATGCAACAA	960
10	ACAGITAGCA	TCTCTGMANG	CCAGTIGGCI	CARACTATT	PERCENCACCA	ACACTACAAG	1020
10	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATI	TICGMONGCA	ACAGIACAAG	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260
15	GGTGCTATTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TCCS CTAATC	CCTTATATOO	AAAATACAGC	GACCAACTICA	TTGTCGACAT	GCCTACTGAT	1380
	IUCACIANIO	OCTIVITATION	COORTS A SMITT	PARTICULAR VALUE	BACRARTART	CNACCACCAC	1440
	AATCCTGAAC	TIGATETTT	CCCIGAATIA	VIIGOVACIO	ANGAMIANI	CAMOUNDONS	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGIGCTACA	1200
	AACCAAATCA	GGAAAAAGGA	ACCCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
20	ACGARATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
	DCAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
	Ch a Comp com	Character	AAATTATTCC	TOTALACTE	TTCTTAGATC	TOCACATATG	1800
	A A COMPORTOR OF	COOCCICITI	AMCCOTTABAT	ACACTETOTA	TARCAGARTA	TORGORGERG	1860
25	MACTIGICUG	GGACTGCAGA	AICCIIAAAI	ACAGITICIA	TANCHOMITA	TGAGGAGGAG CTCCAGTCCC ATTTTCCTCC AAATGCTTCC GGAGGGAAAT AGGCAGAGAG GACAACCAAG GGAAATGCCA TACCCCATCC	1030
23	AGTTTATIGA	CCAGITTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CICOMITCCC	1000
	GCAACTTCTG	CTATCCCATT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTITUCE	1300
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CITATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
30	ACCUPATOR	AGACTAATTA	CACTGAGATA	COTOTTGATG	AATCTGAGAA	GACAACCAAG	2220
50	MOCITICIO	OF CCCCCCTC	CATCHCACAC	COTCCCTCAG	TTACAGATOT	GCAAATGCCA	2280
	TCCTTTTCTG	CAGGCCCAGI	CONTROCCALACT	CACCERACAG	CTCATGCTTT	TROCCCATCC	2340
	CATTATICIA	CCTTTGCCTM	CITCCCAACI	GAGGIANCAC	CICATOCITI	INCCCCATCC	2400
	TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGIGGIAI	ACTUGUNGAU	MACCCAACCG	2400
	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TCCTCTAGTC	2460
35	ACCCCTTTGT	TGCTTGACAA	TCAGATCCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TOGGCCTTGC	ATGCTACGCC	TGTATTTCCC	AGTGTCGATG	TGTCATTTGA	ATCCATCCTG	2580
	TOTAL TO	ATCCTCCACC	TTTCCTTCCA	TTTTCCTCTG	CTTCCTTCAG	TAGTGAATTG	2640
	TOTA GOLDEN	TOCATA CACT	TTCTCABATC	CTTCCACAAG	TTACTTCAGC	TACCGAGAGT	2700
	TITCOCCATC	1GCA IACAGI	monomonda	omogomocoo	CONTRACTOR	ATTACACCCC	2760
40	GATAAGGTGC	CCTTGCATGC	TICICIGCOA	OTGGCTGGGG	GIGNITIGGI	Ch CCCTCCA A	2020
40	AGCCTTGCTC	AGTATTCTGA	TOTOCTGTCC	ACTACTCATG	CIGCIICAGA	GACGCIGGAA	2020
	TTTGGTAGTG	AATCTGGTGT	TCTTTATAAA	ACCCTTATGT	TTTCTCAAGT	TGAACCACCC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCTTCTTA	TGCCFTGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCTGCAAT	GGAAATGCCA TACCCATCC TACCCATCC AACCCAACCG TCCTCTAGTC AAGTAGTGAT AATCCATCCTG TACGGAATGAATTG TACGGAGAGT ATTAGAGCCC GAGCCTGGAA TGAACCACC TGCCTTGTCT ACCTGTGCAT TATACCAATA TGCCCTCCTT	3000
	GATTCTGTGG	GTGTAACTTA	TCAGGGTTCC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
45	CALPUGACAL	COTTANTANC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	CONCERTOCCO	AATOCTOCTOC	ACCORPANCE	CATACTCAAT	TTCTTTACC	TGACACAGAT ATATACAACA TGGAAATGAG	3180
	CCCCMICGCG	COCUMBARCAM	TOCCITCIACT	COTTOTOTOTO	CTGAATTTAC	ATATACAACA	3240
	GGGCTGACAG	CCCTTAACAT	TICTICACCI	WOMEN TO SOME	ADDRESTATE	TOTALATORO	1100
	TCTGTGTTTG	GIGATGATAA	TANGGCGCTT	ICIAAAAGIG	MINIMINIA	1000000000	3366
60	ACTGAACTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CITCIGAAAG	CACAGTUATG	3360
50	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAAGGGCAT	GTTTCCAGGG	TCCCTTGCTC	ATACCACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACTTTTCAG	TTCAACCTAC	ACATACTGTC	3540
	TCTCAAGCAT	CTGGTGACAC	TTCGCTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
	TOCTOTOLOG	CTCCTTCTAC	TELABATETTA	TOTOCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
55	* COTOTONOC	CTTTTTACTAC	TOARGERTS	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3720
33	ACCTCAGCTT	CITTIAGIAC	TOMOGRATIO	CINCARCCIA	ATOTA ATART	COMPONANCO	3700
	GACACCTTGC	TTARARCIGT	TUTTUMGUT	GIGCCCAGIG	AICCARIATI	GGIIGAAACC	3000
	CCCAAAGTTG	ATAAAATTAG	TTCTACAATG	TIGCATCICA	TIGIATCAAA	TTCTGCTTCA	3840
	AGTGAAAACA	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCCTATG	CAAGTGAGAA	ATATGAACCA	3960
60	GTTTTGTTAA	AAAGTGAAAG	TTCCCACCAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAAC	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080
	TOTAL CAL	COCTUTATO	AACTTACTTAA	CTATTABATA	CACTAATAAA	TAAGCTTATA	4140
	TITIGETACAC	CIGITITALC	OTTOTAL COLUMN	ACTUATION	CTCCTAACCT	ATTTGCTGGT	4200
	CATTCCGATG	MOUTTITANC	CICCACCAAA	TOTAL COURT	**************************************	TATACCARAT	4260
15	ATTCCAACAG	TIGCTICIGA	TACATTIGIA	ICIACIGATO	ATTCIGITEC	TATAGGAAAT	4200
65	GGGCATGTTG	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GITCIGTAAC	CICAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
							4500
	AGAGGTAGTG	ATGGCTTATC	CATTCATAAG	TGTATGTCAT	GCTCATCCTA		
	AGAGGTAGTG	ATGGCTTATC	CATTCATAAG	TGTATGTCAT	GCTCATCCTA	TAGAGAATAAT	4560
70	AGAGGTAGTG CAGGAAAAGG	ATGGCTTATC TAATGAATGA	CATTCATAAG TTCAGACACC	TGTATGTCAT CACGAAAACA	GCTCATCCTA GTCTTATGGA	TCAGAATAAT	4560
70	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT	ATGGCTTATC TAATGAATGA ACTCACTATC	CATTCATAAG TTCAGACACC TGAGAATTCT	TGTATGTCAT CACGAAAACA GAAGAAGATA	GCTCATCCTA GTCTTATGGA ATAGAGTCAC	TCAGAATAAT AAGTGTATCC	4560 4620
70	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT TCAGACAGTC	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT	TGTATGTCAT CACGAAAACA GAAGAAGATA CCTGGTAAAT	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC	TAGAGATTAT TCAGAATAAT AAGTGTATCC AAATGGGCTA	4560 4620 4680
70	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT TCAGACAGTC TCCCAAAAGC	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA	TGTATGTCAT CACGAAAACA GAAGAAGATA CCTGGTAAAT AATGACATTC	CTGARTTAC ANATHATIAC ANATHATIAC CTCTGRANG TTCGAGCTAC TTCGAGCTAC TTCGACCTAC TT	TAGAGATTAT TCAGAATAAT AAGTGTATCC AAATGGGCTA TGCTCTGCTT	4560 4620 4680 4740
70	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT TCAGACAGTC TCCCAAAAGC CCTCTCAGCC	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA	TGTATGTCAT CACGAAAACA GAAGAAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA	TAGAGAATAAT AAGTGTATCC AAATGGGCTA TGCTCTGCTT AAGTGGATCA	4560 4620 4680 4740 4800
	AGAGGTAGTG CAGGANANGG CCAATCTCAT TCAGACAGTC TCCCAANAGC CCTCTCAGCC GGGCAAGGTA	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA CCTTAATGAG	TGTATGTCAT CACGAAAACA GAAGAAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT	TCAGAMATAAT TCAGAATAAT AAGTGTATCC AAATGGGCTA TGCTCTGCTT AAGTGGATCA CAGTTTTGCA	4560 4620 4680 4740 4800
	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT TCAGACAGTC TCCCAAAAGC CCTCTCAGCC GGGCAAGGTA GACACTA	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA CCTTAATGAG TGATGGGATC	TGTATGTCAT CACGAAAACA GAAGAAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGCAG	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGA	TCAGAMATAAT TCAGAATAAT AAGTGTATCC AAATGGGCTA TGCTCTGCTT AAGTGGATCA CAGTTTTGCA AATAACTCCT	4560 4620 4680 4740 4800 4860 4920
70 75	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT TCAGACAGTC TCCCAAAAGG CCTCTCAGCC GGGCAAGGTA GACCTAATG	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG AAAAAGATGA	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA CCTTAATGAG TGATGGGATC	TGTATGTCAT CACGAAAACA GAAGAAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGCAG ACTAGCGAGAG	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGA ACTCAGAAGA	TCAGAMATCA TCAGAATAAT AAGTGTATCC AAATGGGCTA TGCTCTGCTT AAGTGGATCA CAGTTTTGCA AATAACTCCT GTTCCACGTT	4560 4620 4680 4740 4800 4860 4920
	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT TCAGACAGTC TCCCAAAAGG CCTCTCAGCC GGGCAAGGTA GACACTAATG	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG AAAAGATGC AGTCCCCAAC	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA CCTTAATGAG TGATGGGATC ATCATCTGTT	TGTATGTCAT CACGAAAACA GAAGAAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGCAG ACTAGCGAGA ACTAGCGAGA	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGAAGT ATTCAGAAGT	TCAGAMATCA TCAGAATAAT AAGTGTATCC AAATGGCTA TGCTCTGCTT AAGTGGATCA CAGTTTTGCA AATAACTCCT GTTCCACGTT TGAGGGGTT	4560 4620 4680 4740 4860 4920 4980
	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT TCAGACAGTC TCCCAAAAGC CCTCTCAGCC GGGCAAGGTA GACACTAATG GGATTCCCAC TCAGAGGCAG	ATGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG ANAAGATGC AGGCCAGTAA AGGCCAGTAA	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA CCTTAATGAG TGATGGATC ATCATCTGTT TAGTAGCCAT	TGTATGTCAT CACGAAACCA GAAGAAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGCAG ACTAGCGAGA GAGTCTCGTA	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGA ACTCAGAAGT TTGGTCTAGA	TCAGAATAAT TCAGAATAAT AAGTGTATCC AAATGGGCTA TGCTCTGCTT AAGTGGATCA CAGTTTTGCA AATAACTCCT GTTCCACGTT TCAGGGGTTG	4560 4620 4680 4740 4860 4920 4980 5040
	AGAGGTAGTG CAGGAAAAGC CCAATAGCACTCTCAGACAGTC GGGCAAAAGC GGCAAAGTAGCACACTAATG GACTACTAGAGCACTAATG GACTCCAGAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGC	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG AAAAAGATG AGGCCCAAC AGGCCAGTAA AGAAGGCAGT	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA CCTTAATGAG TGATGGGATC ATCATCTGTT TAGTAGCCAT TATACCCCTT	TGTATGTCAT CACGARAACA GARGAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGCAG ACTAGCGAGA GAGTCTCGTA GTGATCGTGT	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGA ACTCAGAAGT TTGGTCTAGC CAGCCTGAC CAGCCTGAC	TAMBARTAT TCAGAATAAT AAGTGTATCC AAATGGGCTA TGCTCTGCTT AAGTGGATCA CAGTTTTGCA AATAACTCCT TGTCCACGTT TCAGGGGTTG TTTATCTGT	4560 4620 4680 4740 4860 4920 4980 5040
75	AGAGGTAGTG CAGGAAAGGC CCAATCTCAGCG TCCCAAAAGC CCTCTCAGCG GGGCAAGGTA GACACTAATG GGATTCCCAC TCAGAGGCA GAATCCCAC TCAGAGGCA CAAGAGCAC CTAGTGGTTC	ATGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG AAAAGATGC AGTCCCCAAC AGGCCAGTAA AGAAGGCAGT TTGTGGGTAT	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGA AGCATGGGCA CCTTAATGAG TGATGGGATC ATCATCTGTT TAGTAGCCAT TATACCCCTT TCTCATCTAC	TGTATGTCAT CACGAGAGCA GAGGAGGAACA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGCAG ACTAGCGAGA GAGTCTCGTA GTGATCGTAT TGGAGGAAAT TGGAGGAAAAT	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGA ACTCAGAAGT TTGGTCTAGC CAGCCCTGAC GCTTCCAGAA GCTTCCAGAAG	TAMBARTAT TAMBARTAT ANGTOTATC ANATOGOCTA ANGTOGATCA CAGTTTTGCA ANTACTCCT GTTCCACGTT TCAGGGGTTG TTTTATCTGT TGCACACTTT TGCACACTT	4560 4620 4680 4740 4860 4920 4980 5040 5160
	AGAGGTAGTG CAGGAAAGG CCANTCTCAT TCAGACAGTC TCCCAAAAGC CCTCTCAGGC GGGCAAGGTA GACACTAATG GAATCCCAC TCAGAGGCAG GAATCCGAGA CTAGTGGTTC TACTTAGAGG TACTTAGAGG	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG AAAAAGATGC AGTCCCCAAC AGGCCAGTAA AGAAGGCAGT TTGTGGGTAT ACAGTACATC	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGAT CGTTAATGAG TGATTGGGAT ATCATCTGTT TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTAGAGTT	TGRATGTCAT CACGARAACA GAGGAGGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGCAG ACTAGCGAGA GAGTCTCGTA GTGATCGTGT TGGGGGAAAT ATATCCACAC	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATT GTGACTCAGA ACTCAGAAGT TTGGTCTAGC CAGCCCTGAC GCTTCCAGAC CTCCAGACC	TAMBARTAT TAMBATTAT AMBTGTATCC AMATGGGCTA TGCTCTGGCT TAMGTGGATCA CAGTTTTGCA AMTAACTCCT GTTCCACGTT TGAGGGGTTG TTTTATCTGT TGCACACTTT TATCTTTCCA	4560 4620 4680 4740 4860 4920 4980 5040 5160 5220
75	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT TCAGACAGTC TCCAAAAGG CCTCTCAGCG GGCAAGGTA GAACTCCACA GAATTCCAC TCAGAGGCAG CAAGGTAC TCAGAGGCAG CTAGTGGTTC TACTTAGAGG ATTCCAGAT	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG AAAAAGATGC AGTCCCCAAC AGGCCAGTAA AGAAGGCAGT TTGTGGGTAT ACAGTACAT ATGTCGGAGC ATGTCGGAGC ATGTCGGAGC ATGTCGGAGC ATGTCGGAGC ATGTCGGAGC ATGTCGGAGC	CATTCATAGE TTCAGACACT TGAGAAGT TGAGAAGT AAAAGAGGA AGCATGGGCA CCTTAATGAG TGATGGGATC ATCATCTGTT TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTTAGAGT AATTCCAATA	TGTATGTCAT CACGAAACA GAGGAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGCAG ACTAGCGAGA ACTAGCGAGG ACTAGCGGGAG ACTAGCGGGAGAAT ATGAGGAGAAAT ATATCCACAC AAGCACTTTC AAGCACTTC AAGCACTTTC AAGCACTTC AAGCACTTTC AAGCACTTTC AAGCACTTTC AAGCACTTTC AAGCACTTTC AAGCACTTTC AAGCACTTTC AAGCACTTTC AAGCACTT	GCTCATCCTA GTCTTATGGA ATAGGATCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGA ACTCAGAAGT TTGGTCTAGC CAGCCCTGAC GCTTCCAACACC CAAAGCATGT	TAMAGMITAT TAMAGRATAAT AAGTGTATCC AAATGGGTT AAGTGGATCA CAGTTTTGCA AATAACTCCT GTTCCACGTT TGAGGGGTTG TTTTATCTGT TGCACACTTT TATCTTTCCA TGCACACTTT TATCTTTCCA TGCAGACTTTA	4560 4680 4740 4860 4980 5040 5160 5220 5280
75	AGAGGTAGTG CAGGAAAAGG CCAATCTCAT TCAGACAGTC TCCCAAAAGG CCTCTCAGCC GGGCAAGGTA GACACTAATG GGATTCCCAC GAGTCCCAC GATTCCAGAGG GAATCCGAGA CTAGTGGTTC TACTTAGAGG ATTTCAGATG CTAGGAGGAGTA	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCTAA CCTCAGATAG AGAACGCAGT AGGCCAGTAA AGAAGGCAGT TTGTGGGTAT ACAGTACCAC ATGTCCGAAC ATGTCCGAAC ATGTCCGAAC ATGTCCGAAC ATGTTCGGAGT ATGTTCGAGT ATGTTCGAGT ATGTTCGAGT ATGTTCGAGT AT	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA CCTTAATGAG TGATGGGAT ATCACCTGTT TAGTAGCCCTT TATTACCCCTT TCTCATCTAC CCCTAGAGTT AATTCCAATTA TGAAGAATTT TGAGAAATTT	TGTATGTCAT CACGAAAACA GAGAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGCTT CTGGCAGCAG GAGTCTCGTA GTGATCAGTA GTGATCAGTA GTGATCAGTA GTGATCGTGT TGGAGGAGAAT ATATCCACAC AAGCACTTC	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGA ACTCAGAAGT TTGGTCTAGC CAGCCCTGAC GCTTCCAGAC CTCCAACACC CAAAGCATGT AAGAGGTTTTA	TAMBARTAT TAGARATAT AAGTGTATCC AAATGGCTA TACTCTGCT AAGTGGATCA AATAACTCCT GTTCAACGTT TCAACGGTTT TCAACGGTTT TCAACGGTTT TCAACGGTTT TCAACGGTTT TACCTTTCCA TCCAACATTT TACCTTTCCA TCCAAGATTTA TCCAAGAGTG TCCAAGAAGTG CCAAGGAAGTG	4560 4680 4740 4860 4860 4980 5040 5160 5220 5340
75	AGAGOTAGTO CAGGANAGG CCANTTCAT TCAGACAGTC TCCCANAMGC CCTCTCAGCC GGCAAGGTA GACACTARG GGATTCCAC TCAGAGGCAG GAATCCGACA CTAGTGGTTC TACTTAGAGG ATTTCAGATT CATGCAAGTA CATGCAAGTA	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGG CTGAATCATAC CCTCAGATAG CCTCAGATAG AGTCCCCAAC AGGCCAGTAA AGGACCAGTTA TTGTGGGTAT ACAGTACATC ATGTCGGGGC TTGGGGTTAC CCTGTTAGACC CCTGTAGACC CCTCTACC CC	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAGT AAAAGAGGAA AGCATGAGCAA AGCATGAGCAA TGATGGGAT ATCATCTGTT TAGTAGCAT TATACCCCTT TCTCATCTAC CCCTAGAGTT AATTCCAATTAC AATTCCAATTA	TGTATGTCAT CACGAAACA GAGAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGAG ACTACGGAGA GAGTCTCGTA TGGAGGAGAT TGGAGGAGAT TGGAGGAAAT TATATCACAC AAGCACTTTC GAGACACTGT GAGACACTGT GAGACACTGT GCAGACAGCT CCAGACAGCT CCAG	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGA ACTCAGAAGT TTGGTCTAGC CAGCCCTGAC GCTCCAACACC CAAAGCATTT AAGAGTTTTA ACCAACACCT CAAAGCATCT AAGAGTTTTA ACCAACCACCT CCACACCACCT CAAAGCATCT AAGAGTTTTA ACCAACCACCT CCACCACCT CAAAGCACTCT AAGAGTTTTA ACCAACCACCT CCACCACCT CCACCACCT CAAAGCACCT CAAAGCACTCT AAGAGCACTCT CCACCACCT	TAGGARTAN TAGGARTANT AGTOTATCC ANATOGATCA AGTOTATCA AGTOTATCA AGTATCACGT TTCACGGTT TTTATCTGT TGCACACTT TATCTTCCA TGCAGACTTA TATCTTCCA TGCAGACTTA TGCAGACTTA CCAGGAGTTA CCAGGAGTGA TGCAGACACACACACACACACACACACACACACACACACA	4560 4680 4740 4860 4980 5040 5160 5280 5280 5400
75	AGRIGATAGIS CAGRANAGE CONTITORT TORGACAGTO TOCCARAGE COTOTICAGO GACTICAGO GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG GARTICOCAG CAGGAGT	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGA CCTCAGATAG CCTCAGATAG AGTCCCCAAC AGGCCAGTA AGAAGGCAGT TTGTGGGTAT ACATTGACATC ATGTTGGGTAT CTTGTGGTTTA CTTGTGGTTTA CTTGTGGTTTA CTTGTGGTTTA CTTGTGACT CTGTTGACTT CTTGTTGACTT CTTGTTT CTTGTTGACTT CTTGTTT CTTGTTT CTTGTT C	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA CCTTAATGAG TGATGGGAT TAGTAGCCTT TAGTAGCCTT TATACCCCTT TATACCCCTT AATCCCATT AATCCCATT AATCCCATT AATCCCATT AATTCCAATT AATTCAATT AGAGAATTT GAGAATTT AG	TGTATGTCAT CACGAAACA GAAGAAACA GAAGAAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACTT CTGGCAGCAG ACTAGCAGCAG TGATCGTTA TGAGGAGAAT ATATCCACAC AAGCACTTC GCAGACAGCT TGAGACAGCT TTATGATCATA	GCTCATCCTA GTCTTATGGA ATAGAGTCAC CACCATCAGG GTGATGAAGA CCACAGATTT TTGGTCTAGG GCTTCAGAAGT TTGGTCTAGC CACCCTGAC GCTTCAGAAGT CTCCAGAAGT TTGGTCTAGC CACCCTGAC CAAAGCATTT AAGAGTTTTA CCAACCACCC CAAAGCATTT CCAACCACCC CAAACCACCC CAAACCACCC CAAACCACC	TAGGARTAN TAGGARTAN AGRITATCE TAGCTCCTT AGRIGGATCA AGRITIGGATCA ATANCTCCT GTTCCACGTT TITATCGT TIGACGGGTTG TICACCACTT TACCTTCCA TGCACACTT TACCTTCCA TGCAGACTTA CCAGGARGTG AGACACAGG GCTAGCACACA GCTAGCACACA GCTAGCACACA GCTAGCACACA	4560 4620 4680 4740 4860 4920 4980 5160 5220 5340 5460
75 80	AGAGOTAGTS CAGGAAAAGG CCATCTCAT TCAGACGTC TCCCAAAAGC CCTCTCAGCC GGCCAAGGTA GACATCAGA TCAGAGGTA TCAGAGGAC TCAGAGGAC TCAGAGGAC TCAGAGGAC TACTTAGAGG ATTTCAGATG CATGCAAGTA CAGAGCTGTA CAGAGCTGTA CAGAGCTGTA CAGAGCTGTA CAGAGCTGTA	ATGGCTATC TAATGATGA ACTCACTATC AAACTGGTAT ACAATGGTAT ACAATGATGG CTGAATCCTAA AGCCCGAAC AGCCCGAC AGGCCATAA AGAAGGCAGT TTGTTGGGTAT ACAATGACA ACGGCATAA ACGAGTACA CGGCTAAC ACGGCTAAC ACGGCTAAC ACGGCTAAC ACGGCTAAC ACGGCTAAC ACGGCTAAC ACGGCTAAC ACGGCTAAC CTGTTGACT GATACATAAA	CATTCATAAG TTCAGACACT TGAGACACT TGAGACTCT GGACAGAGT AAAAGAGGAA AGCATGGGGT TATGGGTC ATCACTGTT TAGTAGCCCTT TCTCATCTCC CCTAGAGTT AATTCCAATA TGAAGAATTT TGAGAGATTT TGGATTACC TATGCTTCC TAGTTT TGAGAGATTT TGAGAGATTT TAGGTTGCC TCCCCCCCCCC	TGTATGTCAT CACGAAACA GAGAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGCATC CTGGCAGCAG ACTAGGGAGAG TGTGTCGTA TGGAGGAGAT TGGAGGAAAT ATATCCACAC AAGCACTTC AAGACACTTC AAGACACTTC AAGACACTTC AAGACACTTC AAGACACTTC AAGACACTTT	GCTCATCCTA GTCTTATGGA ATTAGGATCAC CACCATCAGC AGACTGGTAG GTGATGAAGA CCACAGATTT GTGACTCAGA ACTCAGAAGT TTGGTCTAGC CAGCCCTGAC GCTTCCAGAA CTCCAGAAGT TTGAGTCTAGC CCACACACC CAAAGCATGT AAGAGTTTTA ACCAACCACC GCAGGGTTAA	TROBARTANT NAGTOTATICE ANATIGGETA AGENCIGET ANATIGGETA AGENCIGET ANATIGGATCA AGENCIGET TOAGGGTTG GTTCCAGGTT TGAGGGGTTG TGTCAGGTT TGAGGGTTT TATCTTTCCA TGCAGATTT CCAGGAGTTC CCAGGAGTTG CCAGGAGTG GGAGACACAG GCTAGCACACAG GCTAGCACACAG GCTAGCACACAG GCTAGCACAG GCTAGCACAG GCTAGCACAG GCTAGCACAG	4560 4620 4680 4740 4860 4980 5100 5160 5220 5340 5400
75	AGAGGTAGTS CAGGAAAAGC CAATCTCAT TCAGACAGTC TCCGAAAAGC CCTCTCAGCC GGGCAAGGTA GACACTARTG GAATCCGAG TCAGAGGCAG TACTTAGAGG ATTCAGAGT ATTCAGAGT CAGGAGGTAG CTAGTGGTTC CAGGAAGTT CAGGAGGTAG CTAGTGGTTC CATGAAGTA CTAGTGTTC CCCAAGAATT CTTGGTGTAA	ATGGCTTATC TAATGAATGA ACTCACTATC AAACTGGTAT ACAATGATGA CCTCAGATAG CCTCAGATAG AGTCCCCAGA AGGCCAGA AGGCCAGA AGGACGCAT AAAGGCAGT TTGTGGGTAT ACATTCAGAC CTGTTGACAT CTGTGGTTTAC CTGTTGACAT CGATACAT CGATACAT CGATACAT AGGATACAT CGATACAT AGGATGCAA AGGGATGCAA	CATTCATAAG TTCAGACACC TGAGAATTCT GGACAGAAGT AAAAGAGGAA AGCATGGGCA CCTTAATGAG TGATGGGAT TAGTAGCCAT TAGTAGCCAT TATACCCCTT TATACCCCTAGAGTT AATCCCAT AATCCAAT AA	TGTATGTCAT CACGAAACA GAAGAAACA GAAGAAGATA CCTGGTAAAT AATGACATTC GTTCTGACAA AATGAGACAT CTGGCAGCAG ACTAGCGAGA TGATCGTTT TGGAGGAAA TATCCACAC AAGCACTTC GAAGACAGT TATGATCATA TATACAAT TATAC	GCTCATCCTA GTCTTATGGA ATTAGGATCAC CACCATCAGG GTGATGAAGA CCACAGATTT TTGGTCTAGG GCTTCAGAAGT TTGGTCTAGC CACCCTGAC GCTTCAGAAGT CTCCAGAAGT TTGGTCTAGC CAACACCACCA CAAAGCATTT AAGAGTTTTA CCAACACCC GCAGGGTTAA CCAATTATGT	TROBUSTION TORONATION	4560 4680 4740 4800 4920 5040 5160 5220 5340 5460 5520
75 80	AGAGOTAGTS CAGGAAAAGG CCATCTCAT TCAGACGTC TCCCAAAAGC CCTCTCAGCC GGCCAAGGTA GACATCACA TCAGAGGCAG TCAGAGGCAG TCAGAGGCAG TCAGAGGCAG TACTTAGAGG ATTTCAGATG CATGCAAGTA CAGAGCTGTA CAGAGCTGTA CACAAGAATC CTAGCAGGTA AACAAGACCA AACAAGACCA AACAAGACCA	ATGGCTATC TAATGATGA ACTCACTATC AAACTGGTAT ACAATGGTAT ACAATGATGG CTGAATCCTAA AGGCCAGTAA AGGCCAGTAA AGGAGGCAGTAA AGAAGGCAGT ACAGTACCCAAC AGGCCAGTAA ACAGTACATC ATGTCGGGTAA ACAGTACATC CTGTTGACT GATACATAAA AGGATGACTA AGGATTATAT	CATTCATANG TTCAGACACT TGAGACACT TGAGACACT TGAGACTCT GGACAGAGT TAAAAGAGGAA AGCATGGGATC TATTGAGT TATTAGCACT TATTACCCCTT TATTACCCCTT TATTACCCCTT TATTACCACTA TATTCCATA TGAGAGATTT TGAGAGATTT TAGTATTACC TATCGTTGCC ACTGACTGT TGCTCCCCAA	TGTATGTCAT CACGAAAACA GAGGAGATA CATGGTAAAT CATGGTAAAT AATGACATTC TGGCAGCAG GAGTCTCGTA TGGAGGAAA ATATCCACAC AAGACATTCCACAC AAGACATTCCACAC AAGACATTCCACAC AAGACATTTCAACAC AAGACATTTCAACAC AAGACACTTTC AAGACACTTAT AAGACACTTAT AATATCAATAC TATATCAATAC TA	GCTCATCCTA GTCTTATGGA ATTAGGATA ATAGAGTCAC CACCATCAGC CACCATCAGC CACAGAGTT GTGATGAGAGA ACTCAGAAGT TTGGTCTAGC CAGCCCTGAC GCTTCAGAC CTCCAACACC CAAAGCATT AAGAGTTTA ACCACACACC GCAGGGTTAA CCACACACC GCAGGGTTAA AATCACACACACACACACACACACACACACACACA	TROBARTANT PAGRATANT AGTIGTATICE AAATIGGCTA TGCTCTGCTT TGCTCTGCTT TGCACGTT TGCACACTT TGCACACTT TGCACACTT TGCACACTT TGCACACTT TGCACACTT TGCACACTT TGCACACACT TGCAGATTTA AGACACACAC TGCAGACT TGCAG	4560 4620 4680 4740 4860 4920 5040 5160 5220 5340 55400 5520

	AAAGGAAGGA	GAAAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	5700
		CTCAGAAGAG					5760
		CAAAAATAAA					5820
_	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
5		TGAGAAAGGC					5940
		CTGGAGTTGG					6000
		ACGAAGGAAC					6060
		TGGTACAAAC					6120
	GCCATACTTA	GTAAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTCATGCCTA	TGTTAATGCA	6180
10	CTCCTCATTC	CTGGACCAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GCTCCTGAGC	6240
		TACAGCAGAG					6300
	AATCGAACTT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TTGGCATTTC	ATCCCTGAGT	6360
	GGAGAAGGCA	CAGACTACAT	CAATGCCTCC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
	TTCATCATTA	CCCAGCACCC	TCTCCTTCAT	ACCATCAAGG	ATTTCTGGAG	CATGATATGG	6480
15	GACCATAATG	CCCAACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATTGTG	AGAGCTTTAA	GGTCACTCTT	6600
	ATGGCTGAAG	AACACAAATG	TCTATCTAAT	GAGGAAAAAC	TTATAATTCA	GGACTTTATC	6660
	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTITCAGIG	TCCTAAATGG	6720
	CCAAATCCAG	ATAGCCCCAT	TAGTAAAACT	TTTGAACTTA	TAAGTGTTAT	AAAAGAAGAA	6780
20	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
	ACTITCTGTG	CTCTGACAAC	CCTTATGCAC	CAACTAGAAA	AAGAAAATTC	CGTGGATGTT	6900
	TACCAGGTAG	CCAAGATGAT	CAATCTGATG	AGGCCAGGAG	TCTTTGCTGA	CATTGAGCAG	6960
	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAATCCA	7020
	TCCACCTCTC	TGGACAGTAA	TGGTGCAGCA	TTGCCTGATG	GAAATATAGC	TGAGAGCTTA	7080
25	GAGTCTTTAG	TTTAACACAG	AAAGGGGTGG	GGGGACTCAC	ATCTGAGCAT	TGTTTTCCTC	7140
	TTCCTAAAAT	TAGGCAGGAA	AATCAGTCTA	GTTCTGTTAT	CIGITGATIT	CCCATCACCT	7200
	GACAGTAACT	TTCATGACAT	AGGATTCTGC	CGCCAAATTT	ATATCATTAA	CARTGTGTGC	7260
	CTTTTTGCAA	GACTTGTAAT	TTACTTATTA	TGTTTGAACT	AAAATGATTG	AATTTTACAG	7320
	TATTTCTAAG	AATGGAATTG	TGGTATTTTT	TTCTGTATTG	ATTTTAACAG	AAAATTTCAA	7380
30	TTTATAGAGG	TTAGGAATTC	CAAACTACAG	AAAATGTTTG	TTTTTAGTGT	CAAATTTTTA	7440
	GCTGTATTTG	TAGCAATTAT	CAGGTTTGCT	AGAAATATAA	CTTTTAATAC	AGTAGCCTGT	7500
	AAATAAAACA	CTCTTCCATA	TGATATTCAA	CATTTTACAA	CTGCAGTATT	CACCTAAAGT	7560
	AGAAATAATC	TGTTACTTAT	TGTAAATACT	GCCCTAGTGT	CTCCATGGAC	CAAATTTATA	7620
	TTTATAATTG	TAGATTTTTA	TATTTTACTA	CTGAGTCAAG	TTTTCTAGTT	CTGTGTAATT	7680
35	GTTTAGTTTA	ATGACGTAGT	TCATTAGCTG	GTCTTACTCT	ACCAGTTTTC	TGACATTGTA	7740
	TIGIGITACC	TAAGTCATTA	ACTITICITIC	AGCATGTAAT	TTTAACTTTT	GTGGAAAATA	7800
	GAAATACCTT	CATTTTGAAA	GAAGTTTTTA	TGAGAATAAC	ACCTTACCAA	ACATTGTTCA	7860
	AATGGTTTTT	ATCCAAGGAA	TTGCAAAAAT	AAATATAAAT	ATTGCCATTA	AAAAAAAAA	7920
		AAAAAAAAA					
40							

Seq ID NO: 180 Frotein sequence: Protein Accession #: Bos sequence

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		11	21	31	41	51	
45	1	11	11	i .	ī*	ĭ	
43	MOTE WORK NO	IQLLCVCRLD	MANICAADOOD	KINEBIGMEA	TOTALNOUNG	KKYPTCNSPK	60
	PRIDATE	TOVNVNLKKL	ANGE THE SA	PHIPPYUMTON	TUPTNI THINY	DACCCAREMA	120
	GS51MIDEOF	GKCNMSBDGS	MEGOMPKISH	LUMOTYCEDA	DEFEREN	KGKGKLRALS	180
	LUMBELLEUM	LDFKAIIDGV	BUREBOOKLE	ALDERTIANT	LDMOTDKYYT	VMGSLTSDDC	240
50	TEPEVOTEEN	DTVSISBSQL	AUPCRILTIO	ODGALMI MUA	TOWNEDBOOK	KESBONESSA	300
50	IDIADAIAEK	CSSEPERVOA	DOCUMENT IN	ANGEL AUTHOL	THI DVDAULY	COLDGEDORK	360
	TORRETHEAD	LGAILNNLLP	DIEMITADES	TOPMOLYCHY	COOL TANDADT	UNDELDITEDE	420
	REFLIDGIQU	EEEGKDIEEG	PATRICCOUCE	TUTOTTOR	TOTTUVNET	CTICVMEAKTM	480
	PUBLICATION	GKGDVPNTSL	MOTOCUTTELL	ATPENTELTS	COURTED DHT	VEGTSASIAD	540
55	RSPIRGSEFS	MNLSGTAESL	MALOAMBABI	MIDADIGUIO	TOLEDGEGGG	DATCATORIS	600
33	GSKTVLKSPA	SENPETITYD	MIVOIIDIDE	CONTOCCOOR	EGI KDUGARO	MANDOCTOT	660
	ENISOGYIPS	ESPLOTNYTE	ADIDECIMA	ACDO 100000	OCCUPATION ON	DUVCTPAVED	720
	TAQPDVGSGR	SSROODLVST	INVESTIN	MUNICIPALIO	Devections.	UTDLILDNOT	780
	TEVTPHAFTP	DSALHATPVF	DODUSTER	Leevocapit	DECACEGE	LEBHINITUSO	840
60	DATTPAASSS	SDKVPLHASL	POVENDEDE	DOL PORCOIL	COMPUNE COM	PECCEPCULY	900
00	ILPOVISATE	PSSDAMMHAR	PVAGGDIIII	EDMECCONT B	TUCVOCATEU	ungvavavoa	960
	KILMESUVEP	IPKSSLITPT	POLICEMENT	CONCUMENTAL	CDODDIT.DOT	DOLLARIMITES	1020
	SERSGERHIP	TSVFGDDNKA	Variotation	DOLUGING CAN	PRIVICE CALL	MDMMADMANA	1080
	PVSVABETIT	SISSTEGMEP	BOKSETTION	BIBLIGHTOPH	PHOLOGOTA	MOON GODTOT.	1140
65	LNASLQETSV	ASSDPASSEM	CSEMMITTIKV	PROLEGOVER	I T O DODO TEN	U.TVTVI.I.TVTVI	1200
05	KPVLSKNSEP	TPKVDKISST	DSP5 IQUUE E	PIGNOFOIDA	Improvence	TOTAL OCT.	1260
	AVPSDPILVE	PVLLKSESSE	WITHTI A SUBV	EL BOARNIT EL	ALALDAGLIG	WEATOW.CID	1320
	TISTASERIE	INSDEILTST	QVVPSLISND	DUPLIANDEL	MANUALITY	WCHUN TEAUC	1380
	SELVALLINKE	KLLPPSKATS	RSSVIGRVPA	GIPTVASDIP	COLORDODO	DEGENALIAVA	1440
70	PHRIIGSVIST	SQEKVMNDSD	BUSINSAKSDA	GEAGGGEDGD	TOODGOODOO	DEGODODOTE	1500
70	KCMSCSSYRB	PORKHNDOKE	THENSUMDON	NPISISLSEN	SEEDWKATSA	ecocatenet M	1560
	SPUKSPSANG	ADTNEKDADG	RNDIGIGSAT	Denogram	WARTERERA	HOUSE BY CHEE	1620
	ENETSTOPSF	LESEKKAVIP	ILAAGDSEIT	PUPPUSPISS	VISBRSEVER	PVI PDOTEDD	1680
	HESRIGLANG	PISDDVGAIP	PATASWELLI	CHAARACHEL	THREE VERY AR	HOCCERNICA	1740
75	AISTABLLIE	PISODVGAIP	INTERNAVAD	DUNDOOL LUD	PATHAMAMA	YNRPKAYIAA	1800
13	TADSSNHPON	KHKNHYINIV	AYDHSKVKLA	CPURCOUNT	DITMANIANG	NPLVTQKSVQ	1860
	QGPLKSTAED	PAKWIMEHNA	RATAMTINDA	BRGRRRCDQI	WPALOSONO	MA DA YÖVGAĞ	1920
	VLAYYTVRNP	TLRNTKIKKG	SQKGRPSGRV	VIQIHITQWP	DMGVPEISLE	ADTLAKONA	1980
	AKRHAVGPVV	VHCSAGVGRT	GTYIVLDSML	QQIQREGIVN	IFGFLKHIRS	COCHTOCOCON	2040
90	GAALIHDIPA	EAILSKETEV	LDSHIHAYVN	ALLIPUPAGE	TKTRKÖLÖTT	50201700D1	2100
80	SAALKQCNRE	KNRTSSIIPV	ERSRVGISSL	SGEGIDYINA	SATMGAAGSM	RFIITQHPLL	2160
	HTIKDFWRMI	MDHNAQLVVM	IPDGQNMAED	ELALMENKOR	PINCESPRAT	LMAZEHKCLS	2220
	NEEKLIIQDP	ILEATQDDYV	PEAKHEOCEK	WPNPDSPISK	TPELISVIKE	BAANKIXGPM1	2220
	VHDEHGGVTA	GTPCALTTLM	HOLEKENSVD	VYQVAKMINL	MICPGVFADIE	GAĞETAKAIP	2280
0.5	SLVSTROBEN	PSTSLDSNGA	ALPIGNIAES	PESTA			
85							

Seq ID NO: 181 DNA sequence Nucleic Acid Accession #: Eos sequence

WO 02/086443 Coding sequence: 148-4518

	1	11	21	31	41	51	
5	1	CACGCACGAT	1	1	000000000000000000000000000000000000000		60
,	CACACATACG	CACGCACGAT	CTCACTTCGA	CTATACACT	TOACHACCAC	AGGAGGGGGA	120
	CONTRACTOR	ATTTCCTTCG CCGCAGACCG	TCTGGGGGGGG	CTCTCCACTC	AGOSTTTCCT	CCCTTCCATT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTTGCCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
10	AAATATCCAA	CATGTAATAG TGAATCTTAA	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540 600
15	AAATGCAATA	TGTCATCTGA TCTACTGCTT	TGGATCAGAG	CATAGITTAG	AAGGACAAAA	ACCICACTO	660
13							720
	GATTTCAAAG	CGATTATTGA TCATACTGTT TGACATCTCC	TOGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
20	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCTTAC	AATGCAACAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA	960
	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
25	TGGGAAAGAC	CTCGAGTCGT GAGAGGACCA TCAATAATTT	TTATGATACC	ATGATTGAGA	CACATCCCTA	TENTACCAG	1260
23	CAGTIGGATG	TCAATAATTT	CCTACCCAAT	ATGROTTATO	TTCTTCAGAT	AGTAGCCATA	1320
							1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	TTGATCTTTT AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
30							1560
	ACGARATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
35	GAAGGTACTT	GGACTGCAGA	AAATGATGGC	TCTAAAACTG	TTCTTAGATC	ATTCTCTGGA TAAATTAGCC TCACACTGTG TCCACATATG	1860
33							1920
	CCAACTTCTC	CCAGTTTCAA CTATCCCATT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCCTCC	1980
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	GAAGATYCAA	CTTCATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	AAATGCTTCC GGAGGGAAAT AGGCAGAGAG GACAACCAAG GGAAATGCCA	2100
40	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATCTTCCATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTTCTG	CAGGCCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCCTA AGGATTTGGT	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340 2400
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	CAGCTTGCTG	AAAAGGATGG CAAAAGCTTA	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940 3000
55	TACAACAGAC	TGATATGGGA	TATTGCTGCC	CANGGCCCAC	TONORTONE	ANACCTICATA	3060
33	CACARAGORA	GGAGAAAATG	TCATCACTAC	TOCCOTOCOG	ATTEGRACITES	GGAGTACGGG	3120
	A A CTTTCTCC	TCACTCAGAA	GAGTGTGCAA	GTGCTTGCCT	ATTATACTGT	GAGGAATTTT	3180
	ACTOTARGAA	ACACAAAAAT	AAAAAAGGGC	TCCCAGAAAG	GAAGACCCAG	GAGGAATTTT TGGACGTGTG	3240
	GTCACACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
60	GTGCTGACCT	ATCACTACAC TTGTGAGAAA GTGCTGGAGT	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	CCCTGTTGTC	3360
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75							4200 4260
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	CTTTACCAGG	TAGCCAAGAT	CATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
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	CCATCCACCT	CTCTGGACAG TAGTTTAACA	TAATGGTGCA	GCATTGCCTG	ATGGAAATAT	AGCTGAGAGC	4500
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	TGCCTTTTTG	CAAGACTTGT	AATTTACTTA	TTATGTTTGA	ACTAAAATGA	TIGAATTITA	4740
85	CAGTATTTCT	AAGAATGGAA AGGTTAGGAA	TIGIGGTATT	TITTTCTGTA	TIGATTITAA	TOTCALATT	4800 4860
05	CATTIATAG	MUGTTAGGAA	TICCAAACTA	COTACAAAAA	TANCTOTAL	TACAGTAGCC	4920
	TOTALANTA	LIGIAGCAAT	ATATOMOSTIT	CAACATTTTA	CAACTGCAGT	TACAGTAGCC ATTCACCTAA	4920
	TOTANATAAA	MUNCICITUU	MIMIMONIALI	Concentition	- LILLIGUNGI		

	AGTAGAAATA	ATCTGTTACT	TATTGTAAAT	ACTGCCCTAG	TGTCTCCATG	GACCAAATTT	5040
			TTATATTTTA				5100
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_			TTAACTTTGT				5220
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	AAAAAAAAA	AAAAAAAAA	AAAAAA				

10 Seq ID NO: 182 Protein sequence: Protein Accession #: Eos sequence

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			KFQGWDKTSL				120
			EHSLEGQKPP				180
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	TOTVOWIVEK	DTVSISESQL	AVFCEVLTMQ	QSGYVNLMDY	LONNFREQQY	KFSRQVFSSY	300
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	LIGTERLIKE	RERGEDIEEG	AIVNPGRDSA	TNOIRKKEPO	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	OTVTELPPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
25	ENISOGYIFS	SENDETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAOPDVGSGR	ESPLOTNYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPHAFTP	SSROODLVST	VNVVYSQTTQ	PVYNARASNS	SHESRIGLAE	GLESEKKAVI	780
	PLVIVSALTP	ICLVVLVGIL	IYWRKCFQTA	HPYLEDSTSP	RVISTPPTPI	PPISDDVGAI	840
	PIKHPPKHVA	DLHASSGFTE	EFETLKEFYQ	EVOSCTVDLG	ITADSSNHPD	NKHKNRYINI	900
30	VAYDHSRVKL	AQLAEKDGKL	TDYINANYVD	GYNRPKAYIA	AQGPLKSTAE	DPWRMIWEHN	960
	VEVIVMITNL	VEKGRRKCDO	YWPADGSEEY	GNPLVTQKSV	QVLAYYTVRN	FTLRNTKIKK	1020
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	MHOLEKENSY	DVYOVAKMIN	LMRPGVFADI	EQYQFLYKVI	LSLVSTRQEE	NPSTSLDSNG	1440
	AALPDGNIAE						
40							

Seq ID NO: 183 DNA sequence Nucleic Acid Accession #: EOS sequence Coding sequence: 148-4494

	couring sequ	Tellice: 140-4	1474				
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	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
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	GAGATGCAAA	TCTACTGCTT	TGATGCAGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
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70	AATCCTGAAC	TIGATCITIT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG	1440
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	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
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5	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGGAAGTGC	AGAGCTGTAC	TGTTGACTTA	2760
	GGTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	ACAAGAATCG	ATACATAAAT	2820 2880
	ATCOTTGCCT	ATGATCATAG ATATCAATGC	CAGGGTTAAG	CTAGCACAGC	TIGCIGOUN	ACCOUNT TATE	2940
	CTGACTGATT	GCCCACTGAA	CAATTATGTT	CARCATTECT	CONGRECCIAN	ATCCCARACAT	3000
10	DETGCCCAMG	TTATTGTCAT	GATAACAGCI	CTCCTCCACA	PACCANCING	AAAATGTGAT	3060
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	MAGITITIAL	AATATAAATA	TTCCCCATTAA	AAAAAAAAA	AGGGGGGG	AAAAAAAA	5340
	AAA	MINIMAIA	HIGCONTIAN	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	,		
50	AUA.						
50	Sec ID NO:	184 Protein	n sequence:				
		cession #:		e			
	_		21	31	41	51	
55	1	11	11	11	i.	1	
,,	L	IQLLCVCRLD	MANGAAMOON	PLANDALUNGA	TOATMONWO	KKYPTCNSPK	60
	PRILICALIAC	TOWNVNLKKL	PROGRAMMENTOL	PATRIMATOR	TUETNITUDY	RVSGGVSEMV	120
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Seq ID NO: 185 DNA sequence Nucleic Acid Accession #: EOS sequence Coding sequence: 501-4514

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	ACCAAATCAG	WARRINGGAA	ACTRACOGAT	CCCCAACAAG	AGGAAGTGAA	TTCTCTGGAA	1620
	DOCUMENTAL TOTAL	TOTALTACA	TCTTTAAATT	CCACTTCCCA	ACCAGTCACT	AAATTAGCCA	1680
30	CAGAAAAAGA	TATTTCCTTG	ACTTCTCAGA	CTGTGACTGA	ACTGCCACCT	CACACTGTGG	1740
	AAGGTACTTC	AGCCTCTTTA	AATGATGGCT	CTAAAACTGT	TCTTAGATCT	CCACATATGA	1800
	ACTTGTCGGG	GACTGCAGAA	TCCTTAAATA	CAGTTTCTAT	AACAGAATAT	GAGGAGGAGA	1860
	GTTTATTGAC	CAGTTTCAAG	CTTGATACTG	GAGCTGAAGA	ACCOUNTATION	TTTTCCTCCG	1980
35	CAACTTCTGC	TATCCCATTC	ATCTCTGAGA	TENTACCACA	ATCTGCTAGA	AATGCTTCCG	2040
33	AAAACCCAGA	GACAATAACA	TATGATGTCC	CACTABAGGA	TCCTTCTATG	GAGGGAAATG	2100
	AAGATTCAAC	TACCTCTACE	GACATAACAG	CACAGCCCGA	TGTTGGATCA	GGCAGAGAGA	2160
	CCTTTCTCCA	GACTAATTAC	ACTGAGATAC	GTGTTGATGA	ATCTGAGAAG	ACAACCAAGT	2220
	CCTTTTCTGC	AGGCCCAGTC	ATGTCACAGG	GTCCCTCAGT	TACAGATCTG	CCTACTORTA ANGGAGGAG AGTOCTA CAA CCCCATAGGA AGTACTA CAA CCCCATAGGA AGTACTA CAA CAACATTAGA AGACAGGAG CCACATAGGA AGGAGGAGAA AATTCTACCC AGGAGGAGGAGA ACAACCCACACACACACACACA	2280
40	ATTATTCTAC	CTTTGCCTAC	TTCCCAACTG	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340
	CCAGACAACA	GGATTTGGTC	TCCACGGTCA	ACGTGGTATA	CTCGCAGACA	ACCCAACCGG	2460
	TATACAATGA	GGCCAGTAAT	AGTAGCCATG	AGTCTCGTAT	TGGTCTAGCT	THEATCHETC	2520
	AATCCGAGAA	GAAGGCAGTT	ATACCCCTIG	CCACCAAATC	CTTCCAGACT	GCACACTTTT	2580
45	TAGTGGTTCT	CACCACCACCAC	CTAGAGTTA	TATCCACACC	TCCAACACCT	ATCTTTCCAA	2640
73	TTTCAGATGA	TOTOGGAGCA	ATTCCAATAA	AGCACTITCO	AAAGCATGTT	GCAGATTTAC	2700
	ATGCAAGTAG	TGGGTTTACT	GAAGAATTTG	AGACACTGAR	AGAGTTTTAC	CAGGAAGTGC	2760
	AGAGCTGTAC	TOTTGACTT	GGTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	2820
	ACAAGAATCG	ATACATAAAT	ATCGTTGCCT	ATGATCATAC	CAGGGTTAAG	CTAGCACAGC	2880
50	TTGCTGAAAA	GGATGGCAAJ	CTGACTGATT	ATATCAATGO	CAATTATGTT	CALGGCIACA	3000
	ACAGACCAAA	AGCTTATAT	CCTGCCCAAG	GCCCACIGA	CATABCABAC	CTCGTGGAGA	3060
	GGAGAATGAT	ATGGGAACA	AATGTGGAAG	CTGCCGATGC	CACTGAGGAG	TACGGGAACT	3120
	AAGGAAGGAG	MARKITUTUR	CHGINCIGG	TTGCCTATTA	TACTGTGAGG	ACCOMMANDA ANTITHACTO GOTOTIGOTO ANTITHACTO GOTOTIGOTO ANTITHACTO GOTOTIGOTO ANTITHACTO	3180
55	TARGRARCAC	TORGANGAG.	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGGA	CGTGTGGTCA	3240
	CACAGTATCA	CTACACGCAC	TGGCCTGACA	TGGGAGTAC	AGAGTACTCC	CTGCCAGTGC	3300
	TGACCTTTGT	GAGAAAGGC	GCCTATGCCA	AGCGCCATG	AGTGGGGCCT	GTIGTCGTCC	3360
	ACTGCAGTGC	TGGAGTTGG	AGAACAGGC	CATATATTG	GCTAGACAG	ATGTTGCAGC	3420 3480
	AGATTCAACA	CGAAGGAAC	GTCAACATAT	TTGGCTTCT	C AAAACACATC	COTTCACAGA	3540
60	GAAATTATTT	GGTACAAAC	GAGGAGCAA	AIGICITCA:	r TCATGATAC	GTTAATGCAC	3600
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	ACTUALITY	ACACCAGAG	GACTATICIO	CAGCCCTAA	GCAATGCAAG	AGGGAAAAGA	3720
	ATCGAACTTC	TTCTATCAT	CCTGTGGAA	GATCAAGGG	TGGCATTTC	TCCCTGAGTG	3780
65	GAGAAGGCAC	AGACTACAT	AATGCCTCC	* ATATCATGG	3 CTATTACCAC	AGCAATGAAT	3840
•••	TCATCATTAC	CCAGCACCC	CTCCTTCAT/	CCATCAAGG	A TITCTGGAGG	ATGATATGGG	3900 3960
	ACCATAATGO	CCAACTGGT	GTTATGATTC	CTGATGGCC	A AAACATGGC	GAAGATGAAT	4020
	TIGITTACTO	GCCAAATAA	A GATGAGCCT	TAAATTGTG	A GAGCITIAA	GICACICIA	4080
70	TGGCTGAAGA	ACACAAATG	CTATCTAAT	3 AUGAAMAC	r inimilion	CCTAAATGGC	4140
70	TAGAAGCTAG	ACAGGATGA	TATGIACIT	TOTAL CTTA	T AMCTOTTAT	AAAGAAGAAG	4200
	CAAATCCAGA	TAGCCCCAT	T AGIAAAACI	ATGATGAGC	A TGGAGGAGTY	ACGGCAGGAA	4260
	CIGCCARIAC	TOTTACAAC	CTTATGCAC	AACTAGAAA	A AGAAAATTC	C GTGGATGTTT	4320
	ACCAGGTAGG	CARGATGAT	CARTCTGATG	A GGCCAGGAG	T CTTTGCTGA	CATTGAGCAGT	4380
75	ATCAGTTTC	CTACAAAGT	G ATCCTCAGC	C TTGTGAGCA	C AAGGCAGGA	C ATTGAGCAGT A GAGAATCCAT T GAGAGCTTAG T GTTTTCCTCT	4440
	CCACCTCTCT	GGACAGTAA	T GGTGCAGCA	T TGCCTGATG	G AAATATAGC	T GAGAGCTTAG	4500
	AGTCTTTAG:	TTAACACAG	A AAGGGGTGG	G GGGACTCAC	A TCTGAGCAT	T GITTICCICT	4560 4620
	TCCTAAAATT	r aggcaggaa	A ATCAGTCTA	G TTCTGTTAT	C TGTTGATTT	C CCATCACCTG C AATGTGTGCC A ATTTTACAGT	4680
90	ACAGTAACT	TCATGACAT	A GGATTCTGC	C GCCAAATTT	A IAICATTAA	ARIGIGIGOC	4740
80	TTTTTGCAA	ACTIGIAAT	T TACTTATTA	T TOTAL	A TITTANIA	A AAATTTCAAT	4800
	ATTTCTAAG	A ATGGAATTG	C DESCRIPTION	A AAATGTTTC	T TTTTAGTGT	C AAATTTTTAG	4860
	CTATAGAGG	T AGCARTIC	C AGGTTTGCT	A GAAATATAA	C TTTTAATAC	A GTAGCCTGTA	4920
	AATARAACA	C TOTTOCATA	T GATATTCAA	C ATTTTACAR	C TGCAGTATT	C ACCTAAAGTA	4980
85	GAAATAATC	T GTTACTTAT	T GTAAATACT	G CCCTAGTGT	C TCCATGGAC	C AAATTTATAT	5040
	TTATAATTG	T AGATTTTTA	T ATTTTACTA	C TGAGTCAAG	T TTTCTAGTT	A ATTITIACAGI A AAATTICAAT C AAATTITIAG A GTAGCCTGTA C ACCTAAAGTA C AAATTIATAT C TGTGTAATTG T GACATTGTAT	5100
	TTTAGTTTA	A TGACGTAGT	T CATTAGCTG	G TCTTACTCT	A CCAGTTTTC	T GACATTGTAT	5160

	WO 02	/086443 aagtcattaa	COMPAND COMPAND CO.	CONTOURNET	TOTAL CONTENTS	TOCABARTAG	5220
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	ATGGTTTTTA	TCCAAGGAAT	TGCAAAAATA	AATATAAATA	TTGCCATTAA	АЛЛЛАЛАЛ	5340
5	алалалала	AAAAAAAA	AAA				
,	Seg ID NO:	186 Proteir	sequence:				
	Protein Acc	ession #: E	OS sequence	•			
	1	11	21	31	41	51	
10	Ī	1	1	Ī	1	1	
	MVFKASKITF	HWGKCNMSSD ENLOFKATID	GSEHSLEGQK	PPLEMQIYCF	DADRESSEE	AVKGKGKLRA Y1YNGSLTSP	60 120
	PCTDTVDWIV	PKDTVSISES	OLAVECEVLT	MOOSGYVMLM	DYLONNFREC	QYKFSRQVFS	180
15	SYTCKEEIHE	AVCSSEPENV	QADPENYTSL	LVTWERPRVV	YDTMIEKFAV	LYQQLDGEDQ	240 300
13	TKHEFLTDGY	QDLGAILNNL KEREEGKDIE	EGATUNEGED	SATNOTREKE	POISTTTHYN	RIGTKYNEAK	360
	TWDSDTDGSE	PSGKGDVPNT	SUNSTSOPVT	KLATEKDISL	TSOTVTELPP	HTVEGTSASL	420
	NDGSKTVLRS	PHMNLSGTAE	SLNTVSITEY	EEESLLTSFK	LDTGAEDSSG	SSPATSAIPF	480 540
20	DITACUDVES	FSSENPETIT GRESFLQTNY	TETRVDESEK	TTKSFSAGPV	MSOGPSVTDL	EMPHYSTFAY	600
	FPTEVTPKAP	TPSSROODLV	STVNVVYSQT	TOPVYNEASN	SSHESRIGLA	EGLESEKKAV	660
	IPLVIVSALT	FICLVVLVGI ADLHASSGFT	LIYWRKCFQT	ARPYLEDSTS	PRVISTPPTP	IFPISDDVGA	720 780
	TVAYDRSRVK	LAGLAEKDGK	LTDYINANYV	DGYNRPKAYI	AAQGPLKSTA	EDPWRMIWEH	840
25	NVEVIVAITN	LVEKGRRKCD	QYWPADGSEE	YGNPLVTQKS	VQVLAYYTVR	NFTLRNTKIK	900
	RGSQKGRPSG	RVVTQYHYTQ MLQQIQHEGT	WEDWGALFAR	RSORNYLVOT	EEQYVFIHDT	LVRAILSKET	1020
	EVLDSHIHAY	VNALLIPGPA	GKTKLEKQFQ	LLSQSNIQQS	DYSAALKOON	REKNRTSSII	1080
30	PVERSRVGIS	SLSGEGTDY I EDEFVYWPNK	NASYIMGYYO	SNEFILTOHP	LLHTIKDFWR	MIMDHNAQLV	1140 1200
50	VALEABARDOC	PKWPNPDSPI	SKTPELISVI	KEEAANRDGP	MIVHDEHGGV	TAGTFCALTT	1260
	LMHQLEKENS	VDVYQVAKMI	NLMRPGVFAD	1 EQYQFLYKV	ILSLVSTRQE	ENPSTSLDSN	1320
	GAALPDGNIA	ESLESLV					
35	Seq ID NO:	187 DNA sec	quence				
	Nucleic Ac	id Accession	n#: EOS se	quence			
	Coding seq	uence: 148-	4632				
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	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AACGTTTCCT	CGCTTGCATT	180 240
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	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
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50		TGTCATCTGA		CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600 660
	GGAAAAGGGA	TCTACTGCTT AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT TTACATTTAC	780 840
55	TTAGATCCAT	TGACATCTCC	TOCOTTOTA	CCAAACTCAA	ACTGGATTGT	TTTTAAAGAT	900
55	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCTTAC	AATGCAACAA	960
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	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
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65	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG CAGTGCTACA	1440 1500
05	GAAGAGGGAA	GGAAAAAGGA	ACCCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGARATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA TAAATTAGCC	1620 1680
	AAGGGTGATG	TTCCCAATAC	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TAAATTAGCC	1740
70	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACTG	TTCTTAGATC	TCCACATATG	1800
	AACTTGTCGG	GGACTGCAGA CCAGTTTCAA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
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75	GANANCCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
75	GAAGATTCAA	CTTCATCAGG	AGACATARCA	GCACAGO	ATGTTGGATC	AGGCAGAGAG	2100
	ACCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTTCTG	CAGGCCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
80	TCCAGACAAC	CCTTTGCCTA	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
	GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	TOGATOGICA	CAGCCCTGAC	TTTTATCTGT	2520 2580
	TACTTAGAGG	ACAGTACATO	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	2640
85	ATTTCACATG	ATGTCGGAGC	AATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	2700 2760
	CATGCAAGTA	GTGGGTTTAC	AGGTATTACA	GCAGACACTGA	CCAACCACCC	AGACAACAAG	2760 2820
	CHOMOCIGTA	CIGITANCII					

	WO 02/	086443					
	CACAAGAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	2880
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	2940
	AACAGAGCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	3000
	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	3060
5	AAAGGAAGGA	GAAAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	3120
-	TTTCTCCCCC	CTCAGAAGAG	TOTOCAAGTG	CTTGCCTATT	ATACTGTGAG	GAATTTTACT	3180
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10	CACTGCAGTG	CTGGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	3420
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1.5	COCTTAACTC	ATCCTCCTAC	CTCAGCCTCC	CGACTGGCTG	GGACTATACT	CCTGAGCCAG	3780
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	CANCELLCE	ACTACATCAA	TGCCTCCTAT	ATCATGGGGT	ATTACCAGAG	CAATGAATTC	3960
20	A TOTAL COO	AGCACCCTCT	CCTTCATACC	ATCARGGATT	TCTTGGAGGAT	GATATGGGAC	4020
20	CATAATOCCC	AACTGGTGGT	TATCATTCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	4080
	CTTTACTGCC	CAAATAAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACTCTTATG	4140
	CCTCAAGAAC	ACANATGTCT	ATCTAATGAG	GANANACTTA	TAATTCAGGA	CTTTATCTTA	4200
	CANCETACAC	AGGATGATTA	TOTACTTORA	GTGAGGCACT	TTCAGTGTCC	TAAATGGCCA	4260
25	BATCCAGATA	GCCCCATTAG	TABABETTTT	GAACTTATAA	GTGTTATAAA	AGAAGAAGCT	4320
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	ATAGAGGTTA	GGAATTCCAA	ACTACAGAAA	ATGTTTGTTT	TTAGTGTCAA	ATTTTTAGCT	4980
	GTATTTGTAG	CAATTATCAG	GTTTGCTAGA	AATATAACTT	TTAATACAGT	AGCCTGTAAA	5040
	TARABACACTO	TTCCATATGA	TATTCAACAT	TTTACAACTG	CAGTATTCAC	CTAAAGTAGA	5100
	AATAATCTGT	TACTTATTGT	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	5160
40	ATAATTGTAG	ATTTTTATAT	TTTACTACTG	AGTCAAGTTT	TCTAGTTCTG	TGTAATTGTT	5220
	TACTTTAATC	ACGTAGTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTTCTGA	CATTGTATTG	5280
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45	AAAAAAAA	AAAAAAAAA.	A				

Seq ID NO: 188 Protein sequence: Protein Accession #: EOS sequence

50						51	
30	1	11	21	31	41	51	
	MDAY KOM S.C.	IQLLCVCRLD	MYNGAADUUD I	PINDETCHEY	TONTONNO	KKYPTCNSPK	60
	MRILKRPLAC	TOVNVNLKKL	WANGIIRQQR	WINDS AND AND AND AND AND AND AND AND AND AND	TOTAL TATO	DACCURE DATE	120
	OSE THIDEDE	GKCNMSSDGS	PUCT POOVED	LEMOTYCEDS.	DESCRIPTION	KCKCKTRALS	180
55	PRASKITERN	LDFKAIIDGV	EUGDEGALL	ALDERT LINE	LENSTDKYYT	YNGSLTSPPC	240
55	THEPAGIESIA	DTVSISESQL	AVECEVITMO	OSCYVMI MDY	LONNERFOOY	KPSROVESSY	300
	TOVOCTUCAV	CSSEPENVOA	DPENYTSLLV	TWEEPRVVYD	TMIEKPAVLY	OOLDGEDOTK	360
	HERITDGYOD	LGAILMNLLP	NMSYVLOTVA	ICTNGLYGKY	SDOLIVDMPT	DNPELDLPPE	420
	LIGTERITEE	EEEGKDIEEG	AIVNPGRDSA	TNOIRKKEPO	ISTTTHYNRI	GTKYNEAKTN	480
60	RSPTRGSEFS	GKGDVPNTSL	NSTSOPVTKL	ATEKDISLTS	QTVTBLPPHT	VEGTSASLND	540
••	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSG99	PATSAIPFIS	600
	ENISOGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	RSLKOPSMEG	NVWPPSSTDI	660
	TAOPDVGSGR	ESPLOTNYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPHAFTP	SSROODLVST	VNVVYSOTTQ	PVYNEASNSS	HESRIGLARG	LESEKKAVIP	780
65	LVIVSALTFI	CLVVLVGILI	YWRKCPQTAH	FYLEDSTSPR	VISTPPTPIP	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTEE	FETLKEPYQE	VQSCTVDLGI	TADSSNHPDN	KHKNRYINIV	900
	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPLKSTAED	FWRMIWEHNV	960
	EVIVMITHLY	EKGRRKCDQY	WPADGSBEYG	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
	SOKGRPSGRV	VTQYHYTQWP	DMGVPBYSLP	VLTPVRKAAY	AKRHAVGPVV	VHCSAGVGRT	1080
70	GTYIVLDSML	QQIQHEGIVN	IFGFLKHIRS	QRNYLVQTEE	QYVFIHDTLV	eallsketev	1140
	LOSHIHAYVN	ALLIPGPAGK	TKLEKQFQGL	TLSPRLECRG	TISAHCNLPL	PGLTDPPTSA	1200
	SRVAGTILLS	QSNIQQSDYS	AALKQCNREK	NRTSSIIPVE	RSRVGISSLS	GEGTDYINAS	1260
	YIMGYYQSNE	PIITQHPLLH	TIKDFWRMIW	DHNAQLVVMI	PDGQNMAEDE	PVYWPNKDEP	1320
	INCESFKVTL	MAEEHKCLSN	EEKLI IQDPI	LEATQUDYVL	EVRHFQCPKW	PNPDSPISKT	1380
75	PELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TFCALTTLMH	OFEKENSADA	AGAYRWININ	1440
	RPGVFADIEQ	YOPLYKVILS	LVGTRQEENP	STSLDSNGAA	LPDGNIAESL	ESLV	

80 Seq ID NO: 189 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304..831

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85	CCCTGTTCCA	CGAACCCAGG	AGAACTGCTG	GCCAGATTAA	TTAGACATTG	AGGCGGTTAG CTATGGGAGA TCGCTATTAT	60 120 180

	WO 02/						
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	ACGATGCAGC	GGAGACTGGT	TCAGCAGTGG	AGCGTCGCGG	TGTTCCTGCT	GAGCTACGCG	360
-	GTGCCCTCCT	GCGGGCGCTC	GGTGGAGGGT	CTCAGCCGCC	GCCTCAAAAG	AGCTGTGTCT	420
5	GAACATCAGC	TCCTCCATGA TGATCGCAGA	CAAGGGGAAG	TCCATCCAAG	ATTTACGGCG	ACGATTCTTC	480 540
	CCTRACTCCR	AGCCCTCTCC	CAACACAAAG	AACCACCCCC	TOGGATTTGG	GTCTGATGAT	600
	GAGGGCAGAT	ACCTAACTCA GGAAGAAAAA	GGAAACTAAC	AAGGTGGAGA	CGTACAAAGA	GCAGCCGCTC	660
10	AAGACACCTG	CTCGCTCTGC	GAAAGGCAAG	CCCGGGAAAC	GCAAGGAGCA	GGAAAAGAAA	720 780
10	GACCACCTGT	CTGACACCTC GCCTCAGCGG	CACAACGTCG	CTGGAGCTCG	ATTCACGGTA	ACAGGCTTCT	840
	CTGGCCCGTA	GCCTCAGCGG	GGTGCTCTCA	GCTGGGTTTT	GGAGCCTCCC	TTCTGCCTTG	900
	GCTTGGACAA	ACCTAGAATT CTCAGAATAT	TETETECETT	AAAGCAGTAC	CCCCCTACCA	CACACACCCC	960 1020
15	TGTCCTCCAG	CACCATAGAG	AGGCGCTAGA	GCCCATTCCT	CTTTCTCCAC	CGTCACCCAA	1080
	CATCAATCCT	TTACCACTCT	ACCAAATAAT	TTCATATTCA	AGCTTCAGAA	GCTAGTGACC	1140
	ATCTTCATAA	TTTGCTGGAG	CTTACGTTCT	TTCACTTCAA	GGGAGAATAT	AGAAGCATTT	1260
	CATATTATCT	ACABACACTG	CAGAACAGCA	TCATGTCATA	AACGATTCTG	AGCCATTCAC	1320
20	ACTITITATI	TAATTAAATG TTTAAACACA	TATTTAATTA	AATCTCAAAT	TTATTTTATT	GTAAAGAACT	1380 1440
	CCAGCTCATA	CAAAATAAAT	GGTTTCTGAA	AATGTTTAAG	TATTAACTTA	CAAGGATATA	1500
	GGTTTTTCTC	ATGTATCTTT	TTGTTCATTG	GCAAGATGAA	ATAATTTTTC	TAGGGTAATG	1560
25	CCGTAGGAAA	AATAAAACTT	CACATTTAAA	AAAAA			
23							
		190 Protein					
	Protein Acc	cession #: 1	P_002811	•			
30							
	1	11	21	31	41	51	
	MODBINOOMS	VAVFLLSYAV	PECCEPSURGI.	SPRIKPAVSE	HOLLHDEGES	IODLERREPL	60
	HHLIAEIHTA	EIRATSEVSP	NSKPSPNTKN	HPVRFGSDDE	GRYLTQETNK	VETYKEQPLK	120
35	TPGKKKKGKP	GKRKEQEKKK	RRTRSAWLDS	GVTGSGLEGD	HLSDTSTTSL	ELDSR	
	Sea ID NO:	191 DNA sec	mence				
	Nucleic Ac:	id Accession	a #: XM 0593	28			
40	Coding sequ	uence: 52	L023 ··				
70	1	11	21	31	41	51	
	1	1	<u></u>	1	í .	1	
	GGGCTGTCCG	GCCCACTCCC GCCTGGTGGT	CTGGGAGCGC	GAGCGGTGGA	CCCAGGCGGC	CATGTCCCGC ACGCGATGAG	60 120
45	CCTCGCATGC	GCCTGGTGGT AGGCCTTTCT	CACCGCGGGAC GGCCGGGGCT	GAGCGGTGGA GACTTTGGTT GTGACCAGCG	CCCAGGGGGC ACTGCCCGCG TGTCCCTGCT	ACGCGATGAG GGTCAACGGT	120 180
45	CCTCGCATGC GGTATCGTGG GCGGCCACGG	AGGCCTTTCT AGAGCGCGGC	CACCGCGGAC GGCCGGGGCT GGAGCTGGCC	GAGCGGTGGA GACTTTGGTT GTGACCAGCG CGCAGGCACA	CCCAGGCGGC ACTGCCCGCG TGTCCCTGCT GCATCCCCAC	ACGCGATGAG GGTCAACGGT GGGCCTCCAC	120 180 240
45	CCTCGCATGC GGTATCGTGG GCGGCCACGG	AGGCCTTTCT AGAGCGCGGC	CACCGCGGAC GGCCGGGGCT GGAGCTGGCC	GAGCGGTGGA GACTTTGGTT GTGACCAGCG CGCAGGCACA	CCCAGGCGGC ACTGCCCGCG TGTCCCTGCT GCATCCCCAC	ACGCGATGAG GGTCAACGGT GGGCCTCCAC ATCGCTGCTC	120 180
	CCTCGCATGC GGTATCGTGG GCGGCCACGG GCCAACCTGT GGCCCGGAAG GTGGATTTGC	GCCTGGTGGT AGGCCTTTCT AGAGCGCGGC CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG	CACCGCGGAC GGCCGGGGCT GGAGCTGGCC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC	GAGCGGTGGA GACTTTGGTT GTGACCAGCG CGCAGGCACA CCGGCCCGCC GGATTCCGGG GAGGCCCAAC	CCCAGGCGGC ACTGCCCGGT TGTCCCTGGT GCATCCCCAC GTGGCGCCTC AGGCGGTTGGC TAAGCTGCTT	ACGCGATGAG GGTCAACGGT GGGCCTCCAC ATCGCTGCTC GGCCGGAGAC CCGGGAGCTG	120 180 240 300 360 420
45 50	CCTCGCATGC GGTATCGTGG GCGGCCACGG GCCAACCTGT GGCCCGGAAG GTGGATTTGC CTGGGCAGGG	GCCTGGTGGT AGGCCTTTCT AGAGCGCGGC CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG CCCCCACGCA	CACCGCGGAC GGCCGGGGCT GGAGCTGGCC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC CGCGGACGGG	GAGCGGTGGA GACTTTGGTT GTGACCAGCG CGCCCGGC GGATTCCGGG GAGGCCCAAC CACCAGCACG	CCCAGGCGGC ACTGCCCGCG TGTCCCTGCT GCATCCCCAC GTGGCGCTCC AGGCGGTGGC TAAGCTGCTT TGCACGTGCT	ACGCGATGAG GGTCAACGGT GGGCCTCCAC ATCGCTGCTC GGCCGGAGAC CCGGGAGCTG CCCAGGCGTG	120 180 240 300 360 420 480
	CCTCGCATGC GGTATCGTGG GCGGCCACCGG GCCAACCTGT GGCCCGGAAG GTGGATTTGC CTGGGCAGGG TGCCAGGTGT GAGCGCGGTG	GCCTGGTGGT AGGCCTTTCT AGAGCGCGG CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG CCCCCACGCA TCGCCGAGGC TCGCCGAGGC	CACCGCGGAC GGCCGGGGCT GGAGCTGGCC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC CGCGGACGGG GCTGCAGGCC CACTTGGCTG	GAGCGGTGGA GACTTTGGTT GTGACCAGCG CGCAGGCACA CCGGCCCGCC GGATTCCGGG GAGGCCCAAC CACCAGCACG TATGGGGTGC	CCCAGGOGGC ACTGCCCGCG TGTCCCTGCT GCATCCCCAC GTGGCGCCTC AGGCGGTGGC TAAGCTGCT TGCACGTGCT GCTTTACGCG GCGGTGGCCTT	ACGCGATGAG GGTCTACCGGT GGGCCTCCAC ATCGCTGCTC GGCCGGAGAC CCCAGGCGTG ACTGCCGCTG CGCCTGCGCCCC	120 180 240 300 360 420 480 540
	CCTCGCATGC GGTATCGTGG GCGGCCACGG GCCAACCTGT GGCCCGGAAG GTGGATTTGC CTGGGCAGGG TGCCAGGTGT GAGGCGGGTG GTGCAGCCGGTG	GCCTGGTGGT AGAGCGCGGG CCCAAGGGGCCC CCTCATCCT CTCAGGTGCC CCCCACGCA TCGCCGACGCA TCGCCGACGCA TCGCCGACGCA ACGCCCGCGGC	CACCGCGGAC GGCCGGGGCT GGAGCTGGC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC CGCGGACGGG GCTGCAGGCC CACTTGCTGCTG CGCGTGGGG	AGCGGTGGA GACTTTGGTT GTGACCAGCG CGCCCGCC GGATTCCGGG GAGGCCCAC CACCAGCACG TATGGGGTG GAGGCCCCG CACCAGCACG G CACCAGCACCACACACA	CCCAGGCGGC ACTGCCCGCG TGTCCCTGCT GCATCCCCAC GTGGCGCTT AGGCGCTT TGCACGTGCT TGCACGTGCT GCTTTACGCG GCGGTGCCTT GCCACGGCCTC	ACGCGATGAG GGTCAACGGT GGGCTCCAC ATCGCTGCTC GGCCGGAGAC CCCGGGGCTG ACTGCCCCTG GGCCTGCGCC GCGCTGCGCCC GCGGTGGACA	120 180 240 300 360 420 480 540 600 660
	CCTCGCATGC GGTATCGTGG GCCACGG GCCACGG GCCACGGTG GGCCCGGAAG CTGGCAGGG TGCCAGGTGT GAGCGCGGTG GAGCGCGTTG GACCCTTCCG GACCCCTTCCG	GCCTGGTGGT AGGCCTTTCT AGAGCGCGG CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG CCCCCACGCA TCGCCGAGGC TGGGTGGCTG ACGCCCGGAG TGGGCCGGAG	CACCGCGGAC GGCCGGGGCT GGAGCTGGCC CCCGTGGGT TGGCAAGATG GGAGGAGCTC GCGGACGGG GCTGCAGGCC CACTTGGCTG CACTTGGCTG CACTTGGGGC CACTTGGGGC CACTTGGGGC	GAGCGGTGGA GACTTTGGTT GTGACCAGCG CGCAGGCACA CCGGCCCGCC GGATTCCGGG GAGGCCCAC CACCAGCACG TATGGGTGC GAGGCCCCC CCTTCTCCC CGGCACATGT	CCCAGGOGGG ACTGCCOGGG TGTCCCTGGT GCATCCCAC GTGGCGCCTC AGGCGGTGGC TAAGCTGGT TGCACGTGGCT GCTTTACGCG CGCGTGCCT GCCACGGCCT CCCACGCCCT CCCCTCACCG	ACGCGATGAG GGTCAACGGT GGGCCTCCAC ATCGCTGCTC GGCCGGAGCT CCCAGGCGTG ACTGCCGCTG GCCTGCGCCT GCGTGGACA CGCGTGGACA CGCGTGGACA CGTGTCCGGG	120 180 240 300 360 420 480 540
50	CCTCGCATGC GGTATCGTGG GCCACGG GCCACGG GCCACGGG GCCAGGAGG GTGGATTTGC CTGGGCAGGG TGCCAGGTGT GAGCGCGTGT GAGCGCGTGG GACGCCTTCG GCCCTGGGGC	GCCTGGTGGT AGGCCTTCT AGAGGGCGC CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG CCCCACGCA TCGCCGAGGC TGGGTGGCT ACGCCGGGGC TGGGCCTGAG GGGTCCTGAG	CACCGCGGAC GGCCGGGGGT GGAGCTGGGC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC CCCGGGGACGGG GCTGCAGGCC CACTTGGCGC CACTTGGCGC AGGTACCCTA AGGTACCCTA	AGCGGTGGA GACTTTGGTT GTGACCAGCG GGACTTCGGG GGATTCCGGG GGATTCCGGG GAGCCCAAC TATGGGTGG GAGGCCCAC CCCTTCTCCC CGGCACATGT GCGGCCCACA	CCCAGGGGG ACTGCCGGG TGTCCCTGCT GCATCCCCAC GTGGGGCCTC AGGCGGTGGC TAAGCTGCTT TGCACGTGCTT GCCATGGGC GCGTGCCTT CCCCTCACGG	ACSCGATGAG GGTCAACGGT GGGCCTCCAC ATCGCTGCTC GGCCGGAGAC CCCAGGCGTG ACTGCCGCTG CGCCTGCGCCC GCGGTGGACA CGTGTCCGCG CCAGGCTGGACA CGTGCGCC CCAGGCTGGACA CGTGTCCGCG CCAGGCTGACA CCTGCGCC CCAGGCTGACAC CCAGGCTGACGC CCAGGCTGACGC CCAGGCTGACGC CCAGGCTGACGC CCAGGCTGACGC	120 180 240 300 360 420 480 540 600 660 720 780 840
50	CCTCGCATGC GGTATCGTGG GCCACGG GCCACGG GCCACGGG GCCAGGAGG GTGGATTTGC CTGGGCAGGG TGCCAGGTGT GAGCGCGTGT GAGCGCGTGG GACGCCTTCG GCCCTGGGGC	GCCTGGTGGT AGGCCTTCT AGAGGGCGC CCGAGGGCCG GCTTCTTCCT CTCAGGTGCG CCCCACGCA TCGCCGAGGC TGGGTGGCT ACGCCGGGGC TGGGCCTGAG GGGTCCTGAG	CACCGCGGAC GGCCGGGGGT GGAGCTGGGC CCCCGTGGGT TGGCAAGATG GGAGGAGCTC CCCGGGGACGGG GCTGCAGGCC CACTTGGCGC CACTTGGCGC AGGTACCCTA AGGTACCCTA	AGCGGTGGA GACTTTGGTT GTGACCAGCG GGACTTCGGG GGATTCCGGG GGATTCCGGG GAGCCCAAC TATGGGTGG GAGGCCCAC CCCTTCTCCC CGGCACATGT GCGGCCCACA	CCCAGGGGG ACTGCCGGG TGTCCCTGCT GCATCCCCAC GTGGGGCCTC AGGCGGTGGC TAAGCTGCTT TGCACGTGCTT GCCATGGGC GCGTGCCTT CCCCTCACGG	ACSCGATGAG GGTCAACGGT GGGCCTCCAC ATCGCTGCTC GGCCGGAGAC CCCAGGCGTG ACTGCCGCTG CGCCTGCGCCC GCGGTGGACA CGTGTCCGCG CCAGGCTGGACA CGTGCGCC CCAGGCTGGACA CGTGTCCGCG CCAGGCTGACA CCTGCGCC CCAGGCTGACAC CCAGGCTGACGC CCAGGCTGACGC CCAGGCTGACGC CCAGGCTGACGC CCAGGCTGACGC	120 180 240 300 360 420 480 540 660 720 780 840 900
50	CCTOSCATOS GGTATCGTGG GCGGCAGGG GCCAACCTGT GGCCGGGAG GTGGATTTGC TGCCAGGTGT GAGGCGGG GAGGCTTCG GCCTGGCGC GCCTGGCGC TCTCTTGCT GCCAGCTTG GCCAGCTGG	CCTRGTGGT AGAGCGGC CCAAGGCGGC CCCAAGGCGGC CCCCACGGA TGGCCTGGGA TGGCCTAGGA AGGCCCGGGC TGGGTGCTGA AGGCCTGAG AGGCCTGAG AGTCCTGGA CCTACCCCAG CCTAGGAGGG CCCAGGATGG CCCAGGATGG CCCAGGATGG CCCAGGATGG AGGCCCCCAG	CACGGGGAC GGAGCTGGCC CCCGTGGGT TGGCANGATTG GGAGGACTGG GCTGCAGGCC CACTTGGCT CGCGGACGGG CACTTGGCTG CGCGTTGGCC CACTTGGCTG CGCCTTGGCT CGCCTTGGCT CGCCTTGGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGGGC CTGCATGAG CGTGCACTTGAGCCCACT TGAGCCCACT	GAGCGGTGGA GACTTTGGTT GTGACCACCG GGATTCCGGG GAGGCCCACC GGATTCCGGG GAGGCCCACC CACCAGCACG CACCAGCACC CACCACCACC CACCACC CACCACC CACCACC CACCAC	I CCCAGGGGGG CCCAGGGGGGG CCCAGGGGGGGGGGGG	ACGCGATGAG GGGCCTCAC ATCGCTCAC ATCGCTGCTC GGCCGGAGAC CCCGGAGCT CCCAGGGTG GGCGTGAGC GGGTGGACC GGGTGGACC GGGTGGACC CGGTGGACC CGGTGGACC CGGTGGACC CGGTGGACC CCCGAGAGC CCCGAGAGC CCCGAGAGC CTCCAAGAGG CTCCCTACTC	120 180 240 300 360 420 480 540 600 660 720 780 840
50	CCTOSCATOS GGTATCGTGG GCGGCAGGG GCCAACCTGT GGCCGGGAG GTGGATTTGC TGCCAGGTGT GAGGCGGG GAGGCTTCG GCCTGGCGC GCCTGGCGC TCTCTTGCT GCCAGCTTG GCCAGCTGG	CCTRGTGGT AGAGCGGC CCAAGGCGGC CCCAAGGCGGC CCCCACGGA TGGCCTGGGA TGGCCTAGGA AGGCCCGGGC TGGGTGCTGA AGGCCTGAG AGGCCTGAG AGTCCTGGA CCTACCCCAG CCTAGGAGGG CCCAGGATGG CCCAGGATGG CCCAGGATGG CCCAGGATGG AGGCCCCCAG	CACGGGGAC GGAGCTGGCC CCCGTGGGT TGGCANGATTG GGAGGACTGG GCTGCAGGCC CACTTGGCT CGCGGACGGG CACTTGGCTG CGCGTTGGCC CACTTGGCTG CGCCTTGGCT CGCCTTGGCT CGCCTTGGCC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGCGGC CACTTGGGC CTGCATGAG CGTGCACTTGAGCCCACT TGAGCCCACT	GAGCGGTGGA GACTTTGGTT GTGACCACCG GGATTCCGGG GAGGCCCACC GGATTCCGGG GAGGCCCACC CACCAGCACG CACCAGCACC CACCACCACC CACCACC CACCACC CACCACC CACCAC	I CCCAGGGGGG CCCAGGGGGGG CCCAGGGGGGGGGGGG	ACGCGATGAG GGGCCTCAC ATCGCTCAC ATCGCTGCTC GGCCGGAGAC CCCGGAGCT CCCAGGGTG GGCGTGAGC GGGTGGACC GGGTGGACC GGGTGGACC CGGTGGACC CGGTGGACC CGGTGGACC CGGTGGACC CCCGAGAGC CCCGAGAGC CCCGAGAGC CTCCAAGAGG CTCCCTACTC	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020 1080
50	CCTOCATISC GOTATIOTISG GCGCCACGG GCCAACCTGT GCCCAGAGT GTGGCCAGGG TGCCAGGGT GTGGCCAGGG GTGCCAGGGC GCCCTTCG GCCTTCG GCCTTCG GCCTGGCCC GCCAGGTTT GCCAGGGGAG TCCCAGGGAG TCCCAGGGAG TCCCTGCTT	CCTIGGTGGT AGACGCCGC CCAGGCA CCCCCGGCA CCCCCGGCA CCCCCGGCA CCCCCGGCA CCCCCGGCA CCCCCGGCA CCCCGGCA CCCCGGCA CCCCGGCA CCCCGGCA CCCCGGGCA CCCCGGGCA CCCCGGGCC CCCAGGATGG CCCAGGATGG CCCAGGATGC CCCAGGAACACCA CCCAGCACCA CCCAGCACCC	CACGGGGGC GGGGGGT GGAGCTGGCC CCCGGTGGGT TGGCAAGATG GGAGGAGCTC CGCGGACGGG GCTTGAGGCC CACTTGGCTG GGCGTGGGC CACTTGGCTG TGGCACGGC CACTTGGCTG TGGCGCTACGGC CACTTGGCTC TGGACCACA AGGACCTACT TGAGCCCACT AGCACTAATG AGCTGGACCACA	GAGCOGTGGA GACTTTGGTT GTGACCAGCG GGCAGGCACA CCGGCCGCCC CACCAGCCCACC CACCAGCACG AACCAGCACG CACCAGCACG CACCAGC CACCAGCACG CACCAGC CACCAGCACG CACCAGCACG CACCAGCACG CACCAGCACG CACCAGCACG CACCAGC CACCAGCACC CACCAGCACC CACCAGCACC CACCAGCACC CACCAGCACC CACCAGCACACC CACCAGCACC CACCAGCACC CACCAGCACC CACCAGCACC CACCAGCACC CACCACACC CACCACACC CACCACACC CACCAC	CCCAGGCGGG ACTGCCCAG ACTGCCCAG TGACCCCAG GGATCCCCAG GGAGCGCTT GAAGCGGTGGC TAACTGCTT TGCACGTGCT GCCACGGCCC GCCTACAGG CCTGACAG CCCTGACAG CCCTGACAG CCCACAGAAAGGG ACAAAAGGG CAAAAAGGG CACAAAAGGG TCCTGGAAC CAAAAAGGG TCTGTGAC	ACCIGATGAG GGGCTCAAC GGCCGAGAC GCCCGAGAGC GCCGGAGAC GCCCGGAGAC GCCTGCCC GCGTGGAC GCGTGGCC GCGTGGAC GCGTGGAC GCGTGAC GCGCTCAG GCGCTCCAG CCCCAAGAG CTCCAAGAG CTCCAAGAG GTCCCAGGC GAGCTAC GAGCCAGGT TCCCTGGGTA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140
50	CCTCGCATISC GGTATGGGG GGGCCACGG GCCACCGGTGT GGCCGGAAG GTGGATTTGG GGCGGGGGT GGCAGGTGT GGCGGGGGGGGGG	CCTIGOTGGT AGACCTAGA AGACCTAGA AGACCTAGA AGACCTAGA AGACCTAGA AGACCAGA AGACCAGA AGACCAGA AGACCAGA AGACCAGA AGACCAGA AGACCAGA ACCAGACCAG AGACCAGA AGACCAGA ACCAGACCAG ACCAGCAGACCAC ACCAGACCAG ACCACTAGACCAG ACCACTAGACCAG ACCACTAGACCAC ACCAGCACAG ACCACTAGACCAC ACCAGCACAG ACCACTAGACCAC ACCACTAGACAC ACCACTAGACAC ACCACTAGACCAC ACCACTAGACAC ACCACTAGACACAC ACCACTAGACACAC ACCACTAGACACACAC ACCACTAGACACAC ACCACTAGACACAC ACCACTAGACACACAC ACCACTAGACACACAC ACCACTAGACACAC ACCACTAGACACAC ACCACTAGACACACAC ACCACTACACACACA	CACGGGGGC GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAGCOGTIGA GAGTTTCGTT GTGACCAG GAGCACAC CCGCACCACC CACCAGCACAC CACCAGCACAC CACCAGCACAC CACCAGCACA TATGGGTTGC CACCAGCACAT CACCAGCACAT CACCAGCACAT CACCAGCACC CACCACC CACCACC CACCACC CACCACC CACCAC	CCCAGGCGGC ACTGCCGGG ACTGCCGGG ACTGCCGGG GGATCCCCAC GTGGCGCCT GCACGGCCT TGCACGTGGCT GCCACGGCCT GCCACGGCCT GCCACGGCCT ACGGCTGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGATGGAAGG TCACGGATGGAAGG TCATGGAAGG TCTGGAAAGG TCTGGAAGG TCTGGAAGG TCTGGAAGG	ACGGATGAG GGGCTCAC GGGCCTCAC ATGGCTGCTC GGCCGAGAC CCCAGGGTG ACTGCCGTG GCCTGGACT GCCTGGGC GCGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGGGGT CACGGGGT CACGGGGT TCCCAGGAGGT TCCCTTACTC GAGCCAGGAT TCCCTGGGTA AGATTGAGC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1200
50 55 60	CCTCGCATISC GGTATCGTGG GCGACCTGGT GCCACCTGT GGCCCGGAAG GTGGATTTGC GTGGCAGGG GTGCAGGTGT GAGCCCGGTTC GGCCAGGTGT GCCAGGTGT GCCAGGTGT GCCAGGTGT GCCAGGTGC GCCCTGCGCC TCTCTTGCT CCAGGGGAGG TGACCCCTA TTAGTCCTGG GGACACTGCC AGCCTTCT	GCTIGGTGGT AGAGGCGGG GCTTGTTCT AGAGGCGGG GCTTGTTCT CTCAGGTGGGCG CCTCATCTCT TGCGGAGGCG CCTCAGCGCA TGGGCTGCT AGGCTGCCT AGGCTGCCT AGGCCTGAG GCTACCCCAG CCTAGGGATGG CCAGGAATGG AGGTCCCCTG CAGACAACCA CCCAGGCCAG CCTGGGCCGGG CCTGCGGGC CCTGGGCCGGG CCTGCGGGC CCCAGGCCAG CCCAGGCCAG CCCAGGCCAG CCCAGGCCAG CCCAGGCCAG CCCAGGCCAG CCCAGGCCAG CCCAGCCAG	CACCOGGGAC GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAGCOGTIGA GAGTTTCGTT GTGACCAG GAGCACAC CCGCACCACC CACCAGCACAC CACCAGCACAC CACCAGCACAC CACCAGCACA TATGGGTTGC CACCAGCACAT CACCAGCACAT CACCAGCACAT CACCAGCACC CACCACC CACCACC CACCACC CACCACC CACCAC	CCCAGGCGGC ACTGCCGGG ACTGCCGGG ACTGCCGGG GGATCCCCAC GTGGCGCCT GCACGGCCT TGCACGTGGCT GCCACGGCCT GCCACGGCCT GCCACGGCCT ACGGCTGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGATGGAAGG TCACGGATGGAAGG TCATGGAAGG TCTGGAAAGG TCTGGAAGG TCTGGAAGG TCTGGAAGG	ACGGATGAG GGGCTCAC GGGCCTCAC ATGGCTGCTC GGCCGAGAC CCCAGGGTG ACTGCCGTG GCCTGGACT GCCTGGGC GCGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGGGGT CACGGGGT CACGGGGT TCCCAGGAGGT TCCCTTACTC GAGCCAGGAT TCCCTGGGTA AGATTGAGC	120 180 240 300 360 420 660 660 6720 780 840 900 1020 1080 1140 1200
50	CCTCGCATISC GGTATCGTGG GCGACCTGGT GCCACCTGT GGCCCGGAAG GTGGATTTGC GTGGCAGGG GTGCAGGTGT GAGCCCGGTTC GGCCAGGTGT GCCAGGTGT GCCAGGTGT GCCAGGTGT GCCAGGTGC GCCCTGCGCC TCTCTTGCT CCAGGGGAGG TGACCCCTA TTAGTCCTGG GGACACTGCC AGCCTTCT	CCTIGOTGGT AGACCTAGA AGACCTAGA AGACCTAGA AGACCTAGA AGACCAGA ACCAGACCAG AGACCAGA ACCAGACCAG AGACCAGA ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCAGACCAG ACCACAGCCAG ACCACAGCCAG ACCACAGCCAG ACCACAGCCAG ACCACACCAC ACCAGCCAG	CACCOGGGAC GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAGCOGTIGA GAGTTTCGTT GTGACCAG GAGCACAC CCGCACCACC CACCAGCACAC CACCAGCACAC CACCAGCACAC CACCAGCACA TATGGGTTGC CACCAGCACAT CACCAGCACAT CACCAGCACAT CACCAGCACC CACCACC CACCACC CACCACC CACCACC CACCAC	CCCAGGCGGC ACTGCCGGG ACTGCCGGG ACTGCCGGG GGATCCCCAC GTGGCGCCT GCACGGCCT TGCACGTGGCT GCCACGGCCT GCCACGGCCT GCCACGGCCT ACGGCTGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGATGGAAGG TCACGGATGGAAGG TCATGGAAGG TCTGGAAAGG TCTGGAAGG TCTGGAAGG TCTGGAAGG	ACGGATGAG GGGCTCAC GGGCCTCAC ATGGCTGCTC GGCCGAGAC CCCAGGGTG ACTGCCGTG GCCTGGACT GCCTGGGC GCGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGGGGT CACGGGGT CACGGGGT TCCCAGGAGGT TCCCTTACTC GAGCCAGGAT TCCCTGGGTA AGATTGAGC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1200
50 55 60	CCTCGCATIGE GCTGACCTGT GCCGCGGAGG GCCACCTGT GGCCCGGAGG GTGGATTTGC TGGGCAGGG GGCAGCCGG GGCCCCCG GCCCTCG GCCCGGAGT TCCCTTGCT GCCAGGGGGGGGGG	GCTIGOTIGGT AGAGGCCIG CTGAGGGCGG GCTTCTTCTT CTCT TCCT TCGCGAGGCG GCTCTTCTCCT TGGCGAGGC TGGGTGGCTG AGGCCCTGGA GCTCCTGGA GCTCCTGGA GCTCCTGGA CCTCGGGC CCAGGATGGCT AGGCCCCGA AGGCCCCGA AGGCCCCGA AGGCCCCGA AGGCCCCGA AGGCCCCCT AGAGAACA ACTCTGGGGC CCAGGCAGGA ACTCTGGGGC CCAGGCAGGA ACTCTGGGGC CCAGGCAGGA ACTCTGGGGC CCAGGCAGGCA CCATCTGGGGC CCAGGCAGGCA CCATCTGGGGC CCAGGCAGGCA CCATCTGGGGC CCAGGCAGCA CCATCTGGGGC CCAGGCAGGCA CCATCTGGGGC CCAGGCAGCA CCATCTGGGGC CCAGGCAGCA CCATCTGGGGC CCAGGCA CCATCTGGGGC CCAGGCA CCATCTGGGGC CCAGGCA CCATCTGGGGC CCAGGCA CCATCTGGGGC CCATCTGGGGC CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CC	CACCOGGGAC GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAGCOGTIGA GAGTTTCGTT GTGACCAG GAGCACAC CCGCACCACC CACCAGCACAC CACCAGCACAC CACCAGCACAC CACCAGCACA TATGGGTTGC CACCAGCACAT CACCAGCACAT CACCAGCACAT CACCAGCACC CACCACC CACCACC CACCACC CACCACC CACCAC	CCCAGGCGGC ACTGCCGGG ACTGCCGGG ACTGCCGGG GGATCCCCAC GTGGCGCCT GCACGGCCT TGCACGTGGCT GCCACGGCCT GCCACGGCCT GCCACGGCCT ACGGCTGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGATGGAAGG TCACGGATGGAAGG TCATGGAAGG TCTGGAAAGG TCTGGAAGG TCTGGAAGG TCTGGAAGG	ACGGATGAG GGGCTCAC GGGCCTCAC ATGGCTGCTC GGCCGAGAC CCCAGGGTG ACTGCCGTG GCCTGGACT GCCTGGGC GCGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGGGGT CACGGGGT CACGGGGT TCCCAGGAGGT TCCCTTACTC GAGCCAGGAT TCCCTGGGTA AGATTGAGC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1200
50 55 60	CCTCGCATIGE GCTGACCTGT GCCGCGGAGG GCCACCTGT GGCCCGGAGG GTGGATTTGC TGGGCAGGG GGCAGCCGG GGCCCCCG GCCCTCG GCCCGGAGT TCCCTTGCT GCCAGGGGGGGGGG	GCTIGGTGGT AGAGGCGGG GCTTGTTCT CTCAGGTGGGCG GCTTGTTCT CTCAGGTGGGCG CTCAGGTGGGCG CTCAGGTGGGCC TGGGTGGCT AGGCCGAG GCTACCGAG GCTACCGAG GCTACCGAG CTAGGGATGG CCAGGGATGG AGGTCCCTGG AGGCCAG CCAGGCAG CCAGGCCAG CCAG	CACCOGGGAC GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAGCOGTIGA GAGTTTCGTT GTGACCAG GAGCACAC CCGCACCACC CACCAGCACAC CACCAGCACAC CACCAGCACAC CACCAGCACA TATGGGTTGC CACCAGCACAT CACCAGCACAT CACCAGCACAT CACCAGCACC CACCACC CACCACC CACCACC CACCACC CACCAC	CCCAGGCGGC ACTGCCGGG ACTGCCGGG ACTGCCGGG GGATCCCCAC GTGGCGCCT GCACGGCCT TGCACGTGGCT GCCACGGCCT GCCACGGCCT GCCACGGCCT ACGGCTGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGATGGAAGG TCACGGATGGAAGG TCATGGAAGG TCTGGAAAGG TCTGGAAGG TCTGGAAGG TCTGGAAGG	ACGGATGAG GGGCTCAC GGGCCTCAC ATGGCTGCTC GGCCGAGAC CCCAGGGTG ACTGCCGTG GCCTGGACT GCCTGGGC GCGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGGGGT CACGGGGT CACGGGGT TCCCAGGAGGT TCCCTTACTC GAGCCAGGAT TCCCTGGGTA AGATTGAGC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1200
50 55 60	CCTCGCATIGE GCTGACCTGT GCCGCGGAGG GCCACCTGT GGCCCGGAGG GTGGATTTGC TGGGCAGGG GGCAGCCGG GGCCCCCG GCCCTCG GCCCGGAGT TCCCTTGCT GCCAGGGGGGGGGG	GCTIGOTIGGT AGAGGCCIG CTGAGGGCGG GCTTCTTCTT CTCT TCCT TCGCGAGGCG GCTCTTCTCCT TGGCGAGGC TGGGTGGCTG AGGCCCTGGA GCTCCTGGA GCTCCTGGA GCTCCTGGA CCTCGGGC CCAGGATGGCT AGGCCCCGA AGGCCCCGA AGGCCCCGA AGGCCCCGA AGGCCCCGA AGGCCCCCT AGAGAACA ACTCTGGGGC CCAGGCAGGA ACTCTGGGGC CCAGGCAGGA ACTCTGGGGC CCAGGCAGGA ACTCTGGGGC CCAGGCAGGCA CCATCTGGGGC CCAGGCAGGCA CCATCTGGGGC CCAGGCAGGCA CCATCTGGGGC CCAGGCAGCA CCATCTGGGGC CCAGGCAGGCA CCATCTGGGGC CCAGGCAGCA CCATCTGGGGC CCAGGCAGCA CCATCTGGGGC CCAGGCA CCATCTGGGGC CCAGGCA CCATCTGGGGC CCAGGCA CCATCTGGGGC CCAGGCA CCATCTGGGGC CCATCTGGGGC CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CCAGGCA CCACCT CC	CACCOGGGAC GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAGCOGTIGA GAGTTTCGTT GTGACCAG GAGCACAC CCGCACCACC CACCAGCACAC CACCAGCACAC CACCAGCACAC CACCAGCACA TATGGGTTGC CACCAGCACAT CACCAGCACAT CACCAGCACAT CACCAGCACC CACCACC CACCACC CACCACC CACCACC CACCAC	CCCAGGCGGC ACTGCCGGG ACTGCCGGG ACTGCCGGG GGATCCCCAC GTGGCGCCT GCACGGCCT TGCACGTGGCT GCCACGGCCT GCCACGGCCT GCCACGGCCT ACGGCTGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGATGGAAGG TCACGGATGGAAGG TCATGGAAGG TCTGGAAAGG TCTGGAAGG TCTGGAAGG TCTGGAAGG	ACGGATGAG GGGCTCAC GGGCCTCAC ATGGCTGCTC GGCCGAGAC CCCAGGGTG ACTGCCGTG GCCTGGACT GCCTGGGC GCGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGGGGT CACGGGGT CACGGGGT TCCCAGGAGGT TCCCTTACTC GAGCCAGGAT TCCCTGGGTA AGATTGAGC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1200
50 55 60 65	CCTCGCATIGE GCTGACCTGT GCCGCGGAGG GCCACCTGT GGCCCGGAGG GTGGATTTGC TGGGCAGGG GGCAGCCGG GGCCCCCG GCCCTCG GCCCGGAGT TCCCTTGCT GCCAGGGGGGGGGG	GCTIGOTIGGT AGAGGCCIG CTGAGGGCG GCTTCTTCTT CTCTCTT CTCTCTCT TCGCGAGGCG GCTCAGGGC TGGGTGGCTG AGGCCCTGGG GGTTCTGGCT GGGTGGCTG GGGTCCTGGA GCTACCCCAG GCTTCGGGAGG CCAGGATGGCT CAGGAGAGGC CCAGGATGG CCAGGAGAGG CCTCGGGC CCAGGAGAGA	CACCOGGGAC GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAGCOGTIGA GAGTTTCGTT GTGACCAG GAGCACAC CCGCACCACC CACCAGCACAC CACCAGCACAC CACCAGCACAC CACCAGCACA TATGGGTTGC CACCAGCACAT CACCAGCACAT CACCAGCACAT CACCAGCACC CACCACC CACCACC CACCACC CACCACC CACCAC	CCCAGGCGGC ACTGCCGGG ACTGCCGGG ACTGCCGGG GGATCCCCAC GTGGCGCCT GCACGGCCT TGCACGTGGCT GCCACGGCCT GCCACGGCCT GCCACGGCCT ACGGCTGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGCTGGAAGG TCACGGATGGAAGG TCACGGATGGAAGG TCATGGAAGG TCTGGAAAGG TCTGGAAGG TCTGGAAGG TCTGGAAGG	ACGGATGAG GGGCTCAC GGGCCTCAC ATGGCTGCTC GGCCGAGAC CCCAGGGTG ACTGCCGTG GCCTGGACT GCCTGGGC GCGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGGACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGTGAACA CGGGGGGT CACGGGGT CACGGGGT TCCCAGGAGGT TCCCTTACTC GAGCCAGGAT TCCCTGGGTA AGATTGAGC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1200
50 55 60 65	CCTGCANTC GOTATCCTG GOCGACCACG GOCGACG GOCGACCACG GOCGACCACG GOCGACG GOCGACG GOCGACC GOCGACG GOCGACG GOCGACG GOCGACG GOCGACC GOCGACG GOCGACC GOCGACG GOCGACC GOCGACG GOCGACC GOCGACG GOCGACG GOCGACC GOCGACG GOCGACC GOCGACG GOCGACC GOCGACC GOCGACG GOCGACC GOCGACG GOCGACC GOCGACG GOCGACC GOCGACG GOCGACC GOCGACG GOCGACC GOCGACG GOCGACC GOCGACG GOCGACC GOC	GCCTGGTGGT AGAGGGGGC CCGAGGGGGG GCTCTTTCCT CCGAGGGGGG GCTCTTCCT TGGAGGGGG GCTCGAGGGGG GCTCGAGGGGG GCTCGAGGGGG CCGAGGGGG CCGAGGGGGGGGGG	CACCOGGGAC GOCCOGGGAC GOCCOGGGAC GOCCOGGGAC GOCCOGGGAC GOCCOGGAC GOCCOGCAC GOCCOGGAC GOCCOGCAC GOCCOGGAC GOCCOGCAC GOCCOGCAC GOCCOGCAC GOCCOC GOCCOGCAC GOCCOC GO	GAGCGGTGGA GACTTGGTT GTTGTTTGGTT GTGACCAGC GGAGTGGCAC GGAGTGGCAC GGAGTGGGCAC GGAGTGGGCAC GGAGTGGGCAC GGAGTGGGCAC CCCTTTTCCC GGGCCCCCT TGGGGCCCCC CCTTTTCCC GGGGCCCAC ACCGGCCAC TGGGCCCCCC CTGGCCCCCC CTGGCCCCCCC CTGGCCCCCCC CTGGCCCCCCC CCTTTCCC CCCTTTCCC CCCTTCCCC CCCTTCCCC CCCTTCCCC CCCTTCCCC CCCTTCCCCC CCCTTCCCCC CCCTTCCCCC CCCTTCCCCC CCCTTCCCCC CCCTTCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCCC GGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGGCCCCCC TGGCCCCCCC TGGGCCCCCC TGGCCCCCCC GGCCCCCC TGGCCCCCCC TGGCCCCCCC TGGCCCCCCC TGGCCCCCCC TGCCCCCCC TGCCCCCCCC	CCCAGGGGGG ACTGCCGGG ACTGCCGGG ACTGCCGGG ACTGCCGGG GCATCCCCAG AGGCGGTGGC AGGCGGTGGG CCCTGCGGGGCCC CCCTGACGG CCCTGACGGCC CCCTGACGGC CCCTGACGCC CCGGGGCACGGC CCGGGGCACGGC CAGGGACGGC CAGGGACGC CAGGGCACGC CGGGGCACGCG CGGGCACGCG CGGGCACGCG CGGGCACGCG CGGGCACGCG CCCTGACGCC CGGGCACGCG CCCTGGCC CCCTGACGCC CCCTGACGCC CCCTGCC CCTGCC CCCTGCC CCCTCC CCCTGCC CCCTGCC CCCTGCC CCCTCC CCCTCC CCCTGCC CCCTCC C	AGGGANTANA GGTCAACGT GGTCAACGT GGTCAACGT GGCCGAAGAT ACCGCTGCT GGCCGAAGAT ACCGCTGCT GGCCGAAGAT ACCGCGCT CCCGAAGGT CCCGAAGGT CCCGAAGGT CCCGGAAGGT CCCGAAGGT CCCCGAAGGT CCCGAAGGT CCCAAGGT CCCCAAGGT CCCAA	120 120 240 300 420 480 540 660 720 960 1020 1080 1140 1200 1320
50 55 60 65 70	CCTCGCANCE GCGANCTG GCGANCTG GCGANCTG GCGANCTG GCGANCTG GCGANCTG GCGANCTG GCGANCTG GCGANCTG GCCGANCTG GCCCGANCTG GCCCANCTG GCC	GCCTGGTGGT AGAGGGGGC CCGAGGGGGG GCTCTTTCCT CCCAGGTGGCGG GCTCGAGGGGG GCTCGAGTGGG GCTCGAGTGGGG AGGCCGAGGG AGGCCGAGGG AGGCCCGGG CCGAGGGGGGG AGGCCCGGG AGGCCCGGG AGGCCCCGG AGGCCCCGG AGGCCCCGG AGGCCCGGG AGGCCCCGG AGGCCCCGG AGGCCCCGG AGGCCCCGG AGGCCCCGG AGGCCCCGG AGGCCCCGG AGGCCCCGG AGGCCCGGG AGGCCCCGG AGGCCCGGG AGGCCCGGG ACCCCTGGGG ACCCCTGGGC CCGGGATGCG ACCCCTGGGC ACCCCTGGGC ACGCGGGG ACCCCTGGGG ACCCCTGGGC ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGGG ACGCGGG ACGCGGG ACGCG AGGG ACGCGGG AGGCG AGGG AGGCG AGGG AGGCG AGGG A	CACCOGGGAC GOGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAGCIGOTIGA GACTTIGITT GTIGACCAGG CONTROLLAGO CONTROLLAGO CONTROLLAGO GAGCICCOAC GAGCICC	CCCGAGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGG	AGSCRATGAR GOSTCALCEST GOSTCALCE GOSTCALCEST GOSTCALCE GOSTCALCEST GOSTCALCE GOS	120 180 240 300 480 540 660 720 940 940 960 1020 1140 1260 1320
50 55 60 65	CCTCGANTCC GCTATCCTGANTCC GCCCCACCTG GCCCCCACCTG GCCCCCCACCTG GCCCCCCACCTG GCCCCCCACCTG GCCCCCCACCTG GCCCCCCACCTG GCCCCCCCACCTG GCCCCCCCCACCTG GCCCCCCCCACCTG GCCCCCCCCCC	GCCTGGTGGT AGAGGGCGC CCGAGGGGGG GCTCTTTCCG GCTCTTTCCG GCTCGTGGTGGCT TGGCTGAGGGGG GCTCTTTCCG GCCCAGGGG TGGCCGAGGC TGGCCGAGGC TGGCCGAGGC TGGCCGAGGC GCGCAGGC GCGCAGGC GCGCAGGC GCGCAGGC CCCAGCCCA GCCCCAGCCC CCAGCCCAG ACCTCTGGCC GCGAGCCA CCATCTGGCC CCAGCCCAG CCAGCCCAG CCAGCCAG CCAGCCAG	CACCOGGGAC GENCOGGAC GENCOGCAC GENCOGGAC GENCOGCAC GENCOGGAC GENCO	AGCOGTOGA GACTTTGGTT GTTTGGTT GTTGGTT GTTGGTT GTGGTCGGC GGGCGCGC GGGCGCGCC GGGCCGCC GGGCCCCC GGGCCCCCC	CCCAGGGGGG ACTGCCCAGG ACTGCCCAGG ACTGCCCAGG ACTGCCCAGG ACTGCCAGG ACTGCCAGGGGG ACTGCCAGGGGGG ACTGCCAGGGGGGGGGG	AGGGANTANA GGOTCALCORI GGOTCAL	120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1020 1180 1200 1320
50 55 60 65 70	CCTOCANGE GCORACCIO GCORAC	GCCTGGTGGT AGAGGGCTCC AGAGGGCT AGAGGGCTCC AGAGGGCC CCCCACGGGCC CCCCACGGGCC AGGGCCC AGGGCCC CCCCACGGGCC CCCCACGGGCC CCCACGGGCC CCCACGGGCC CCCACGGCC CCCACGCC CCCCACGCC CCCACGCC CCCACGCC CCCACGCC CCCACGCC CCCACGCC CCCACGCC CCCCACGCC CCCACGCC CCCACGCC CCCACGCC CCCACGCC CCCACGCC CCCACGCC CCCCACGCC CCCACGCC CCCACGCC CCCACGC CCCCACGC CCCACGC CCCACGC CCCACGC CCCCCC CCCCC CCCCC CCCCCC CCCCC CCCCC CCCC	CACCOGGGAC GOCCOGGGAC GOCCOGGGAC GOCCOGGGAC GOCCOGGAC GOCCOGCAC GOCCOGCAC GOCCOGCAC GOCCOGCAC GOCCOC GOCCOGCAC GOCCOCCOC GOCCOC	AGGOGOTIGA GACTTIGITT GTTACCAGG GGCGCCAG GGGGCCCAG GAGGCCCCAG GAGGCCCCAG GAGGCCCCAG CGCACACAG GGGGCCCAG CGGGCCAA ACGGGGGCC CCTGGACCCT CCTGGACCT CCTGACCT CCTGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACT CCTGGACCT CCTGA	CCCGAGGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAA	AGGGARTANA GOSTCALCORT GOSTCAL	120 180 240 300 360 420 660 660 720 780 960 1020 1140 1260 1320
50 55 60 65 70	CCTCGACACC GCGACACCG GCGACACGG GCGCCACAGG GCGCCCACGG GCGCCCACGG GCGCCCACGG GCGCCACGG GCGCCACGG GCGCCACGG GCCCACGGC GCCCACGCC GCCCACGCC GCCCACGCC GCCCACGCC GCCCACGCC GCCCACGCC GCCCACGCC AGCCTTCC CCACGCCAC AGCCTTCC CCACGCC CACGCC CACGCC CACGCC CCACGC CCACGC CCACGC CCACCC CCACGC CCACC CCACGC CCACGC CCACC	GCCTGGTGGT AGAGGGCGC CCGAGGGGGG GCTCTTTCCG GCTCTTTCCG GCTCGTGGTGGCT TGGCTGAGGGGG GCTCTTTCCG GCCCAGGGG TGGCCGAGGC TGGCCGAGGC TGGCCGAGGC TGGCCGAGGC GCGCAGGC GCGCAGGC GCGCAGGC GCGCAGGC CCCAGCCCA GCCCCAGCCC CCAGCCCAG ACCTCTGGCC GCGAGCCA CCATCTGGCC CCAGCCCAG CCAGCCCAG CCAGCCAG CCAGCCAG	CACCOGGGAC GOACCTSGCC ACCTGCCCC ACCTGCCCC GOACCTGCCC GOACCTGCCC GOACCTGCCC ACCTGCCCC GOACCTGCCC GOACCTGCCC GOACCTGCCC GOACCTGCCC GOACCTGCCC GOACCTGCCCC GOACCTGCCC GOACCTCC GOACCTGCCC GOACCTCC	AGGOGOTIGA GACTTIGITT GTTACCAGG GGCGCCAG GGGGCCCAG GAGGCCCCAG GAGGCCCCAG GAGGCCCCAG CGCACACAG GGGGCCCAG CGGGCCAA ACGGGGGCC CCTGGACCCT CCTGGACCT CCTGACCT CCTGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACCT CCTGGACT CCTGGACCT CCTGA	CCCGAGGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAA	AGGGARTANA GOSTCALCORT GOSTCAL	120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1020 1180 1200 1320
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50 55 60 65 70	CCTOCANTOC GOTATOCTOCA GOTATOCTOCA GOTATOCTOCA GOTATOCTOCA GOTATOCTOCA GOTATOCTOCA GOTATOCTOCA GOTATOCTOCA GOTATOCTOCA GOTATOCA G	GCCTGGTGGT AGAGGCTCTA AGAGGCTCTA AGAGGCTCTA AGAGGCTCTA CCCCAAGGC CCCCAAGGC CCCCAAGGC AGGCCCTAAG AGAGCCTAAG AGAGCCTAAG AGAGCCCTAA AGAGCCCTAAG AGGCCCTAAG AGGCCCTAAG AGGCCCTAAG AGGCCCCTAA AGGCCCCTAC CCCAAGCCCAA AGGCCCCTAC CCCAAGCACAC CCCAAGCCCAC CCCAAGCCACAC CCCAAGCACAC CCCAAGCACAC CCCAAGCACAC CCCAAGCACAC CCCAAGCACAC CCAAGCACAC CCCAAGCACAC CCCAAGCAC CCCAACCAC CCCAACC	CACCOGGGAC GORACTESCOT GORACT GORACTESCOT GORACTESCOT GORACTESCOT	AGGOSTIGA GASTINIA GA	CCCGAGGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAA	AGGGARTANA GOSTCALCORT GOSTCAL	120 180 240 300 360 420 660 660 720 780 960 1020 1140 1260 1320
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50 55 60 65 70	CCTOCANTOC GOTATOCTOC GOTATOCTOC GOTATOCTOC GOTATOCTOC GOTATOCTOC GOTATOCTOC GOTATOCTOC GOTATOCTOC GOTATOCTOC GOTATOCT CCAGGOGGAG GOTATOCT CCAGGOGGAG GOTATOCT CCAGGOGGAG GOTATOCT CCAGGOGGAG GOTATOCT CCAGGOGGAG GOTATOCT CCAGGOGGAG GOTATOCT CCAGGOGGAG GOTATOCT CCAGGOGGAG GOTATOCT CCAGGOGGAG GOTATOCT CCAGGOGGAG GOTATOCT	GCCTIGNTGOT AGRICULTURA AGRICU	CACCOGGIAC GORACTESCOT GORACT GORACTESCOT GORACTESCOT GORACTESCOT GORACTESCOT GORACTESCOT	BAGOGOTIGA GAGORITAGA	CCCAGGGGGG ACTOCCOCCAG ACTOCCOCCAG ACTOCCOCCAG ACTOCCAG A	AGGIGATGAA GOTTAACGT ATGGTTATC AGGICTACT AGGIC	120 180 240 300 360 420 660 660 720 780 960 1020 1140 1260 1320
50 55 60 65 70	CCTOCATCO GOTATOCTO OTATOCT GO	GCCTIGGTGGT AGGCCTTGCT CCAGGTGGCC CCAGGGCCG CCAGGGCCG CCAGGGCCG CCAGGCCCG CCAGGCCGC CCAGGCCGC CCAGGCCGC CCAGGCCCG CCAGGCCCGC CCAGGCCCGC CCAGGCCCGC CCAGGCCCG CCAGCCCCG CCAGGCCCG CCAGCCCCG CCAGCCCCG CCAGCCCCG CCAGCCCCG CCAGCCCCG CCAGCCCCG CCAGCCCCG CCAGCCCCC CCAGCCCCG CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCCC CCAGCCC CAGCC CCAGCCC CCAGCC CCACCC CACCC CACCC CACCOGGIAC COCCOGGIAC COCCOCCOGGIAC COCCOGGIAC COCCOGGIAC COCCOGGIAC COCCOCOC COCCOCOC COCCOCCOC COCCOCOC COCC	AGACCIOTICA GACTITICATO GACTITICATO GACTITICATO GACTITICATO GACCICA GA	CCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	AGGIGANTANA GOTTOALOGIT AGGITALOGIT AGGITA	120 240 360 360 360 422 480 600 720 900 1020 1020 1260 1320	
50 55 60 65 70 75 80	CCTOCANTOC GOTATOCTOC GOTATOCT CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC CCAGGGAGG GOTATOCC CCAGGGGAGG GOTATOCC GOTATOCC CCAGGGGAGG LOCAGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GCCTIGNTGOT AGRICULTURA AGRICU	CACCOGGIAC GORGOGGIAC	AGOSTOGO GARAGOGO GARAGO GARAGOGO GARAGO GARAGO GARAGOGO GARAGOGO GARAGOGO GARAGOGO GARAGOGO GARAGOGO GARAGOGO	CCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	AGGIGATGAA GOTTAACGETT AGGITTAACGET AGGICTACT GOCCOGAGACT GOCCAGACAT GOCAGAGACT GOCAGACT GOC	120 180 240 300 360 420 660 660 720 780 960 1020 1140 1260 1320

	****	006443					
	WO 02/	O86443 GGATATCGAC	ATACCA NA AC	ACTATATCAT	CCCCAGTCCT	GGGTATAGAA	180
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5	TCTCTCTTGA	TGCCTCCATG TCATGGCTTG	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	ANACACCAGG	360 420
,	ACCCAGTGGA	CAATGCTGGG	CTTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
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	ACGAGTCTTC	TGACGTGAAC AGACGCTGCT	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
10	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TOGCTTCAGT	GGACCAGCCT	720
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	TGTTGTTAGT	GCTGGGCCTC GAATTACCGA	CTCCTGACGG	AAATCGTGCG	GTCTTGGTCG	CTTGCACTGA	840 900
	TTANGAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
15	TTTGCTCCAA	CGATGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCCTGGG	ATCAGCTGTT TTTCAGGAGA	PARTCCTCT	COCCACGA	TCARCETCE	CAGAAGATGA	1140 1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
20	AGAGTGTTCA	AAAAATCCGC	GAGGAGGAGC	GTCGGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAC	TGTGGGTGTG GACCCTGGGC	GCTCCCATTG	TGGTGGTGAT	TGCCAGOGTG	GTGACCTTCT	1380 1440
	TOTTYCAATTC	CATGACTTTT	CCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
0.5	AAGCCTCAGT	GGCTGTTGAC	AGATTTAAGA	GTTTGTTTCT	AATGGAAGAG	GTTCACATGA	1560
25	TARAGRACAR	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620 1680
	ACAAGAGGGC	CCACTCCAGT	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	ACCCCCCCCCC	GGCAGAGCAG	ARAGGCCACC	TOCTOCTOGA	CAGTGACGAG	CGGCCCAGTC	1800
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30	ACAGCATCGA	TCTGGAGATC	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1920 1980
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35	ACAGCTGCTG	CCTGAGGCCT	GACCTGGCCA	TTCTTCCCAG	CAGCGACCTG	ACGGAGATTG	2160 2220
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40	CCATTTTTAL	TAACCTGTTG	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
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	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
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45	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAACACCAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
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50	TGGATGAAGT	TGACGTGCGG	CIGCOGTICC	AGGCCGAGAT	GITCATCCAG	AACGITATCC	3120
	TGGTGTTCTT	CTGTGTGGGA	ATGATCGCAG	ACATIGICAC	CAGGGTCCTC	ATTOGGGAGG	3180
	TGAAGCGTCT	GGACAATATC	ACGCAGTCAC	CTTTCCTCTC	CCACATCACG	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	ANGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
55	AGCTGCTGGA	TGACAACCAA GGACCTCATC	GCTCCTTTTT	TTTTGTTTAC	CACGGGGGCTG	ATTATOTTO	3420 3480
	TTATGCACCG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAACCCCCCC	GTTCCAGTTT	ACCIOTCAGAC	TOGCATCTGA	GACAGAAGCT	CGATTCACCT	3600
60	CGGTGGAGAG	GATCAATCAC TCCCTCCCCT	TACATTAAGA	CTCTGTCCTT	GGAAGCACCT	GCCAGAATTA	3660 3720
00	AGRICAGGEA	CYCAGAAAAC	CTCCCTCTTG	TCCTAAAGAA	ACTATCCTTC	ACGATCAAAC*	3780
	CTAAAGAGAA	GATTGGCATT	GTGGGGGGGA	CAGGATCAGG	GAAGTCCTCG	CTGGGGATGG	3840
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65	TOTTCAGTGG	CACTGTCAGA	TCAAATTTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
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70	GTACCATGCT	CACCATTGCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
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	GTTCCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	CATTOCCTOC	CTGGGGGGGG	4500
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75	GTTCCGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTTCTTA	ATTGCACTCT	AAAAGGTTCA	4680 4740
	TCTATATATA	ATTATAATTG ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
00	STAGGGTTAT	AGCACTGTGC	TARTARCAGT	CCATATTCCT	TTCTATCATT	TTTGTACAGT	4860
80	TTGCTGTACT	AGAGATCTGG	TITTGCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCATTCTT	4920 4980
	ATACTAGCTGG	TGGTTTCACG	GIGCCAGGTT	COCTCCCCAC	AGCCGCTCCA	GGGGTGGCT	4980 5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGCAG	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCCTT	5100
85	CTGTCCTGGT	GTCACTTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCCT	5160
93	TITCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	ATCAGTCTAT	CCACAGAGAG	5220 5280
	TCCCACTGCC	TCAGGTTCCT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	CCACAGAGAG TCCAAGACCT	5340

	GTTGGTTCCA	AGCCCTGGAG	CCAACTGCTG	CTTTTTGAGG	TGGCACTTTT	TCATTTGCCT	5400
	ATTOCCACAC	CTCCACAGTT	CAGTGGCAGG	GCTCAGGATT	TCGTGGGTCT	GTTTTCCTTT	5460
	CTCACCCCACAG	TOGTOGCACA	CTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
	CACCTCTTGC	TAATCAGTGT	CTCACACTGG	CGTAGAAGTT	TTTGTACTGT	AAAGAGACCT	5580
5	ACCTCAGGTT	COTGGTTGCT	GTGTGGTTTG	GTGTGTTCCC	GCAAACCCCCC	TTTGTGCTGT	5640
-	GOGGCTGGTA	CCTCAGGTGG	GCGTGGTCAC	TGCTGTCATC	AGTTGAATGG	TCAGCGTTGC	5700
	AUCTOCTOAC	CARCTAGACA	TTCTGTCGCC	TTAGCATGTT	TGCTGAACAC	CTTGTGGAAG	5760
	CARABATCTG	BARATGTGAA	TAAAATTATT	TTGGATTTTG	AAAAAAAA	AAAAAAAA	5820
	AAAAAAAAA						

10 Seq ID NO: 194 Protein sequence: Protein Accession #: NP_005679.1

15	1	11	21	31	41	51	
	ī	Ĩ.	1	1	1	1	
	MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFRR	TRPLECQUAL	ETAARAEGLS	60
	I DE CHUCOT D	TIDDEUDKOK	VHHGLGALKP	IRTTSKHOHP	VDNAGLFSCM	TFSWLSSLAR	120
	UNITED OUT, OM	POWER, CERTS	SSDVNCRRLE	RLWOEELNEV	GPDAASLRRV	VWIFCRTRL1	180
20	LOTUCEMETO.	LAGESCRAFM	VKHLLEYTOA	TESNLCYSLL	LVLGLLLTEI	VRSWSLALTW	240
20	AT MANDENESSED T.	DOSTITURERY	KILKLKNIKE	KSLGRLINIC	ENDGORMPEA	AAVGSLLAGG	300
	MINIS TLOMIY	MUTTLGDTGP	LGSAUFILFY	PAMMPASRLT	AYFRRKCVAA	TDERVQKMIE	360
	THE WALKEART	VANUVARROS	VOKTREEERR	TLEKAGYFOG	ITVGVAPIVV	VIASVVTFSV	420
	VIIIIRFIRM	ACAPTICITIES	NSMTFALKVT	PPSVKSLSEA	SVAVDRPKSL	PLMEBVHMIK	480
25	THE PARTY OF THE PARTY	PHYMATT AWD	SCHESTONED	KLTPKMKKDK	RASRGKKEKV	RQLQRTEHQA	540
23	NKPASPHIKI	Inchespose	EEEGKHIHLG	HURLORTLHS	IDLEIOEGKL	VGICGSVGSG	600
	VLANDRORLID	OMENT TECRTA	ISGTFAYVAQ	CAWTINATIO	DNTL PGKEYD	EERYNSVLNS	660
	KTSLISAILG	CMIPPEGRI	RGANLSGGOR	OD TOTABALV	SDESTALLDD	PLSALDAHVG	720
	CCLRPDLAIL	PSSDLTEIGE	THOLOYLVDC	DEALEMKEAL	TTERGTHEEL	MNLNGDYATI	780
30	NHIFNSAIRK	HUNSKIVDEV	SGSQKKSQDK	CUNTOCUNAN	KANKBERGOL	VOLEEKGOGS	840
30	PNNLLCETP	PVEINSKRET	VIMALEMENV	COMP DOMINIT	CAMILAUGUS	TTUTRGNETS	900
	VPWSVYGVYI	QAAGGPLAFL	SMAUMLILKA	GSIAFSIWWD	I DA CODI DOD	T.PDDTT.DCPM	960
	VSDSMKDNPH	MCTAVELAND	EVDVRLPFQA	INGVVEVIGI	PROTONTACU	POWET-VAUGE	1020
	KPPDTTPTGR	ILNRFSKDMD	REDNITOSPF	EMPIQUATES	T A TOTAL PARTY	OPPLUDYORI.	1080
2.5	LVILFSVLHI	VSRVLIRELK	RUDNITOSPE	LSHITSSIQG	DAI INTING	TATOVAVOLT	1140
35	LDDNOAPFFL	FTCAMRWLAV	RLDLISIALI	TITGLMIVLM	HGQIPPAIAG	DETAINANT	1200
	GLFQFTVRLA	SETEARFTSV	ERINHYIKTL	SLEAPARIKN	KAPSPDWPQE	GEVTPENAEM	1260
	RYRENLPLVL	KKVSFTIKPK	EKIGIVGRIG	SGKSSLGMAL	LKPART2000C	IKIDGVRISD	1326
	IGLADLRSKL	SIIPQEPVLF	SGTVRSNLDP	PNOALEDGIM	DALERTHMER	CIAQLPLKLE	138
	SEVMENGONE	SVGERQLLCI	ARALLRHCKI	LILDRATAAM	DIRIDEPIGE	TIREMPADEL	1300
40	MLTIAHRLHT	VLGSDRIMVL	AQGQVVEPDT	PSVLLSNDSS	REYAMPAAAB	NKVAVKG	

Seq ID NO: 195 DNA sequence Nucleic Acid Accession #: NM_006470 Coding sequence: 228..1922

43							
	1	11	21	31	41	51	
	ī	ī	1	1	1	1	
	CONTROCTGA	GCCTGAGTAC	TCTAGCTGCC	TTGTCGCCAT	CGCATCTGGC	TGCCATCCAG	60
50	GGGGGAGGAGA	CACTAATCAC	TOGGOGAGGT	TCCTCTGGGA	GGGAGGAAAC	AGTTAAAATC	120
	THE CARCAGE	TYCK ATTCATC	TAGGCGTGGT	TCTCTTGTCT	GACTIGGGCT	GUALAGATCC	180
	TOTOGCC N N C/C	GACAGAAGAA	AGACAGCCTA	GGAGCAGAGC	CTCCCAGATG	GCTGAGTTGG	240
	A PROPER BATTORIC	TOCAGGGGCCA	CTGCCCAGGG	CCACTGCTCA	GCCCCCAGCC	CCTCTCAGCC	300
	CACACTCTYCC	CTCACCCAGC	CCAGATTCTG	GGTCAGCCAG	CCCAGTGGAA	GAAGAGGACU	360
55	TO CO COTO COTO	CONGNECTT	CCCACCGAGA	CGGAGGAACA	GGACAGCGAC	TCTGCAGAGC	420
	ACCCCCA TCC	TOCTOCTORS	CCCAAAGAGG	TCCTGTGTGA	CITCIGCCTT	GATGACACCA	480
	CARCACTCAR	CCCACTGAAG	TCCTGTCTAA	CCTGCATGGT	GAATTACTGT	GAAGAGCACT	540
	magaz coccos	TOTALOTOTALO	ATCABACTGC	AAAGCCACCT	GCTGACCGAG	CCAGTGAAGG	600
		COCKERN CTCC	CONGCOCACC	ACAGCCCACT	CTCTGCTTTC	TGCTGCCCTG	660
60	1 mar agr age	AND THE PROPERTY OF THE PROPER	CACTCTTCCC	AGGAGCACAG	TGGCCACACC	ATAGTCTCCC	720
	macan macan ac	CCCCAGGGAC	AAGGAGGCTG	AACTCCAGTG	CACCCAGTTA	GACTIGGAGE	780
	GG CTG	CONTRACTOR D	A ATCCCATCT	CCAGGCTCCA	GGCTAACCAA	AAGTCTGTTC	840
							900
	CONTRACCAR	GGCCCAGGCC	AATGTGATGC	TCTTCTTAGA	GGAGAAGGAG	CAAGCTGCGC	
65	MONOCON COC	CRACCICTATIC	AAGGCCCACC	TGGAGTACAG	GAGTGCCGAG	ATGGAGAAGA	1020
	GCAAGCAGGA	GCTGGAGAGG	ATGGCGGCCA	TCAGCAACAC	TGTCCAGTTC	TTGGAGGAGT	1140
	ACTGCAAGTT	TAAGAACACT	GAAGACATCA	CCTTCCCTAG	TGTTTACGTA	GGGCTGAAGG	1200
	ATAAACTCTC	GGGCATCCGC	AAAGTTATCA	CGGAATCCAC	TGTACACTTA	ATCCAGITGC	1260
	moon on home	TRACKARAGO	CTCCAGGAGT	TTTCCAAGGA	AGAGGAGTAT	GACATCAGAA	1320
70	CTCAAGTGTC	TGCCGTTGTT	CAGCGCAAAT	ATTGGACTTC	CAAACCTGAG	CCCAGCACCA	1380
	GGGAACAGTT	CCTCCAATAT	GCGTATGACA	TCACGTTTGA	CCCGGACACA	GCACACAAGT	1440
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	TCTCCTGGAG	CCTCCAATGG	AACGGGAAGG	AGTTCACGGC	CTGGTACAGI	GACATGGAGA	1740
	CCCCACTCAA	AGCTGGCCCT	TTCCGGAGGC	TCGGGGTCTA	TATCGACTTC	CCGGGAGGGA	1800
	TCCTTTCCTT	CTATGGCGTA	GAGTATGATA	CCATGACTCT	GGTTCACAAG	TTTGCCTGCA	1860
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	AGACTCCAGG	AGCCATATCC	CAGACCTTTC	CCAGCTACAG	TGATGGGAT	TGCATTTTAG	2040
	GGTGATTTGT	GGGCAGAAAT	AACTGCTGAT	GGTAGCTGGC	TTTTGAAATC	CTATGGGGTC	2100
	TCTGAATGAA	AACATTCTCC	AGCTGCTCTC	TTTTGCTCCA	TATGGTGCTG	TTCTCTATGT	2160
0.5	GTTTGCAGTA	ATTCTTTTT	TTTTTTTTG	GACGGAGTCI	CGCACTGTTC	CCCAGGCTGG	2220
85	AGAGCAGTGC	CGCGATCTTC	GCTCACTGC	AGCTCCGCCT	CCCGAGTTC	AGCAATTCTC	2220
	CTGCCTCAGG	CTCCCGAGT	GCTGGGATT	CAGGTGCCTG	CCACCACAC	CAGCTAATGT	2340
	TTTGTATTT	TAGTAGAGAT	GGGGTTTCA	CATGITGGCC	AGGCAGATC	CAAACTCCTG	2340

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5	COCCEDECT	GCACCCACCT GTTTGTAGTA TTCAGGTAAA AAAGATTGCA	ATTITUTE	ACCABATCEC	CCTCATCTTC	TAGTGCCATT	2400 2460 2520
		196 Proteir cession #: 1					
10	DSAFOGDPAG	11 PLPRATAQPP EGKEVLCDFC	LDDTRRVKAV	KSCLTCMVNY	CEEHLOPHOV	NIKLOSHLLT	60 120
15	EPVKDHNWRY LDLERKLKLN EQAALSQANG VGLKDKLSGI EPSTREQPLQ	CPAHHSPLSA ENAISRLQAN IKAHLEYRSA RKVITESTVH YAYDITFDPD	PCCPDQQCIC QKSVLVSVSB BMEKSKQELB LIQLLENYKK TAHKYLRLQB	QDCCQEHSGH VKAVAEMQFG RMAAISHTVQ KLQEFSKEEE ENRKVINTIP	TIVSLDAARR ELLAAVRKAQ FLEBYCKPKN YDIRTQVSAV WEHPYPDLPS	DKEABLQCTQ ANVMLFLEEK TEDITFPSVY VQRKYWTSKP RFLHWRQVLS	180 240 300 360 420 480
20	SDMETPLKAG NA IR IVDLGE	PPRRLGVYID EPEKPAPSLG	PPGGILSPYG VTAP	VEYDTMTLVH	KFACKPSEPV	YAAFWLSKKE	540
25	Nucleic Ac:	197 DNA sec id Accession uence: 433-	1 #: NM_0043				
	1	11	21	31	41 	51 	
30	CCCGAGACCC	GGCGCAAGAG	AGOGCAGCCT	TAGTAGGAGA	GGAACGCGAG	ACGCGGCAGA	60 120
30	GCGCCAGCGG	CAGCCTCACA	CGCGAGCGCC	ACGCGAGGCT	CCCGAAGCCA	ACCCGCGAAG	180
	DODDAGGGGG	AGGGAGGAGG	AGGCGGCGTG	CAGGGAGGAG	AAAAAGCATT	TTCACCTTTT	240
	TTGCTCCCAC	TCTAAGAAGT	CTCCCGGGGA	TTTTGTATAT	TOCACCCAAG	TTCCGTCAGG	3 <i>0</i> 0 360
35	GTCCCCCTCG	CGGGCCCCGC	ACCTCGCGTC	CCGGATCGCT	CTGATTCCGC	GACTCCTTGG	420
	CCGCCGCTGC	GCATGGAAAG	CTCTGCCAAG	ATGGAGAGCG	GCGGCGCCGG	CCAGCAGCCC	480 540
	CAGCCGCAGC	CCCAGCAGCC	CTTCCTGCCG	CCCGCAGCCT	CTTTCTTTGC	GCAGGGGGGGGA	540 600
	CAGCAGCAGC	AGCAGCAGCA	GCAGGCGCCG	CAGCTGAGAC	CGGCGGCCGA	CGGCCAGCCC	660
40	TCAGGGGGGG	GTCACAAGTC	AGCGCCCAAG	CAAGTCAAGC	GACAGCGCTC	CTCTTCCCCC	720
	GAACTGATGC	GCTGCAAACG CCGCCGTGGC	CCGGCTCAAC	TTCAGCGGCT	TTGGCTACAG	CANGTEGGE	780 840
	AACCTGGGCT	TTGCCACCCT	TOGGGAGCAC	GTCCCCAACG	GCGCGGCCAA	CARGAAGATG	900
							960
45	GACGAGCATG	ACGCGGTGAG	CGCCGCCTTC	CAGGCAGGCG	TCCTGTCGCC	CACCATCTCC	1020 1080
	COCCARCTACT	CCAACGACTT CTTACGACCC	GAACTCCATG	GECGGETEGE	AGCTTCTCGA	CTTCACCAAC	1140
	TGGTTCTGAG	GGGCTCGGCC	TGGTCAGGCC	CTGGTGCGAA	TGGACTTTGG	AAGCAGGGTG	1200
c0	ATOTO CACAAC	CTCCATCTTT	P CALAST CALABADACAD	TOTCAGTGGG	GTTGGGAGGG	GGAGAAAAGG	1260
50	AAAAGAAAAA	AAAAGAAGAA	GAAGAAGAAA	AGAGAAGAAG	AAAAAAACGA	AAACAGTCAA GAAAACGGGA	1320
							1440
	ACCREAGRED	ATCCCCA NA N	TOCACCTTCT	GTGCDADAGC	AGTGGGCTCC	TGGCAGAAGG	1500
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60	Seq ID NO: Protein Ac	198 Protei cession #:	n sequence: NP_004307				
	1	11	21	31	41	51	
	MEGGAVMEGG	GAGQQPQPQP	OODELDDAAC	PRATAAAAA	AAAAAAAA	0000000000	60
65	QQQQAPQLRP AVARRNERER	AADGQPSGGG NRVKLVNLGF LSPTISPNYS	HKSAPKQVKR	QRSSSPELMR AANKKMSKVE	CKRRLNPSGF	GYSLPQQQPA ALQQLLDEHD	120 180
70	Nucleic Ac	199 DNA se id Accessio uence: 1-10	n #: NM_0070	015			
	1	11	21	31	41	51	
75	1	1	1	1	1		
75	ATGACAGAGA	ACTCCGACAA CGGCGTACGC	AGTTCCCATT	GCCCTGGTGG	GACCTGATGA	CGTGGAATTC	60 120
							180
	GCCTTCTACT	TCTGGAAGGG	GAGCGACAGT	CACATTTACA	ATGTCCATTA	CACCATGAGT	240
80	ATCAATGGGA	AACTACAAGA	TGGGTCAATG	GAAATAGACG	CTGGGAACAA	CTTGGAGACC	300 360
ου	TITAAAATGG	GAAGTGGAGC GTTTTGCTGG	TURAGRAGEA ACCACAGAGA	TOCTACATTA	AAGCGCAAGT	GAAGGCTCGT	420
	ATTCCTGAGG	TGGGCGCCGT	GACCAAACAG	ACCATCTCCT	CCAAACTGGA	AGGCAAGATC	480
	ATGCCAGTCA	AATATGAAGA	AAATTCTCTT	ATCTGGGTGG	CIGIAGAICA	GCCTGTGAAG	540
85	GACAACAGCT	CCTATCCAAA	TAAGGTGTTA	GAACTCTGCG	GIGACCTICC	AAGAAAAATT	600 660
05	GTTCCA ACTA	CCACAAAAAA	ACCACACAGT	GGACCACGGA	GCAACCCAGG	CGCTGGAAGA	720
	CTGAATAATG	ANACCAGACO	CAGTGTTCAA	GAGGACTCAC	AAGCCTTCAA	TCCTGATAAT	780

5 10 15	CONTROL OF THE PROPERTY OF THE	NO CARACTECTS 960 CARACTECTS 960 CARACTECTS 1080 CATTERATOR 1080 CATTERATOR 1180 CATTERATOR 1200 CATTERATOR 12
25	LENETREVQ EDSQAFNEDN PYMQQUESM IFDERNAMA ICCIDAR GGYYPNPYNY QGCRSACRVI MPCSWWVARI LGMV	SY TECONICEPL 300
	Nucleic Acid Accession #: NM_000728.2 Coding sequence: 112495	51
30	GTAATAAGAG CGGGGTCTCC GCGGGGAAGG CGCCCACAGC AGGTGTGG GTCGACCGGC CGCTCGAGAC TCTAGTCGCC AGAGAGG CGGAAGTTCT CCCCCTTCCT GGCTCTCAGT ATCTTGGTCC TGTACCAG	GC GGCAGCCTC 180 CAC ACTCAGTAAA 240
35	GAGGACGCC GCTCCTGCT GGCTGCACTG GTCCAGGCT ATTACAGG AGACTGAAGC AGGAGCAGGA GACACAGGGC TCCAGCTCCG CTGCCCAG AGACTGCCA CCTGTGTGAC TCATCGGCTG GCAGGCTTGC TGAGCAG GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTTGG GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTTGGC	AT GRANGCERGE 360 ATC AGGGGGGCATG 420 CAG GCGCCGCAGG 480 TTA AATCCAATGA 540
40	CATATCCTTA TANGAGNITC ACTCAGAIGA CACATUTGGA GAGAGUE AGGAGGCA AGCCAGGA AGTCTGTGTC TACCAGAGC CAGAATC TGGAAGAGA GCAGCCTGC TGACACCTAG AGTTTGGACT TCCAGCTI GAGAATAATT TCTGTTGTTT TAGCCACA AGTTTGGACT AATTGGT CADATUTAT TCAGTAGTT TCAGTTTAT TCGGTAAAT GCCTTGG	ACA GAACAGTCTC 660 FCC AGAACTGTGA 720 FAT GACAGCCCTA 780 AGT GGGATTGCTG 840
45	GGTTATTIGG AAAGTGIGTA TITAACTCTG TAAGAAACTI CCAAACTI ACTIGACCAC TICGCCTTCT TGCCAGCCAC AIATGAGAGC CTCHAGTAI GTATGTAGCA GTATCTCATT GCTGTTTTAA TITGTATTC CCCAATGI AGCATCTATT TTACCATATG TTATCACCT TIATTGAGGG GTCTGTT. TAGACCAT	TTT TCCGAGIG 960 TTT CCACAATAG 960 ACT AATGACGTTG 1020 TAA ATCTTCTGCT 1080 TCT TTATATGTTG 1140
50	TEGATECAG ATTETTTCA GATATATAT TREGARACTI CUTTUCU TRECTITTC ATTITCTAG CAGNOTCIC CACAGADAA AGTTOT CCAATCAT CITTITTT CUTTATOTA TOGGCTIT AGTTCAT CACATCAT CACATCAT CACATCAT CACATCAT CACATCAT CACATCAT CACATCAT CACATCAT CACATCAT	AAT TTGAATAAGA 1260 3TC TAAGAACTCT 1320
55	TRISONAPPO ATATTATAT GENARTHAN GENERATTI GROTINA TRISONAPPO ATATTATA GROTINA TRISONAPPO GENERATTI GROTINA TRISONAPPO ATATTATA GENERAT TRISONAPPO AGRICIAN TRICOCATTI ARTECOCCE CONCENT. TRISONAPPO ATATTATO GENERATI ATATTATO GENERATI ATATTATO GENERATI ATATTATO GENERATI ATATTATO GENERATI ATATTATO GENERATI ATATTATO GENERATI ATATTATO GENERATI ATATTATO TRISONAPPO ATATTATO O ATATTATATO ATATTATATATA	ATT CATTGATTTG 1620
60	TICTGATGAG ATTITTAATG GGATTGTGT AAGTCAGTGG GTTAATTCA CATATTAATA ATATTAAGTC GTTCAATTCA TGAACACAAT ACATGIT CATATTAATA ATATTAAGTC GTTCAATTCA TGAACAC	TTC ACTTATTTAG 1920
65	GTTTTCTCG TTTTTTTTT ITTALAGNOUT TTTTCGTGCT ARTGTAL ATTTTTGTT TTAATTGTC ATTGCTGCTA GATAGNATA CANTATT ARAAANANA RAANANANAN ANNANANANA Seq ID NO: 202 Protein sequence:	TAA AATATTAGGA 2100
70	Protein Accession 8: NP_000719.1 1 11 21 31 41	51
75	MOFRKESPEL ALSILVLYQA GSLQAAPERS ALESSEDPAT LSKEDA KASELKQEQE TQGSSSAAQK RACNTATCVT HRLAGILLSRS GGMVKS RREDLQA	RLLL ÄALVQDYVQM 60 NFVP TNVGSKAPGR 120
80	Seq ID No: 203 DNA sequence Nucleic Acid Accession #: NM_001741 Coding sequence: 71496 1 11 21 31 41	51
85	CTCTOGCTOG ACGCCGCCGC CGCCGCTCCC ACCGCCTCTG ATCCAAGCGCGCGC ACGCCGCTCCC ACCGCCTCTC ACCGCCACCACCACCACCACCACCACCACCACCACCACCA	BAGA GCAGCCCAGC 180 BCAC TGGTGCAGGA 240

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	GGAGGACTTC	AGATCTAAGC AACAAGTTTC	ACACGTTCCC	CCAAACTGCA	ATTGGGGTTG	GAGCACCTGG	360 420 480
_	CCAGAATGCC	GATATGTCCA AACTAAACTC	CTCCCTTTCC	TTCCTAATTT	CCCTTCTTGC	ATCCTTCCTA	540
5	TTCCTTGTGG	CATGTGGTTT	CTCAAACTTC	AGATGGGAGG	AAAGAGAGCA	GGACTCACAG	600 660
	GTTGGAAGAG	AATCACCTGG GAGCTCCTCT	GAAAATACCA	GAAAATGAGG	GCCGCTTTGA	GTCCCCCAGA	720 780
10	TATTTTTCCC		diccident	TOWNTOTOCI	unichiliun	0000000000	
10				•			
	Seq ID NO: Protein Ac	204 Protei: cession #: 1	sequence: P_001732				
15	1	11	21	31	41	S1	
	MGFQKFSPFL	ALSILVLLQA	GSLHAAPFRS	ALESSPADPA	TLSEDEARLL	LAALVQDYVQ	60
20	MKASELEQEQ DMSSDLERDH	EREGSSLDSP RPHVSMPQNA	RSKRCGNLST N	CMLGTYTQDP	NKPHTFPQTA	IGVGAPGKKR	120
20	Seq ID NO:	205 DNA 860	quence				
	Nucleic Ac Coding seq	id Accession uence: 1-94	1 #: NM_0053	61			
25	1	11	21	31	41	51 	
	ATGCCTCTTG	AGCAGAGGAG GCCTGGTGGG	TCAGCACTGC	AAGCCTGAAG	AAGGCCTTGA	GGCCCGAGGA	60 120
20	TCCTCTTCTA	CTCTAGTGGA	AGTTACCCTG	GGGGAGGTGC	CTGCTGCCGA	CTCACCGAGT	180
30	CCTCCCCACA	GTCCTCAGGG ATGAGGGCTC	AGCCTCCAGC	GAAGAGGAGG	GGCCAAGAAT	GTTTCCCGAC	240 300
							360 420
	AGAAATTGCC	ATCGAGCCAG AGGACTTCTT	TCCCGTGATC	TTCAGCAAAG	CCTCCGAGTA	CTTGCAGCTG	480
35	GTCTTTGGCA	TCGAGGTGGT TCTCCTACGA	GGAAGTGGTC	CCCATCAGCC	ACTIGIACAT	CCTTGTCACC	540 600
	CTCCTGATAA	TOGTCCTGGC	CATAATCGCA	ATAGAGGGGG	ACTGTGCCCC	TGAGGAGAAA	660
	CATCCCAGGA	AGCTGAGTAT AGCTGCTCAT	GCAAGATCTG	GTGCAGGAAA	ACTACCTGGA	GTACCGGCAG	720 780
40	GTGCCCGGCA	GTGATCCTGC TGAAAGTCCT	ATGCTACGAG	TTCCTGTGGG	GTCCAAGGGC	CCTCATTGAA	840 900
	TACCCACCCC	TGCATGAACG	GGCTTTGAGA	GAGGGAGAAG	AGTGA		
45	Seq ID NO: Protein Ac	206 Protein cession #: 1	n sequence: NP_005352				
45	Seq ID NO: Protein Ac	206 Protein cession #: 1	n sequence: NP_005352 21	31 	41 1	51 I	
-	Protein Ac	cession #: 1 11 KPEEGLEARG	NP_005352 21 EALGLVGAQA	PATEEQQTAS	 SSSTLVEVTL	GEVPAADSPS	60
45 50	Protein Ac	11 KPEEGLEARG	NP_005352 21 EALGLVGAQA	PATEEQQTAS	SSTLVEVIL	GEVPAADSPS	120 180
-	Protein Ac MPLEORSONC PPHSPOGASS LLKYRAREPV CLGLSYDGLL HPRKLLMODL	11 KPEEGLEARG FSTTINYTLW TKAEMLESVL GDNQVMPKTG VQENYLEYRQ	NP_005352 21 EALGLVGAQA RQSDEGSSNQ RNCQDFFPVI LLIIVLAIIA	PATEEQQTAS EEEGPRMPPD FSKASEYLQL IEGDCAPEEK	SSSTLVEVTL LESEFQAAIS VFGIEVVEVV IWEELSMLEV	GEVPAADSPS RKMVELVHPL PISHLYILVT PEGREDSVPA	120
-	Protein Ac MPLEORSONC PPHSPOGASS LLKYRAREPV CLOLSYDGLL	11 KPEEGLEARG FSTTINYTLW TKAEMLESVL GDNQVMPKTG VQENYLEYRQ	NP_005352 21 EALGLVGAQA RQSDEGSSNQ RNCQDFFPVI LLIIVLAIIA	PATEEQQTAS EEEGPRMPPD FSKASEYLQL IEGDCAPEEK	SSSTLVEVTL LESEFQAAIS VFGIEVVEVV IWEELSMLEV	GEVPAADSPS RKMVELVHPL PISHLYILVT PEGREDSVPA	120 180 240
50	Protein Ac I PERSONCE PPHSPQGASS LLKYRAREPV CLGLSYDGLL HPRKLLMQDL YPPLHERALR Seq ID NO: Nucleic Ac	11	NP_005352 21	PATEEQQTAS EEEGPRMPPD FSKASEYLQL IEGDCAPEEK PLWGPRALIE	SSSTLVEVTL LESEFQAAIS VFGIEVVEVV IWEELSMLEV	GEVPAADSPS RKMVELVHPL PISHLYILVT PEGREDSVPA	120 180 240
50 55	Protein Ac I PERSONCE PPHSPQGASS LLKYRAREPV CLGLSYDGLL HPRKLLMQDL YPPLHERALR Seq ID NO: Nucleic Ac	11	NP_005352 21	PATEEQQTAS EEEGPRMPPD FSKASEYLQL IEGDCAPSEK FLWGPRALIE	SSSTLVEVTL LESEFQAAIS VRGIEVVEVV IWEKLSMLEV TSYVKVLHHT	GEVPAADSPS RKMVELVHPL PISHLYILVT PEGREDSVFA LKIGGEPHIS	120 180 240
50	Protein Ac I I I MPLEQRSQHC PPHSPQGASS LLKYRAREEV CLGLSYDGLL HERKLIMODL HERKLIMODL NUCLEIC AC Coding seq I	11 REPEGLEARG FSTINYTLW TKARMLESVL GDNQVMPKTG VQENYLEYTQ EGEE 207 DNA seid Accessionuence: 743	NP_005352 21	PATECOTAS EEEOPRMFPD FSKASEYLQL IEGDCAPEEK FLWGPRALIE	SSSTLVEVIL LESEPÇAAIS VFGIEVVEVV IWEKLSMLEV TSYVKVLHHT	GEVPAADSPS GEVPAADSPS REMVELVHPL PISHLYILVT PEGREDSVPA LKIGGEPHIS	120 180 240 300
50 55	PROTEIN AC I MPLEQRSQHC PPHSPQGASS LLKYPARREPV CLGLSYDGIL HPRKLLMQDL YPPLKERALR Seq ID NO: Nucleic Ac Coding seq 1 AAAGGAAGGG	11 KPEEGLBARG PSTTINYTLW TKABMLESVIL GDNQVMPKTG VQENYLEYRQ EGEE 207 DNA sei id Accessiouence: 743-:	NP_005352 21 EALGLVGAQA RQSDEGSSNQ RNCQDFFFVI LLITVLATIA VPGSDPACYE quence n #: NM_021: 2893 21 AAAAGGAGAAAA	PATERQUIAS EBEGGRMFPD FSKASEYLQL IEGDCAPBEK FLMGPRALIE	SSSTLVEVTL LESEPOAAIS VFGIEVVEVV IWEELSMLEV TSYVKVLHHT	GEVFAADSPS REMVELVHPL PISHLYILVT PEGREDSVFA LKIGGEPHIS	120 180 240
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50 55	Protein Ac I	11 KPEEGLEARG PSTIINYTHW TKAEMLESVL GDNQWMPKTG VQENYLEYRQ EGEE 207 DNA sei dd Accession uence: 743-: 11 AGGGAGGAGGAG TTAGGAGGGC CTGGTGTTCTT CCTTACCTCC GAGAGAGTGG	NP_005352 21	PATERQUIAS PATERQUIAS PATERQUIAS PERCENTED PSKASEYLQL IEGDCAPEE FLMGPRALIE 115 31 TTGGTTTAGA GTCTGACAGC CCAAGATGCT AGCCCGGAG CCCCAGTTCC	SSSTLVEVTL LESEPQAAIS VFGIEVVEVV TSYVKVLHHT 41	GEVPAADSPS GEVPAADSPS GEVPAADSPS GEVPAADSPS JEGRESSVFA LKIGGEPHIS 51 ACGAGCTTTG CCTAAATCTC CGGAAATGCT	120 180 240 300 60 120 180 240 300
50 55 60	Protein Ac I MILEORSONC PPHSPQGASS LLKYRAREEV LLGLSYDGLL YPPLHERALR Seq ID NO: A Coding seq I AAAGGAAGGG GGGACCGCC CCCAAACTAA CCCTTGGGT GCACCCTGGAG GGGAGGTG	11 PERCHERAGE PARCE PARCE	NP_005352 21	PATEDOTAS EEEGPRMPPD PSKASEYLQL ILGDCAPEEK PLMGPRALIE 31 TTGGTTTAGA GTCTGACAGC CCCAGTTCC CTCTGCACAT	SSTIVEVIL LESEFOAAIS VFGIEVVEVV IWESLISMLEV TSYVKVLHHT 41 GGCCAGCCGG AGGTGAAGGT CTTCCCGAGG AGAGGCAGTCT CACAGTCGG	GEVEAADSPS RKMVELVHPL PISHLYILLVI PEGREDSVFA LKIGGEPHIS 51 ACGAGCTTTG CCTAAATCTC GAGATGCTA CCTGGCAAAGA CGCAAGGA CGCACTGTC	120 180 240 300
50 55 60 65	Protein Ac I MPLEQRSQHC PPHSPQGASS LLKYRAREPV CLGLSPYDGLL HPRKLMXDBL VPFLHERALR Seq ID NO: Nucleic Ac Coding seq Coding seq GGOACGSCCC CCAAACTAA CCCTTGGGT GCACCCTGGAA AGGGGGGGCGCCC ACGGCGCCT ACGGCTGCTA TTGGGTCCAAG	11 PERCOLARIO	NP_005352 21	PATEDOTAS EEEGPRMPPD PSKASEYLQL IEGDCAPEEK PLMGPRALIE 31 1 TOGTTTAGA GTCTGACAGC CCCAGTTCC CTCTGCACAT GCAGCCTTG GCAGCTGAGG	SSSTLVEVIL LESEFQAAIS VFGIEVVEVV IWESLISMLEV TSYVKVLHHT 41 GGCCAGCCGG AGGTGAAGGT CTTCCCGAAGG AGAGGCAGTCC CACGAGTCGC CACGAGTCGC CCCCAAGG CCCAAGGCCA CCCCAAGGCCA CCCCAAGGCCA CCCCAAGGCCA CCCCAAGGCCA CCCCAAGGCCA CCCCAAGGCCA	GEVPAADSPS RIGWELVHPL PISBLYTLUT PEGGEDSVFA LKIGGEPHIS 51 ACGGCTTTG GAGANGCTAG GUGGAAGGG CUTGAAATGCTAG GAGACGGTGT AGAAACTGCC CCTCCGCAGC	120 180 240 300 60 120 180 240 300 360 420 480
50 55 60	Protein Ac I MPLEGREGHC MP	11 KPEBGLEARG KPEBGL	NP_05352 21 1 EALGLIVANAN EALG	PATEROOTAS EEGGRMPPD FSKASEYLQL TEGCAPEK FLMGPRALIE 115 31 TTGGTTTAGA GTCTGACAGC CCAAGATGCT CTCTGCACAT GCACGCTTGCACAT GCACGCTTTGCACAT GCACGCTTGCACAT GCACGCTTGCACAT GCACGCTTGCACAT GCACGCTTGCACAT GCACGCTTGCACAT GCACGCTTCACACAT GCACGCTTCACACAT GCACGCTTCACACAT GCACGCTTCACACAT GCACCCACAT GCACCCACAT GCACCCACACC GCACCCACCACC GGACCCCACCC GGACCCCCACC GGACCCCCACC	SSTILVEVIL LESEPOANIS VPGIEVVEVIL LESEPOANIS VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEVVEVIL VPGIEV VPGIE	GEVEAADSPS RIGWELVHPL PISBLYTLY PEGREDSVFA LKIGGEPHIS 51 ACGGCTTTG GAGANGCTAG GUGGAAGGG CUTGAAAATGCTAG GAGACGGTGT AGAAAATGCTAG GAGACGGTGT CAGCCCTGTC AGAAACTGCC CCTCCCCCCCC CCTCCCCAGC AGGAGGCATC AGGAGGCATC	120 180 240 300 60 120 180 240 300 420 480 540 500
50 55 60 65	Protein Ac I MPLEGREGHC MP	THE CONTROL OF THE CO	NP_05352 21 1 EALGLIVAGAA EALGLIVAGAA ROGERSSENQ ENCODEPPVI LLTIVLAITA VPG5DFACTS TUPENCE A # I: NM_021: 883 21 1 AAAGGAGAAG TTCTCCTCTTT TOCCTCTAGA TTGCCTCTCTTT TOCCTCTAGC COGGGGGACCC COGGGGACCC COGGGGACCC COGGGGACCC COGGGGACCC COGGGACCC COGGCACCCAC COGGACCC COGGCACCCAC COGGACCC COGGCACCCAC COGGACCC COGGCACCCAC COGGACCCAC COGCACCAC COGGACCCAC COGCACCAC COGGACCCAC COGGACCCAC COGGACCCAC COGGACCCAC COGGACCCAC COGCAC COGGACCCAC COGGACCCAC COGGACCCAC COGGACCCAC COGGACCCAC COGGA	PATEROTAS EEGGRAPPO FEKASEYLÖL IEGDCAPSIK FLMGPRALIE 115 31 TTGGTTTAGA GTCTGACAGC CCCAGATGCC CCCAGGTGCC CCCCAGGTGC GCAGCTGAG GCACCCTTG GCAGCTGAG GCACCCTG GCAGCTGAG GGACCCCATG GCAGCTGAG GGACCCCATG GCAGCTGAG GGACCCCATG	SSTILVEVIL LESERGAAIS VEGIEVVEVV IWESLISMLEV TSYVKVLEHT OCCCAGCAGCCGG AGFTGAAGGT AGAGGCAGTCG CAGGAGATCG CCCCAGAAGACAC CCTACAACAC CCTACACAC CCTACAACAC CCTACACAC CCTACACAC CCTAC	GEVFAADSPS RKWVELVHPL PISRLYTLVT PEGREDSVFA LKIGGEPHIS S1 ACGAGCTTTG CCAAAGC CCGCAAAGC CCGCAACCCCTGTC AGAGCCTGTC AGAGCCCC	120 180 240 300 60 120 180 300 340 480 540 660
50 55 60 65 70	Protein Ac Principal Control PERSON #: 1 11 12 12 13 14 15 15 15 16 17 17 17 17 17 17 17 17 17	NP_005352 21 1 EALGLIVIAGA EAL	PATEROTAS EEGGRAFPD FASSETUL IEGGCAPEK FIMGPRALIE 115 31 1 TOGSTTAAA GTCTUACAGC CCAARGAGC CCCAARGAGC GCACCCTTTAGA GCACCCTTAGA GTCTUACAGC CTCTUACAGC GCACCTTTAGA GCACCCTTTAGA GCACCCTTTAGA GCACCCTTTAGA GCACCCTTTTAGA GCACCCTTTTAGA GCACCCTTTTAGA GCACCCTTTTAGA GCACCCTTTTAGA GCACCCTTTTTAGA GCACCCTTTTTAGA GCACCCTTTTTTAGA GCACCCTTTTTTAGA GCACCCTTTTTTAGA GCAGCCCCCC GGAGCCCCCC GGAGGCCCCCC GGAGGCCCCCC GGAGGCCCCCC GGAGGCCCCCC	SSSTIVEVTL LESEROALS VEGIEVEEV IMBELSMLEV TSYVEVLMET TSYVEVLMET 41 GCCCACCAGG AGGTGAAGGC TCACCAGGAGGA CCCAGGAGGA CCCCCCAGA CCCCCCCAGG CCCCCCCAGGAGGA CCCCCCCAGGAGGAA CCCCCCCC	GEVPAADSPS RKWELVHPI. PISHLYILVY PEGREDSVPA LKIGGEPHIS S1 ACHAGCTTIG ACHAGCTTIG COTANANCIC GAGATGCTA CTGGCAAAGA CGGAAGTGCT CTGCCAAAGA CGGCACCCT AGAGGCCAGA CCTCCCCCTCTCCT AGAGGCCAGA CCGCACCCCT AGAGGCCAGA CCAGCCCCCAT	120 180 240 300 120 180 240 360 480 540 660 720	
50 55 60 65	Protein Ac I PRIMEROGICE PRINSPONS PRIMERO PRINSPONS Req I No. Req I No. Red I No. Re	Dession #: 1 11 12 13 14 15 17 17 17 17 17 17 17 17 17	NP_005352 21 21 21 21 21 21 21 22 22 23 24 24 24 21 21 21 21 21 21 21 21 21 21 21 21 21	PATEROTAS EEGERHPPP PATEROTAS EEGERHPPP PSKASETLGI IEGGCAPEK 115 31 THE PATEROTAS GEOGRAPH GEOGRA	SSSTIVEVTL LESSEQALIS VEGLEVEZ INVELENTE TSYVEVLENT TSY	GENPAADSPS RIONELVIEL FISHLYLIN FERRENSVFA LITICATE LACAGETTTE CHARTCHAR 120 180 300 60 120 180 300 360 480 540 660 720 780 840 840	
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50 55 60 65 70 75	Protein Ac I PRIEGROUGE PRINGOASS LLEYTAREPY CLALEYTOGLA PRINGOASS LLEYTAREPY CLALEYTOGLA PROTEIN PROLEGATION MUCIEI AC COCING ANAGOMOCO COCOMOCTA COCOMOCT	cession #:1 The continue of the continue of	RP_005352 21 EALSTAVOADA ROBESSENO	PATEROTAS EEGERHPPP PATEROTAS EEGERHPPP PENASETLAI IEROCAPEK 115 115 115 116 117 117 117 117	SSSTLVEVIL LESSEQALIS LESSEGALIS VEGIEVEVEL LESSEGALIS VEGIEVEVEL TSTVEVILIST 15 VEGIEVEVEL GOCCAGCOG GOCCAGCOG CTTCCCCAGC CCCCAACA CCCCCAACA CCCTCCAACA CCTCCAACA CCCTCCAACA CCTCCAACA CCCTCCAACA CC	ST COMPACTOR OF COMPACT OF COMPAC	120 180 240 300 60 120 240 300 420 360 420 720 840 960 1020
50 55 60 65 70	Protein Ac I PRESENCIA I PRES	Dession #: 1 11 12 12 13 14 17 18 18 18 18 18 18 18 18 18	RP_005352 I I I I I I I I I	PATEROTAS EEGERHPPP PATEROTAS EEGERHPPP PENSASEILGI IEGECAPER 115 115 115 116 117 117 117 117	SSSTIVISVIL LESSEDALIS SSSTIVISTIC SSSTIVIS LESSEDALIS SS	GENPAADS PROMETURE IN THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF T	120 180 240 300 60 120 180 360 480 660 660 720 780 900 960
50 55 60 65 70 75	PROCESS AC PRISOCASS INTERPRETATION PRISOCASS LIMITABEUR SEQ ID NO NUCLOIC AC COLING ME SEQ ID NO NUCLOIC AC COCAMACTICA COCTITION ACCOCCAMACTICA COCTITION ACCOCCAMACTICA ACCO	CONTRACTOR CONTRA	RP_065352 21 1 ELICITYON ARGENTS SHOW ARGENT SHOW ARGENTS SHOW ARGENTS SHOW ARGENTS SHOW ARGENTS SHOW ARGENT SHOW ARGENTS SHOW ARGENTS SHOW ARGENTS SHOW ARGENTS SHOW ARGENT	PATEROTAS EEGGRAPPP PATEROTAS EEGGRAPPP PINGRALIE 11520-CAPEK PINGRALIE 115 115 115 115 115 115 115 116 117 116 117 116 117 116 117 116 117 116 117 116 117 116 117 117	SSSTIVEVIL LESSEGALIS VEGIEVORY TYSTIEVEN TYSTIEVEN TSTVAVLHET TST	SI ACAGACTTTG COTAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	120 180 240 300 120 180 240 360 600 600 6720 780 900 1080 1020 1080 1140 1200
50 55 60 65 70 75	Protein Ac PRINCIPAL	CONSTRUCTION OF TO ACCUMACO A A ACCUMACO A A ACCUMACO A A ACCUMACO A A ACCUMACO A A A ACCUMACO A A A A A A A A A A A A A A A A A A	RP_005352 I L L L L L L L L L L L L L L L L L L	PATEROTAS BEDGERNEPD PATEROTAS BEDGERNEPD PERCENTER PERCENTER PERCENTER PERCENTER PERCENTER PERCENTER PERCENTER PERCENTER PERCENTAGE PERCENTER PER	SESTIVISTIL LESSEDALIS SESSIVISTIL SESSIVISTICA SESSIVISTIL LES SESSIVISTICA S	STANDARD SPRINGER STANDARD SPRINGER SPR	120 180 240 300 60 120 180 240 300 340 660 720 780 900 901 901 902 1140 11260 11320 11320
50 55 60 65 70 75	Process Ac INTERPROCESS INTERPR	CONTRACTOR CONTRA	RP_065352 I L L L L L L L L L L L L L L L L L L	PATEROTAS BERGERIA PO BERGERIA	SESTIVESTIL LESIEROAL IS SESTIVESTIL LES SESTIVESTIL LES SESTIVESTIL LESIEROAL IS SESTIVESTIL LES SESTIVES SESTI	STANDARS REPORTED THE TOTAL OF	120 180 240 300 60 120 180 300 420 420 420 420 420 960 1080 1140 1200 1200 1200

	GCATGACAAG	GACAGGATGA	COGTTCACAG	CGGGCAGACC	AACAAGTCAG	CTCTTCTCTA	1620
	CGACTCCCTT	CAAACCGAGA	GTGTCCCTTT	TGAGGGCCTG	CTGAGCGAAG	GCAACACCAT	1680
	CCGCATCGAG	TTCACGTCCG	ACCAGGCCCG	GGCGGCCTCC	ACCTTCAACA	TCCGATTTGA	1740 1800
5	AGCGTTTGAG	AAAGGCCACT TATAACATTG	GCTATGAGCC	CTACATCCAG	AATGGGAACT	COCLOTACATC	1860
,	GGACCAGGGC	CCGGCCATCA	TOGASTGCAT	CAATCTGCGG	GACCCATACT	GGAATGACAC	1920
	AGAGCCCCTG	TGCAGAGCCA	TGTGTGGTGG	GGAGCTCTCT	GCTGTGGCTG	GGGTGGTATT	1980
	GTCCCCAAAC	TGGCCCGAGC	CCTACGTGGA	AGGTGAAGAT	TGTATCTGGA	AGATCCACGT	2040
10	GGGAGAAGAG	AAACGGATCT	TCTTAGATAT	CCAGTTCCTG	AATCTGAGCA	ACAGTGACAT	2100
10	CTTGACCATC	TACGATGGCG CAGAAACTGT	ACGAGGTCAT	GCCCCACATC	TTGGGGCAGT	ACCTTGGGAA	2160
	CAGTGGCCCC	CAGAAACTGT	ACTCCTCCAC	GCCAGACTTA	ACCATCCAGT	TCCATTCGGA	2220
	CCCTGCTGGC	CTCATCTTTG	DARAGGGCCA	CATCCAGAAT	CCCTCCAAAA	CCACCTCCCA	2340
	CACCGACTTC	GTGCGGGGAG	CCAGAATCAC	CTACCAGTGT	GACCCCGGCT	ATGACATOGT	2400
15							2460
	TGAGAAAATT	ATGTACTGCA CTGCTGGTGG	CCGACCCCGG	AGAGGTGGAT	CACTCGACCC	GCTTAATTTC	2520
	GGATCCTGTG	CTGCTGGTGG	GGACCACCAT	CCAATACACC	TGCAACCCCG	GTTTTGTGCT	2580
	TGAAGGGAGT	TCTCTTCTGA	CCTGCTACAG	CCUTGAAACA	GGGACTCCCA	TCTGGACGTC	2640 2700
20	TOGCCTGCCC	CACTGCGTTT ATCTTCATCC	CAGAAGCGGC	AGCAGAGACG	TCGCTGGAAG	CACCCTACAT	2760
20	TTACATCACA	AGATGTCGCT	ACTATTCCAL	CCTCCGCCTG	CCTCTGATGT	ACTCCCACCC	2820
	CTACAGCCAG	ATCACCCTCC	ABACCGAGTT	TGACAACCCC	ATTTACGAGA	CAGGGGGAAC	2880
	CCAAAAGGTT	TAGGGTTTCA	TTTAAAAAGA	GGTACCCTTT	AAAAAGGGGC	TTGTGAACTC	2940
~ -	AACCCCAATT	TAGGGTTTCA TCCCCGAGAC	ATTTATCCAA	AGGCCCTGGG	GGCCTTGATT	TARACCCCCA	3000
25	AAAGGCGGCT	GTTTTTTGGT	TAAACTTTTT	AACAAAGGGT	TACGGGTTTT	TTCCCCGGAT	3060
	TTAAAATT	TTAAAAGTG					
	Sea ID NO:	208 Protein	sequence:				
30	Protein Acc	cession #: 1	IP 066938				
	1	11 .	21	31	41	51	
		SPMALMDKGE		000000000000000000000000000000000000000		DAT CONCERNA	60
35	PROVINGENY	PLLPLNNFLE	CTYNUTUYTG	AGALILATII	NISDGRLLSI	RGVDGPTLTV	120
-	LANOTLLVEG	OVIRSPINTI	SVYFRTFODD	GLGTPOLHYO	AFMLSCNFPR	RPDSGDVTVM	180
	DLHSGGVAHF	QVIRSPINTI HCHLGYELQG	ARMITCINAS	KPHWSSQEPI	CSAPCGGAVH	NATIGRVLSP	240
	CADEMENTOCO	POTESTUADE	CUALTITUDED	TALLUTATION	VUSCOTNESA	LLYDSLOTES	300
40	VPFEGLLSEG	NTIRIEPTSD HSLEQGPAII	QARAASTFNI	RPEAPERGHC	YEPYIONGNP	TTSDPTYNIG	360 420
40	TIVEFTCDPG	IHVGEEKRIF	ECTIVAEDDAM	NDTEPLCRAM	ELMBUTT COV	TOMOGROWS S	480
	CCTDDLTYOU	INVGERERIT	RECOGRIMMAL	RASBNUSCED	LPRIONGWET	TSHTELVEGA	540
	RITYOCDPGY	HSDPAGLIFG DIVGSDTLTC	OWDLSWSSDP	PECEKIMYCT	DPGEVDHSTR	LISDPVLLVG	600
							660
45		FVLEGSSLLT AYIYITRCRY					660
45	VLIISLLLGG	AYIYITRCRY	YSNLRLPLMY				660
45	VLIISLLLGG Seg ID NO:	AYIYITRCRY	YSNLRLPLMY Tuence	SHPYSQITVE			660
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45 50	VLIISLLLGG Seq ID NO: Nucleic Ac:	AYIYITRCRY	YSNLRLPLMY YSNLRLPLMY Tuence 1 #: NM_001	SHPYSQITVE		GGTQKV	660
	VLIISLLLGG Seq ID NO: Nucleic Ac:	AYIYITRCRY 209 DNA second Accession	YSNLRLPLMY YSNLRLPLMY Tuence 1 #: NM_001	SHPYSQITVE			660
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	TTIQYTCNPG VLIISLLEGG Seq ID NO: Nucleic Ac: Coding seq	AYIYITRCRY 209 DNA secid Accession uence: 89-6:	CYSRETGIPI YSNLRLPLMY Zuence 1 #: NM_001: 31 21	SHPYSQITVE 327.1 31 GAGAATACCT	TEFONPIYET 41	S1 GACCTTCTCT	60
50	TTIQYTCNPG VLIISLLEGG Seq ID NO: Nucleic Ac: Coding seq	AYIYITRCRY 209 DNA secid Accession uence: 89-6:	CYSRETGIPI YSNLRLPLMY Zuence 1 #: NM_001: 31 21	SHPYSQITVE 327.1 31 GAGAATACCT	TEFONPIYET 41	S1 GACCTTCTCT	60 120
	TIQYTCNPG VLIISLLLGG Seq ID NO: Nucloic Ac: Coding sequ AGCAGGGGGC CTGAGAGCCG GACGGGCGAT	AYIYITRCRY 209 DNA sected Accession uence: 89-6: 11	YSNLRLPLMY Tuence 1 #: NM_001: 31 21 CCGAGAATAC CCGGAGCCAT CAGGAGGCCAT	SHPYSQITVE 327.1 31	41 CGTGGGCCCT GGCCGGGCA GATGGCCCAG	S1 GACCITCICI CAGGGGGITC CAGGGGGITC CAGGGGGITC	60 120 180
50	TIQYTCNPG VLIISLLLGG Seq ID NO: Nucloic Ac: Coding sequ AGCAGGGGGC CTGAGAGCCG GACGGGCGAT	AYIYITRCRY 209 DNA sected Accession uence: 89-6: 11	YSNLRLPLMY Tuence 1 #: NM_001: 31 21 CCGAGAATAC CCGGAGCCAT CAGGAGGCCAT	SHPYSQITVE 327.1 31	41 CGTGGGCCCT GGCCGGGCA GATGGCCCAG	S1 GACCITCICI CAGGGGGITC CAGGGGGITC CAGGGGGITC	60 120 180 240 300
50	TTIQTTCNPG VLIISLLIGG Seq ID NO: Nucleic Ac: Coding sequ AGCAGGGGGC CTGAGAGCGG GACGGCGAT TGGCGGCCCA AAGGGCCTCA AAGGGCCTCA CTTGAATGGA	PULBUSSLUT AYIYITRCRY 209 DNA sec id Accession usnce: 89-6: 11 GCTGTGTGTA GGCAGAGGCT GCTGATGGCC GGAGAGGCGGGG GGGCCGGGAG GGGCCGGGAG GGGCCGGGAG	TYSNLRLPLMY TYSNLRLPLMY TUENCE 1 #: NM_001: 1 21 CCGGAGCATA CCGGAGCCAC CAGGAGCCCC GTGCCACGGG GAGGGCCCC GTGCCACGGG GAGGGCCCCACGGG GAGGGCCCCACGGG GAGGGCCCCACGGG	SHPYSQITVE 327.1 31 GAGAATACCT GCAGGCCGAA TGGCATTCCT CGGCAGAGGT GCGGGGTCCG GGGGGCCGGAGAGGT	41 	S1 GACCITCTCT CAGGGGTTC CAGGGGCATGC CGGCTTCAGG	60 120 180 240 300 360
50	TIIQTICHE VLIISULIGE Seq ID NO: Nucloic Ac: Coding sequil AGCAGGGGGC CTGAGGGGCGT TGGCGGCCCA AAGGGCCTCG GCTGAATGGA	PVLEGGSLLT AYIYITRCRY 209 DNA sec id Accession uence: 89-6: 11 GCTGTGTGTA GGCAGAGGCT GCTGATGGCC GGGAGAGGCG GGGCCGGAG TGCTGCAGAT TGCTGCAGAT	TYSNLRLPIMY TYSNLRLPIMY TYSNLRLPIMY THE PIN M 001: 1 #: NM 001: 21 CCGAGAATAC CCGAGGCAT CAGGAGGCCAT CAGGAGGCCCC GCGGGGCCAG GAGGGGCCCC GCGGGGCCAG CACCATGGA	SHPYSQITVE S127.1 31 GAGAATACCT GCAGGCGAA TGGCATCCT CCCCCAGAGGT CCGCGGGGTCCG GGGGCCGGAG AGCAGAGGT AGCAGAGGT	41 Garagecca Garagecca Garagecca Garagecca Garagecca Garageca Garageca Garageca Garageca Garageca Garageca Garageca Garageca	51 GACCTICTCT CAGGGGTTC CAGGGGCATGC CGCCTTCAGG TTGAGTTCTA	60 120 180 240 300 360 420
50	TIQUTCHE Seq ID NO: Nucleic Ac: Coding sequilibrian AGCAGGGGG CTGAGGCGG AGGGGCGAT TGGCGGCCCA AGGGGCTGG CCTGAATGGA CCTCGCCATG	PVLESSELT AYIYITRCRY 209 DNA sec dd Accession uence: 89-6: 11 GCTGTGTGTA GGCAGAGGGG GGCCCGGAG GGGCCGGAG GGCCCGGAG GGCCCGGAG CGCTGCTGCAGAT CCTTTGCGAAT	TYSNERLPIMY TYSNERLPIMY TYSNERLPIMY TYSNERLPIMY THE STATE OF THE STATE	SHPYSQITVE 327.1 31 GAGAATACCT GCAGGCCGAA TGGCATTCCT CGGCAGAGGT GGGGCCGGAG AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT	41 	S1 GACCTTCTCT CAGGGGATGC CAGGGGTTCAGG TTCAGGTCTA CCTGGCCCA RETCCGGCCAGCAGC CAGGCGGAGAGC CAGGCGGAGAGC CAGGCGAGAGCAGAGCAGAGAGAG	60 120 180 240 300 360 420 480
50	TIQUTCHE Seq ID NO: Nucleic Ac: Coding sequilibrian AGCAGGGGG CTGAGGCGG AGGGGCGAT TGGCGGCCCA AGGGGCTGG CCTGAATGGA CCTCGCCATG	PVLESSELT AYIYITRCRY 209 DNA sec dd Accession uence: 89-6: 11 GCTGTGTGTA GGCAGAGGGG GGCCCGGAG GGGCCGGAG GGCCCGGAG GGCCCGGAG CGCTGCTGCAGAT CCTTTGCGAAT	TYSNERLPIMY TYSNERLPIMY TYSNERLPIMY TYSNERLPIMY THE STATE OF THE STATE	SHPYSQITVE 327.1 31 GAGAATACCT GCAGGCCGAA TGGCATTCCT CGGCAGAGGT GGGGCCGGAG AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT AGCAGAGGT	41 	S1 GACCTTCTCT CAGGGGATGC CAGGGGTTCAGG TTCAGGTCTA CCTGGCCCA RETCCGGCCAGCAGC CAGGCGGAGAGC CAGGCGGAGAGC CAGGCGAGAGCAGAGCAGAGAGAG	60 120 180 240 300 360 420 480 540
50	Seq ID NO: Nucleic Ac: Coding seq I AGCAGGGGGA TGGGGGGA TGGGGGGA TGGGGGGCA AGGGGCGA AGGGCCTG GCTGAATGGA CCTCGCCATG GATGGCCCATG GATGCCCA CATACTGACT CTCTCCCAG	PVLEGGSLLT 209 DNA set id Accession uence: 89-6: 11 GCTGTGTGTA GGCAGAGGCG GGCAGAGGCG GGAGAGGCG GGCCGGGAG CGTTCCGGA CCGTTCCGGA CAGCTTCCG CAGCTTCCGCA CAGCTTCCCG CAGCTTCCCGCA CAGCTTCCCGCA CAGCTTCCCCC CCGCTACCCCCCCCCC	TYSHURLPLMY TYSHURLPLMY TYSHURLPLMY TYSHURLPLMY THE STATE OF THE STATE	SHPYSQITVE SHPYSQITVE 327.1 J GAGAATACCT GCAGGCCGAA TOGCATCCT COGCCAGAGCTCCG GGGGCCGCAG GCCCGCAG GCTCTCTGAAG CCACCGCCAA GATCAGCCAG GCCCCACAGCTCCCCCACAGCCCACACCCCCACACCCCCACACCCCCACACCCCCC	41	S1 GACCTTCTC CAGGGGGTTC GGGCAATGC CAGGGGCAG GCCTTCAGG TTGAGGTTCTA GCCTGGCCA TGTCGGCAG CATCAGGTC CAGGGTTTTT CTGAGGTCT CAGGGTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCAGGTC	60 120 180 240 306 420 480 540 600
50 55 60	Seq ID NO: Nucleic Ac: Coding seq I AGCAGGGGGA TGGGGGGA TGGGGGGA TGGGGGGCA AGGGGCGA AGGGCCTG GCTGAATGGA CCTCGCCATG GATGGCCCATG GATGCCCA CATACTGACT CTCTCCCAG	PVLEGGSLLT 209 DNA set id Accession uence: 89-6: 11 GCTGTGTGTA GGCAGAGGCG GGCAGAGGCG GGAGAGGCG GGCCGGGAG CGTTCCGGA CCGTTCCGGA CAGCTTCCG CAGCTTCCGCA CAGCTTCCCG CAGCTTCCCGCA CAGCTTCCCGCA CAGCTTCCCCC CCGCTACCCCCCCCCC	TYSHURLPLMY TYSHURLPLMY TYSHURLPLMY TYSHURLPLMY THE STATE OF THE STATE	SHPYSQITVE SHPYSQITVE 327.1 J GAGAATACCT GCAGGCCGAA TOGCATCCT COGCCAGAGCTCCG GGGGCCGCAG GCCCGCAG GCTCTCTGAAG CCACCGCCAA GATCAGCCAG GCCCCACAGCTCCCCCACAGCCCACACCCCCACACCCCCACACCCCCACACCCCCC	41	S1 GACCTTCTC CAGGGGGTTC GGGCAATGC CAGGGGCAG GCCTTCAGG TTGAGGTTCTA GCCTGGCCA TGTCGGCAG CATCAGGTC CAGGGTTTTT CTGAGGTCT CAGGGTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCAGGTC	60 120 180 240 300 360 420 480 540
50	Seq ID NO: Nucleic Ac: Coding seq I AGCAGGGGGA TGGGGGGA TGGGGGGA TGGGGGGCA AGGGGCGA AGGGCCTG GCTGAATGGA CCTCGCCATG GATGGCCCATG GATGCCCA CATACTGACT CTCTCCCAG	PVLEGGSLLT 209 DNA set id Accession uence: 89-6: 11 GCTGTGTGTA GGCAGAGGCG GGCAGAGGCG GGAGAGGCG GGCCGGGAG CGTTCCGGA CCGTTCCGGA CAGCTTCCG CAGCTTCCGCA CAGCTTCCCG CAGCTTCCCGCA CAGCTTCCCGCA CAGCTTCCCCC CCGCTACCCCCCCCCC	TYSHURLPLMY TYSHURLPLMY TYSHURLPLMY TYSHURLPLMY THE STATE OF THE STATE	SHPYSQITVE SHPYSQITVE 327.1 J GAGAATACCT GCAGGCCGAA TOGCATCCT COGCCAGAGCTCCG GGGGCCGCAG GCCCGCAG GCTCTCTGAAG CCACCGCCAA GATCAGCCAG GCCCCACAGCTCCCCCACAGCCCACACCCCCACACCCCCACACCCCCACACCCCCC	41	S1 GACCTTCTC CAGGGGGTTC GGGCAATGC CAGGGGCAG GCCTTCAGG TTGAGGTTCTA GCCTGGCCA TGTCGGCAG CATCAGGTC CAGGGTTTTT CTGAGGTCT CAGGGTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCAGGTC	60 120 180 240 360 420 480 540 600
50 55 60	Seq ID NO: Nucleia Ac- coding seq l ACAGGGGG CTNAAGGGGG CTNAAGGGGGA AGGGGGAA AGGGGCAA AGGGGCAA AGGGGCAA	PVLEGISSLIT AYINITRCRY 209 DNA set id Accession usence: 89-6: 11 GCTGTGTGTA GGCAGAGGGT GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA ACCGGTTCCC CCTCAGGGC CCTGAGGGC CCTGAGGGA GGGGGGGGGG	TYSNICHPLMY TRUCKER TO THE TO	SHPYSQITVE SHPYSQITVE 327.1 J GAGAATACCT GCAGGCCGAA TOGCATCCT COGCCAGAGCTCCG GGGGCCGCAG GCCCGCAG GCTCTCTGAAG CCACCGCCAA GATCAGCCAG GCCCCACAGCTCCCCCACAGCCCACACCCCCACACCCCCACACCCCCACACCCCCC	41	S1 GACCTTCTC CAGGGGGTTC GGGCAATGC CAGGGGCAG GCCTTCAGG TTGAGGTTCTA GCCTGGCCA TGTCGGCAG CATCAGGTC CAGGGTTTTT CTGAGGTCT CAGGGTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCAGGTC	60 120 180 240 360 420 480 540 600
50 55 60	Seq ID NO: Nucleic Ac: Coding seq AGCAGGGGGC TGGGGCGAT TGGCGCCCA AAGGGCCTGGATGGA CCTGGATGGAT GGATGCCCCA CATACTGACT CGTTGTCCCAG GCTCCTCCC Seq ID NO:	PVLESSSLLT AYINITRCRY 209 DNA set 1d Accession uence: 89-6: 11 GCTGTGTGTA GGCAGAGGGT GCTGATGGCC GGAGAGGCG GGGCCGGAG TGCTGCAGA CGGCTTCCCG ATCCGACTTCCG ATCCGACTTCC CCTTCAGGC CCCTCAGGGC CTAGGGAATGA CAGCTTTCCC CCTCAGGGC CTAGGGAATGA CAGCTTTCCC CCTCAGGGC CTAGGGAATGA CAGCTTTCCC CCTCAGGGC CTAGGGAATGA CAGCTTCCCC CCTCAGGGC CTAGGGAATGA CAGCTTCCCC CCTCAGGGC CTAGGGAATGA CAGCTTCCCC CCTCAGGGC CTAGGGAATGAA CAGCTTCCCC CCTCAGGGC CTAGGGAATGAA CAGCTTCCCC CCTCAGGGC CTAGGGAATGAA CAGCTTCCCC CCCTCAGGGC CTAGGGAATGAA CAGCTTCCCC CCCTCAGGGC CTAGGGAATGAAGAC 210 Protein	TYSNELPIMY THERE IS M. OOL 1 S: NM_OOL 21 COGAGAATAC COGAGGCAT CAGGAGGCCC GTGCCACGGG GAGGGCCCC GCGGGGCCAC GAGGGCCCC GCGGGGCCAC GCGCGACCAC GAGGGCCCC GCGGGGCCAC GGCTACAAC GCCTACAAC AGAGGCCAC GCCTACAAC TO TO TO TO TO TO TO TO TO TO TO TO TO T	SHPYSQITVE SHPYSQITVE 327.1 J GAGAATACCT GCAGGCCGAA TOGCATCCT COGCCAGAGCTCCG GGGGCCGCAG GCCCGCAG GCTCTCTGAAG CCACCGCCAA GATCAGCCAG GCCCCACAGCTCCCCCACAGCCCACACCCCCACACCCCCACACCCCCACACCCCCC	41	S1 GACCTTCTC CAGGGGGTTC GGGCAATGC CAGGGGCAG GCCTTCAGG TTGAGGTTCTA GCCTGGCCA TGTCGGCAG CATCAGGTC CAGGGTTTTT CTGAGGTCT CAGGGTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCAGGTC	60 120 180 240 360 420 480 540 600
50 55 60	Seq ID NO: Nucleic Ac: Coding seq AGCAGGGGGC TGGGGCGAT TGGCGCCCA AAGGGCCTGGATGGA CCTGGATGGAT GGATGCCCCA CATACTGACT CGTTGTCCCAG GCTCCTCCC Seq ID NO:	PVLEGISSLIT AYINITRCRY 209 DNA set id Accession usence: 89-6: 11 GCTGTGTGTA GGCAGAGGGT GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA GGGCCGGGA ACCGGTTCCCG ATCGGACTGA ACCGGCTTCCC CCTTAGGGAC CCTTAGGGAC GGGGGGGGGG	TYSNELPIMY THERE IS M. OOL 1 S: NM_OOL 21 COGAGAATAC COGAGGCAT CAGGAGGCCC GTGCCACGGG GAGGGCCCC GCGGGGCCAC GAGGGCCCC GCGGGGCCAC GCGCGACCAC GAGGGCCCC GCGGGGCCAC GGCTACAAC GCCTACAAC AGAGGCCAC GCCTACAAC TO TO TO TO TO TO TO TO TO TO TO TO TO T	SHPYSQITVE SHPYSQITVE 327.1 J GAGAATACCT GCAGGCCGAA TOGCATCCT COGCCAGAGCTCCG GGGGCCGCAG GCCCGCAG GCTCTCTGAAG CCACCGCCAA GATCAGCCAG GCCCCACAGCTCCCCCACAGCCCACACCCCCACACCCCCACACCCCCACACCCCCC	41	S1 GACCTTCTC CAGGGGGTTC GGGCAATGC CAGGGGCAG GCCTTCAGG TTGAGGTTCTA GCCTGGCCA TGTCGGCAG CATCAGGTC CAGGGTTTTT CTGAGGTCT CAGGGTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCT CAGGGTTTTT CTGAGGTCAGGTC	60 120 180 240 360 420 480 540 600
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50 55 60 65 70	TITOTURE TITOTURE Seq ID NO. Nuclair Acc Coding seq I I I IIICANOSOSC CTCANOSOSC CTCANOS	PULBUSSILLY ATTITIENCY 299 DNA sectl di Accession usence: 89-6: 11 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	CYSINATOTHY TYSINATOTHY TYSINA	SIETEGUTVE 327.1 31 GAGANTACCT GCAGCCGUA 31 AGANTACCT GCAGCCGUA AGCAGCCGUA AGCAGCCGUA AGCAGCCGUA AGCAGCGCGA AGCAGCGAG AGCAGCGCGA AGCAGCGCGA AGCAGCGCGA AGCAGCGCGA AGCAGCAGCA AGCAGCGCGA AGCAGCAGCA AGCAGCAGC	41 COTOGOCCCT GOCCOGOGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCCAGO AGCOCCCAGO AGCOCCCCAGO AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TACATAAAATAA	S1 OACCITICAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTATCA TOTCOGGCA TARACTARACTA TARACTARACTA TARACTARACT	60 120 180 240 300 420 480 540 600 720
50 55 60 65	TITOTURE TITOTURE Seq ID NO. Nuclair Acc Coding seq I I I IIICANOSOSC CTCANOSOSC CTCANOS	PULBUSSILLY ATTITITISMY 209 DNA secial di Accession incer: 89-6: 11 11 11 12 12 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15	CYSINATOTHY TYSINATOTHY TYSINA	SIETEGUTVE 327.1 31 GAGANTACCT GCAGCCGUA 31 AGANTACCT GCAGCCGUA AGCAGCCGUA AGCAGCCGUA AGCAGCCGUA AGCAGCGCGA AGCAGCGAG AGCAGCGCGA AGCAGCGCGA AGCAGCGCGA AGCAGCGCGA AGCAGCAGCA AGCAGCGCGA AGCAGCAGCA AGCAGCAGC	41 COTOGOCCCT GOCCOGOGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCCAGO AGCOCCCAGO AGCOCCCCAGO AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TACATAAAATAA	S1 OACCITICAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTATCA TOTCOGGCA TARACTARACTA TARACTARACTA TARACTARACT	60 120 180 240 300 420 480 540 600 720
50 55 60 65 70	TITOTICHER TITOTICHER TITOTICHER Seq ID NO: Nuclaic Ac. Coding seq GAGGGGGGA GAGGGGGAA GAGGGGGAA GAGGGGCTA GAGGGGCTA GAGGGGCTA GAGGGGCTA GAGGGGCTA GAGGGGCTA GAGGGGTA GAGGGGTGA GAGGGGGTA GAGGGGGGAA GAGGGGGTA GAGGGGGGAA GAGGGGGGGAA GAGGGGGGGGGG	PULBUSELLY ATTITIENCY 209 DNA secid di Accession cuence: 89-6: 11 11 0CTOTOTOTTA GGCAGAGGCT GGCAGAGGCT GGCAGAGGCC GGAGAGGCCG GGAGAGGCCG GGAGAGGCCG GGCAGAGGCC CCCTCAGGGC CCCTTCAGGAC CCCTCAGGGC CCCTCAGGGC CCCTCAGGGC CCCTCAGGGAC CCCCCAGGGC CCCCCAGGGC CCCCCAGGGC CCCCCAGGGAC CCCCCCAGGGAC CCCCCCAGGGAC CCCCCCAGGGAC CCCCCCAGGGAC CCCCCCAGGGAC CCCCCCAGGAC CCCCCCCAGGAC CCCCCCCC	CYSIGNOTHY PROBLEDIES PROBLEDIES 1	SIETEGUTVE 327.1 31 GAGANTACCT GCAGCCGUA 31 AGANTACCT GCAGCCGUA AGCAGCCGUA AGCAGCCGUA AGCAGCCGUA AGCAGCGCGA AGCAGCGAG AGCAGCGCGA AGCAGCGCGA AGCAGCGCGA AGCAGCGCGA AGCAGCAGCA AGCAGCGCGA AGCAGCAGCA AGCAGCAGC	41 COTOGOCCCT GOCCOGOGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCCAGO AGCOCCCAGO AGCOCCCCAGO AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TACATAAAATAA	S1 OACCITICAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTATCA TOTCOGGCA TARACTARACTA TARACTARACTA TARACTARACT	60 120 180 240 300 420 480 540 600 720
50 55 60 65 70	TITOTIONS Seq ID NO: Nuclais A: Coding seq AGCAGGGGGC CTGAGAGCGG CTGAGAGCGG ACGGGGGAT TGGCGGCCAN TGGCGGCCAN TGGCGGCCAN TGGCGGCAN TGGCGGCCAN TGGCGCCAN TGGTGAGCGG CCTGCTGAGCG CCTGCTGAGCG CCTGCTGCAG TGGTGCGCA TGGTGAGCG CCTGCTGAGCG CCTGCTGCAG TGGTGCGCA TGGTGAGCG CCTGCTGCAG TGGTGAGCG CCTGCTGCCG CCTGCTGCCG CCTGCTGCG CGGTGAGGGGG CCTGCGCG CGGTGAGGGGGG CGGTGGGGGGGGGG	PULBUSELLY ATTITIENCY 209 DNN sed dd Accession usnce: 89-6: 1 GCTOTOTOTA GCCAGAGGCT GCGAGAGGCT GCGAGAGGCA GCAGAGGCA GCAGAGCAC GCAGAGGCA CCGATTCCG ACCGATTCCG ACCGATTCCG ACCGAGAGGCA CCGAGAGGAGGCA CCGAGAGGAGCA CCAGAGGAGGCA CCAGAGGAGGAG TH 1 STODAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	CYSIGNOVITI VENERALISIA VENER	SIETROLIVE 327.1 31 GRANATACCT GCAGGCGGAN 31 GRANATACCT GCAGGCGGAN GCAGGCGGAN AGCAGAAGGT GCAGCCGGAN AGCAGAGGT GCAGCGGGAN AGCAGAGGT GAGTCGGGGA AGCAGGCGGAN SAGGGGAGAT YLAMGFATON SCLQQLSLIM	41 COTOGOCCCT GOCCOGOGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCCAGO AGCOCCCAGO AGCOCCCCAGO AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TACATAAAATAA	S1 OACCITICAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTATCA TOTCOGGCA TARACTARACTA TARACTARACTA TARACTARACT	60 120 180 240 300 420 480 540 600 720
50 55 60 65 70 75	THIGHTUNE Seq ID NO: Nucleic Ac. Coding seq I AGCAGGGGC CTGAAGACCG AGCAGGGCCCAG AGCAGGCCCAG AGGGCCCAG CCTGAATGAC CCTGCCCAG AGGGCCCAG CCTGCCCAG CCTGCCCAG CCTGCCTGCC CCTGCCTGCC CCTGCCTGCC CCTGCCTG	PULBUSELLY ATTITIENCY 299 DNA sect did Accession selections of the control of the	CYSIGNOTHI VENNERDIHEN IN M. (001) 1	SIETROLIVE 327.1 31 GRANATACCT GCAGGCGGAN 31 GRANATACCT GCAGGCGGAN GCAGGCGGAN AGCAGAAGGT GCAGCCGGAN AGCAGAGGT GCAGCGGGAN AGCAGAGGT GAGTCGGGGA AGCAGGCGGAN SAGGGGAGAT YLAMGFATON SCLQQLSLIM	41 COTOGOCCCT GOCCOGOGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCCAGO AGCOCCCAGO AGCOCCCCAGO AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TACATAAAATAA	S1 OACCITICAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTATCA TOTCOGGCA TARACTARACTA TARACTARACTA TARACTARACT	60 120 180 240 300 420 480 540 600 720
50 55 60 65 70	THIGHTUNE Seq ID NO: Nucleic Ac. Coding seq I AGCAGGGGC CTGAAGACCG AGCAGGGCCCAG AGCAGGCCCAG AGGGCCCAG CCTGAATGAC CCTGCCCAG AGGGCCCAG CCTGCCCAG CCTGCCCAG CCTGCCTGCC CCTGCCTGCC CCTGCCTGCC CCTGCCTG	PULBUSELLY ATTITIENCY 209 DNN sed dd Accession usnce: 89-6: 1 GCTOTOTOTA GCCAGAGGCT GCGAGAGGCT GCGAGAGGCA GCAGAGGCA GCAGAGCAC GCAGAGGCA CCGATTCCG ACCGATTCCG ACCGATTCCG ACCGAGAGGCA CCGAGAGGAGGCA CCGAGAGGAGCA CCAGAGGAGGCA CCAGAGGAGGAG TH 1 STODAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	CYSIGNOTHI VENNERDIHEN IN M. (001) 1	SIETROLIVE 327.1 31 GRANATACCT GCAGGCGGAN 31 GRANATACCT GCAGGCGGAN GCAGGCGGAN AGCAGAAGGT GCAGCCGGAN AGCAGAGGT GCAGCGGGAN AGCAGAGGT GAGTCGGGGA AGCAGGCGGAN SAGGGGAGAT YLAMGFATON SCLQQLSLIM	41 COTOGOCCCT GOCCOGOGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCCAGO AGCOCCCAGO AGCOCCCCAGO AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TACATAAAATAA	51 CAGGGGGTTCC GGGGCAATC GGGGGGTTCC GGGCGAATC GGGGGGTTCC GGGCGAATC GGGGGGTTCC GGGCCGAATC CCTAGGCC TTCAGTCC TTCAGTCA TTCCGGCA TTCAGTCA TTCCGGCA TTCAGTCA TCA TTCAGTCAGTCA TTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCA	60 120 180 240 300 420 480 540 600 720
50 55 60 65 70 75	THIGHTUNE Seq ID NO: Nucleic Ac. Coding seq I AGCAGGGGC CTGAAGACCG AGCAGGGCCCAG AGCAGGCCCAG AGGGCCCAG CCTGAATGAC CCTGCCCAG AGGGCCCAG CCTGCCCAG CCTGCCCAG CCTGCCTGCC CCTGCCTGCC CCTGCCTGCC CCTGCCTG	PULBUSELLY ATTITIENCY 299 DNA sect did Accession selections of the control of the	CYSIGNOTHI VENNERDIHEN IN M. (001) 1	SIETROLIVE 327.1 31 GRANATACCT GCAGGCGGAN 31 GRANATACCT GCAGGCGGAN GCAGGCGGAN AGCAGAAGGT GCAGCCGGAN AGCAGAGGT GCAGCGGGAN AGCAGAGGT GAGTCGGGGA AGCAGGCGGAN SAGGGGAGAT YLAMGFATON SCLQQLSLIM	41 COTOGOCCCT GOCCOGOGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCAGO AGCOCCCAGO AGCOCCCAGO AGCOCCCCAGO AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TTCATTCTGC AGCOCCCT TACATAAAATAA	S1 OACCITICAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTTCAT CAGGGGTATCA TOTCOGGCA TARACTARACTA TARACTARACTA TARACTARACT	60 120 180 240 300 420 480 540 600 720
50 55 60 65 70 75	TTIQTCHAPS Seq ID NO: Nuclais A: Lack Andrews Seq CO No: No: No: No: No: No: No: No: No: No:	PVLBISSILLY ATTITINGNY 299 DNN secial di Accession usence: 89-6: 11	CYSHEATHY MANAGEMENT OF THE STATE OF THE STA	NISHINGUY SERVENCE OF THE SERV	THEORETAINS THEORETAINS 1 PROJECTED GROCOGOGOGO GROCOGOGOGO GROCOGOGOGO GROCOGOGOGO TOCTICACTO	S1	600 120 1800 240 3001 420 450 540 660 720
50 55 60 65 70 75	TTIQTCHAPS Seq ID NO: Nuclais A: Lack Andrews Seq CO No: No: No: No: No: No: No: No: No: No:	PVLBISSILLY ATTITINGNY 299 DNN secial di Accession usence: 89-6: 11	CYSHEATHY MANAGEMENT OF THE STATE OF THE STA	NISHINGUY SERVENCE OF THE SERV	THEORETAINS THEORETAINS 1 PROJECTED GROCOGOGOGO GROCOGOGOGO GROCOGOGOGO GROCOGOGOGO TOCTICACTO	S1	600 120 120 240 300 420 480 540 660 660 6720
50 55 60 65 70 75 80	TITOTIONS Seq ID NO: Nuclaids Accordance AGAGGGGGGCA AAGGGGCTCA COTGANTON COTTANTON Seq ID NO: Nuclaids ACCORDANCE AAGGGGCTCA AAGGGCTCA AAGGTCA AAGGGCTCA AAGGCTCA AAGGGCTCA AAGGCTCA AAGGGCTCA AAGGCTCA AAGGGCTCA AAGGG	PULBUSELLY ATTITITION 7. 299 DNN secial di Accession 89-6: 11	CYSREADING WINDOWN WHITE 1 1 1 1 1 1 1 1 1 1	NISHABATAS 317-1 31	41 INTERPRETATION ATTEMPTED ATTEMP	ST	600 120 1800 3001 420 450 540 660 720
50 55 60 65 70 75	PROTECTIONS Seq ID NO: MULTISHING MULTISHING MULTISHING I J J J J J J J J J J J J J J J J J J	PVLBSSLLY ATTITICAN 209 DNA section (14 Accession ence: 89-6: 11	CYSHICTOTH Y SPECIAL STATE OF THE STATE OF T	STREAM TO SERVICE SERV	41 INTEGRATION	ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK CONTRIBUTION ST CANDENDOCK ST	600 120 120 240 300 420 480 540 660 660 6720
50 55 60 65 70 75 80	TTOTTCHES TTOTTCHES TTOTTCHES Seq ID NO MUCLOIA SEC JGCAGGGGGAT TGCAGGGGGGAT TGCAGGGGGGAT GGAGGGGGAT GGAGGGGAT GGAGGGGGAT GGAGGGGGAT GGAGGGGGAT GGAGGGGGAT GGAGGGGGAT GGAGGGGGAT GGAGGGGGAT CCCCCTCGCGCGAT CCCCCTCGGGGGGAGGGGGAAGGCCAGGGGAAGGCCAGGGAAGGCCAGGGAAGGCCAGGGAAGGCCAGGGAAGGCCAGGGAAGGCCAGGGAAGGCCAGGGGAAGGCCAGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGAAGGCCAGGGGGG	PVLBUSELLY ATTITITION, 299 DNN section (in Accession 11 11 11 11 11 11 11 11 11 11 11 11 11	CYSHICTOPY TYPERCEPTUR THE PROPERCEPTUR THE PROPERCEPTUR TO THE PROPERCEPTUR THE PROPERCEPT	STREAM TO THE TOTAL OF THE TOTA	1 TERRIPITEDE TERRIPITED TE	ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK ST CANDENDOCK CONTRIBUTION ST CANDENDOCK ST	600 120 180 240 300 480 540 660 660 720

	GACAGCCGCC	TGCTTCAGTT	COGACTORACT	GCTGCAGACC	ACCCCCAACT	GCAGCTCTCC	360
	ATCACCTCCT	CTCTCCACCA	COTTTCCCTC	TTCATCTCCA	TCACGCAGTG	CTTTCTGCCC	420
	GTGTTTTTGG	CTCAGGCTCC CTCCTCCCCT TTGTCGCTGG	CTCAGGGCAG	AGGCGCTAAG	CCCAGCCTGG	CGCCCCTTCC	480
_	TAGGTCATGC	CTCCTCCCCT	AGGGAATGGT	CCCAGCACGA	GTGGCCAGTT	CATTGTGGGG	540
5	GCCTGATTGT	TTGTCGCTGG	AGGAGGACGG	CTTACATGTT	TGTTTCTGTA	GAAAATAAAG	600
	CTGAGCTA						
		212 Protein					
	Brotein Acc	ession #: 1	r seduence:				
10	Process Acc		son nedactic	-			
	1	11	21	31	41	51	
	1	1	1	1	1	1	
	MOAEGOGTGG	STGDADGPGG	PGIPDGPGGN	AGGPGEAGAT	GGRGPRGAGA	ARASGPRGGA	60
15		AQDGRCPCGA	RRPDSRLLQF	RLTAADHRQL	QLS1SSCLQQ	LSLLMWITQC	120
13	PLPVFLAQAP	SGQKK					
	Sec ID NO:	213 DNA sec	mence				
	Nucleic Ac	d Accession	#: NM 0005	55			
	Coding sequ	ence: 416.	.1498				
20							
	1	11	21	31	41	51	
	CTTATTTTT	ATGAATGTCG	CATAGONGCA	CCACCTTGGT	GGGGAAAGGG	TTTGATGAAT	60
	AGCACAAAGA	CACTGGCTGT	TCCCTGGAGG	CTGTCCCTTT	AAAGGAGAAT	CTTAGTTTAT	120
25	TCTGGGGGGA	CACTGGCTGT GGGGATGCAC	ACATTAGAGT	AGGAAAGAGG	GCTTGGAATA	AAATGAAAAC	180
	ACTCCCCCTT	CATAGTCATT	GTACTGAAAT	GCAAAGACTG	CTTCCTAAGC	TGGAGATGCT	240
	AACCTTGGGT	AGCTCCTTCT AGTCATGTGG	GTTCTCTTCA	AGGGGAATTT	TGTCAGGCTA	TGGATTCATT	300 360
	TACAACTGTT	CAATTTGATA	GCATGTGTGA	GGAAACAGAT	BOCKBOCK CO	AIGIAITTAG	420
30	ACTTGATTTT	GGACACTTTG	ACGRARGEGE	TANGACATCC	AGGAACATGC	GAGGCTCCCG	480
-	GATGAATGGG	GGACACTTTG TTGCCTAGCC	CCACTCACAG	CGCCCACTGT	AGCTTCTACC	GAACCAGAAC	540
	CTTGCAGGCA	CTGAGTAATG	AGAAGAAAGC	CAAGAAGGTA	CGTTTCTACC	GCAATGGGGA	600
	CCCCTACTTC	AAGGGGATTG GACCTGACGC	TGTACGCTGT	GTCCTCTGAC	CGTTTTCGCA	GCTTTGACGC	660
35	CTTGCTGGCT	ACCATTGATG	GATCTCTGTC	TGACAACATC	AACCTGCCTC	AGGGAGTGCG	720 780
33	CGARAGCTAT	GECKSTRATE	CAGACAACTT	CTTTABABAG	GTGGAGTACA	CCARGARTGT	840
	CAATCCCAAC	TGGTCTGTCA	ACGTAAAAAC	ATCTGCCAAT	ATGAAAGCCC	CCCAGTCCTT	900
	GGCTAGCAGC	GTCTGTTCCT TGGTCTGTCA AACAGTGCAC	AGGCCAGGGA	GAACAAGGAC	TTTGTGCGCC	CCAAGCTGGT	960
40							1020
40	GACAGCCCAC	TCTTTTGAGC AAAAAACTCT GATGATGTGT	AAGTCCTCAC	TGATATCACA	GAAGCCATCA	AACTGGAGAC	1080
	CGGGGTTGTC	AAAAAACTCT	ACACTCTGGA	TGGAAAACAG	GTAACTTGTC	TCCATGATTT	1140
	TOTAL	CTGGATGAAA	ATTRACTOR	AGTCATGAAG	GGAAACCCAT	CAGCCACAGC	1200 1260
							1320
45	CCGAAGCAAG	TCTCCAGCTG CAGTCTCCCA CTGCCTCTGT	ACTCAGCAAA	CGGAACCTCC	AGCAGCCAGC	TCTCTACCCC	1380
	CAAGTCTAAG	CAGTCTCCCA	TCTCTACGCC	CACCAGTCCT	GGCAGCCTCC	GGAAGCACAA	1440
	GGACCTGTAC	CTGCCTCTGT	CCTTGGATGA	CTCGGACTCG	CTTGGTGATT	CCATGTAAAG	1500
	GAGGGGAGAG	TGCTCAGAGT	CCAGAGTACA	COTTTCAAGCC	TATCATTUTA	TTOTTOTTOT	1560 1620
50	TATTTTGAAA	TGTCCAACAG AACACATTGT	AATATGTTGG	GTTTATTTTC	CTGTGATTTC	TCCTCTGGGC	1680
							1740
	TCCAGGGATG	CAAAATGTGC	TAGTCCATGA	CCTTTCAATG	GAAAGCTTAG	GGGCCTGGGG	1800
	TAAATTTGCC	CAAAATGTGC CCGTTTAAAT TAAAAAGTTT	TTGCCCAAAC	AGTTTTCCTT	TTGTAGAGGG	GTGTTTAAAT	1860 1920
55	ATACAGCAAT	TAAAAAGTTT	TOTOTOGGGAA	TCAACAACT	TOCACCACCC	TOCAMORATO	1980
55	GCAAGGCAGC	GTGCCCCTTT TCCCCAGCCT	CACTCTTCAC	TCCTGATTGA	GGCCCGGGTT	TGTTGTCCAG	2040
	CACCAATTCT	GGCTGTCAAT	GGGGAGAAAT	AAACCAACAA	CTTATAATTG	TGACACCAGA	2100
	TGCTTAGGAT	CCTGGTGCTG	GGTTAGCTAA	GAGAATAGAC	AGAATTGGAA	AATACTGCAG	2160
60	ACATTTCCGA	AGAGTITATA ATAAGCAATT	AAGCACAGTG	AATTCCTGGT	CAATCTCTCC	ACTGAGGCAA	2220
00	TITGGAATCA	TGTCTAACAT	GATAATAGTT	TUGAGTAAGG	GACTICATAT	CATCTATCTC	2280 2340
	TOTTCTATTO	AATGCCTTGT	TAACAGCCAA	CACTGAAAAC	ACTGTGAGAA	TITGITTICA	2400
	GGTCTGACAC	AATGCCTTGT CTTTCAGTCT	CTITTTATAG	CAAGAAATCA	ATATCCTTTT	TATAAAAATT	2460
							2520
65	TTTTGTCTAA	AAAACACATG GAAATTATGC	TTTAAAADAA	ACCAGAAAAA	DAAAAAAAA	CCGAAGAATA	2580 2640
	AIGTTATITA	GCCAATTCAA	TAGRATCACTGCC	THETTERGATEAC	CITCAGGAGA	CTTATCCTTC	2700
	CATTABTABT	TTCAATGTGG	ACCAGACATT	CTAATTATAT	TTTAAATGAA	ATGTTACAGC	2760
	DAATTTTAAG	TTCAATGTGG CAACTCTTTT	TATCTATAAT	CCTAATATTT	CATACTGAAG	ACACAGAAAT	2820
70	CTTTCACTTG	TCTTTAACAT	TAGAAAGGAT	TTCTCTTTAC	TAAGGACTGA	TCATTTGAAA	2880
	TAGTTTTCAG	TCTTTTGAGA	TACAGGTTTA	TAACACTGCT	TTTTTTTCC	TGTAAACATA	2940
	GCCCATAATG	GCAAAAACAA AATATAAAAA	CTAATTTTAA	TTGAAGGTCT	TGCTTGCCAN	TCCTGTGTTG	3000
	GCTTTNACCA	AAACCAAGCT	TTCCCTTATT	TACTORATOR	GGIGCAMAIN	TTTCCTCCACT	3120
75	CTARATGGAR	TGAGCTTGCT	GIGIGIGIGI	GTGGTGGTGG	TGGGAGGGG	TGGTGCATGT	3180
	GIGIGIGIGI	TGAGCTTGCT GTGTGCATCT	GCAGCTGCTT	CAAAATTAAG	AAATACTACA	AGACACCCCT	3240
	GTARTGGATT	GGTGGCAACT	GGGTGGCACT	GCTGATGTGC	ACTGTGTAGG	GGGGAACCCA	3300
	GTGGTGGTGG	GGTATCTCAA TTCAAGAAAA	ATGCCCCTAG	ACAAGCTTCA	GATGTCTGTA	GCTACCAAAA	3360
80	ACATTTTCGG	TTCAAGAAAA ATGAGGATCT	GIGAGATGAT	GGTAGTACTG	GITTCTGGTG	CCATTCARA	3420 3480
30	CCATTANTA	GCCCATTTTA	CTANCOCCT	ATTICITION	AGAAGCTCAG	GGTTTNCTTA	3540
	GTGCCTCCCA	NAACATTTTG	TAGTTAATTG	GGAAAAGTG	ATACTTGGAT	GGTTTNCTTA TAGGGGGTGT	3600
							3660
0.5	CACCCATAGT	NTCACTTTAG	GTCTCATTTA	GTCCATCACC	TTTATTTAA	GTTGAGGAAG	3720
85	TGGAGGCTGG	TAAAGAGCAG	GACCAGAGGA	AGAATCCAGA	TTTCCTTATG	CTTGGGCCTC	3780 3840
	ACACTAGCTC	TNTGAGTATT	AACCTTGATTG	CCARCAATAT	TCAATAACAA	TAGTACATAT	3900
	~minintTT	-CIII I MONIAT	ALC: 1 TORK	- Commonthi	- 301170000		3300

	TCCATCTTAC	TTTTAATCGA	GTATAAGGAA	ATGTTTCTTT	ATGGCCATTT	TGGAGGGAGC	3960
	AGGGGATGAG	GCTTGGCATA	GTCCAAAATT TTCAAGGCAA CAATTTTACC	TAAGNCTCCA	TTAATTAATT	GCATTTTAAA	4020
	TTGTTTTAAA	TTGGCCCACT	TTCAAGGCAA	TTTTTTTTTTTTTTT	GTGTCTGTAA	CTGAGCTCCT	4080
	CCACCCCTGT	CATTCACTTC	CAATTTTACC	CAATCCAATT	TTAGCACTCA	AGTTCCATTG	4140 4200
5	OCCUPATION ASSESSMENT	TOCHOCOCO	ACACACAMCA	PCMCPCCB PC	CAMPTOCOCAC	CACTCCCTAT CTCTTGCTTG GAAGGGGAAA	4200
	IGITAATITI	TOCACOGICI	ACACACATCA	MUTCAGCOOKS	CATTIGCCAL	CACTCCCTAT	4200
	ACTICICCCT	CITTITIACA	CACACACACA	CACACACACA	CACAATCCAT	CTCTTGCTTG	4260
	TTCCTACCTC	CCTGATTTTT	CTTCCCTACA	GAAATAGAAA	TAGGGACAAA	GAAGGGGAAA	4320
	ATGTATATAT	TGGGGCTGGG	CTGAACAACT	AACTTCATAA	GTAGTATTAA	CTAGGGGTAA	4380
	ATTGAGAGAA	AACCTCCTTT	TCTCTTCACT	GTTTTGGAAA	GGATAGCCAT	TAGCATGACT	4440
10	COTTTCTCTC	CTTATCCACT	TTACTATTAC	CCTAGATTGA	ATTATACCCT	TTTTCTAGCT	4500
	arrear room	mananana.ca	MCAMOMA CONC	COLUMN CONCORD	a a management	mamanaga	4560
	GINGGINCCI	IMMUNICACA	TCATCTACTC	CICIACICCA	MILITERAL	TCTTCMGGCC	4360
	AGGAAACCGA	GACACAGAGG	TAAAGTAATT	TCCCCCAAGGT	CACACAGCTG	GCTGGGGCAG	4620
	GATTGGGTTT	ACAACCCACA	TCTCCTGGCT	CTTATTCCAG	GGCCTTTTCC	CACTAAGTAG	4680
	TATTGCCTTC	CATTAGGCTC	CTGAGAGTTA	TTTCTCAGGG	TCATGTTGCA	TCTTGGAGCC	4740
15	ACATGCTGCT	CCCCTCATCT	CACTGGGAAA	THUCACCUAGO	ABCCTAATAC	ACCOCCUTTT	4800
10	acamaca mara	1000010MTor	CTTCCCTACA CTGAACAACT TCTCTTCACT TTAGTATTAG TCATCTACTC TAAAGTAATT TCTCCTGGCT CTGAGAGTTA CAGTGGGAACA CAGTGGGAATA	COMMOGRACAM	CONCORNOLING	**************	4860
	CCCTGCATTC	ACCIGGITCE	CATCCACATG ATGGGGTCCC TCTGAATAGC	GG11GCHGM1	OT CCTTORNO	AGAGIGAGGC	4000
	ATTGAGGGCC	AATAGGAGCA	ATGGGGTCCC	TOGCCTTGTC	CATCIGATIC	AGGAGATCAC	4920
	TGCTCCATCG	TGAGGAGCCC	TCTGAATAGC	CCCCCACTGA	ATGCTTGCCT	TGCCCAAATG	4980
	GAATGGAGGA	AGATTGATTT	TCTCCATCAG	TTCACCTTGT	GTCATCTCAT	AATGGTTGGT	5040
20	CTTTCCAGGC	TGAGGGAAAT	GTTTCTTGTT	TCCANAGTAN	AAAAAAGAAA	GAGTGGAACA	5100
	ATANCTITGT	TCATCCTAAC	TTTCTGAGAT	GGCTTTTCAA	CATTTAAAAA	AAACTAGTGT	5160
	COTACCATTC	ACTOCOMICA	TTTMTTTTAG	BATATGGGAG	TARGATGAGG	TAGAGAAAAT	5220
	11 COMOCHIC	ar and and and	200000000000000000000000000000000000000	ACT TOGGOUS	Change	OMCOMMON.	5280
	AACCIGGICI	CACTGIGGIT	GCCCTCATCC	ACMATGICCE	CHANGCCATC	CIGCINIGAL	5200
25	GAGGACAATT	TCCAGGTATA	AGCAAGGGGC	TITGIGACAA	AAATGTACCC	TGGCTGATGT	5340
25	TAAACATTGG	CTCCTGTGTT	TGCACCAAAA	TAGCAAGCTG	TGTGCTCTAT	ACACTCTTCC	5400
	CATCGTCTTG	TGTACACTGC	TCCTGTGGCC	TTCCACAGCA	GAAACCAGGG	CAAAAGGGTC	5460
	CAAACACATG	GTTTTCCTTG	CTGCAAGGCT	NTTCCTGGGA	ACTAAGGGGG	TATTTATTAG	5520
	TTCAGTTATA	AGAGACCTCC	TTCTGGGCTT	ACCCCACTCC	TCACCTACTT	CTCTCTCCTT	5580
	2000111111	CONCORCE CONCORCE	101000011	*****************	**********	MCM1CCM1TT	5640
30	COTCUTTCTC	CICCACAGTC	ACAMOTANCC	ANGUMACCIG	WWW. CONTROL	TGCCAAATG AATGGTTGGT GAGTGGAACA AAACTAGTGT TAGAGGAAAT CTGCTNTGAT TGGCTGATGT ACACTCTTCC CAAAAGGGTC TATTTATTAG CTCTCCTT TGTAGCTATT TCTTAGACCA CAATACTNTG	5700
30	TUAAGAAGGC	AAGGAACCCT	GAGATTCTTC	TTTGAATCCT	TIAGTCCAAG	TUTTAGACCA	5700
							5760
	GGTACAATGC	TCCCAATCAC	CCTGCACATT	TGATTCTAAA	TGGCTTTTAT	TTTTTAAAAA	5820
	TCCATATCCC	TAGGACAAGA	NAACAGGATG	CCTATATCCC	CAAAATGAGC	TCCAGGACAC	5880
	TAADSSTADT	GATCYCAANG	ATCACCCCAC	CTCAGAAAAC	GTCTGTGCCA	ANAGACTTCC	5940
35	CCACATACAA	MCACTOGGAC	ACTYCCTTYCA	ACCIAC PROPER	TTATCCTTCT	CCACTTTCCT	6000
55	CCAGAIAGAA	ALACTOGOAC	MOTOGITION	ALGRETTETT	Chacomomom	mmagaar as m	5050
	ATGGARATAA	ANGGCATTGA	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	AMGATGATTG	GAACCIGICI	TIGGCCACAI	6060
	AGGGCCACTT	GGATCCATTT	CCAGGCCTTA	CTCATATATT	GCCTTCACTG	AAGGGCTTTG	6120
	GCTTTAAGTC	CCAGACTGGT	CTCCCAAGTG	AACCATAAGT	GTTTTGGAGC	TCATCTGGGG	6180
	TGAGGCATGA	GAATGTTGCC	CCATCTATCC	CTTCAGGAAA	AGGTGCCTTC	TTTTAAAAA TCCAGGACAC ANAGACTTCC CCAGTTTGCT TTGGCCACAT AAGGGCTTTG TCATCTGGGG CCTCCCTTTC GGTCTTTATA ATGCANACCT CTTTTTTTTT ACAATCTTGG	6240
40	TCCTAAAGCC	TGGTCCCCAA	AAATTGTTTT	TGTCTCCAAA	AGTCTAGTAT	GGTCTTTATA	6300
	CACCCANACT	CTTACTCTTC	COTCCTGCCT	TOTTTCCTTG	TTAAGGATCT	ATGCANACCT	6360
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CHENCOTAGO	CTCACATTCC	CTATCATTTC	ACABCACTAA	Calabaranana	6420
	CCCGCTTTGG	CTIMOCIMOC	GIGACATIGG	CIMICATITO	ACAROACTAN	CITITITITI	6480
	Trrrrrr	ACTGAGTCTC	CCTCTGTCAC	CTAGGCTGGA	GIGCAGIGGE	ACAATCTIGG	6480
45	CTCGCTGCAA	CCTTCACCCT	TCACCTCCCA	GGTCGAAGCG	ATTCTCCTGC	CTCAGTCTCC	6540 6600
45	CGAGTAGCTG	GGATTACAGG	CGTGCGCCAC	CAAATCTGGC	TATTTTTTTA	CTTITTTTT ACARTCTIGG CTCAGTCTCC TTATTATTAT TTGGCCTCAA ACCATGCCCA TGGAATCAGA TCAGATGGCA TTCTCCATTAC TTTGTGTAT CTAGTTATC CTAGTTATC CTAGTTATC CTAGTTATC CATGTCCCT CATGTGCCTC CATGTGCCTC ACTCCAGCCC ATCCCTGCCC ATCCCTGCCC ATCCCTGCCC	6600
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	ATTATCTGCC	CACCTCGGCC	TCCCAAAGTG	CTGGGATTAC	AGGCATGAGC	ACCATGCCCA	6720
	CCTCACAACA	CALT TALLES TALL	ATTOTTTCCT	TTATTCCTT	CAACATCTTC	TOGRATORGA	6780
	COMO MONTON	monms commo	CARCOGREAG	A CTRA COCCAC	TATACAATTC	CAATTOOTAA	6840
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50	TTAAGGCATC	TITCTGCTCC	TGATCAGAAG	GGCAGGTTAG	TIGGGRGRGG	TCAGATGGCA	6900
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55	CTTATTATCT	TTATTTCTAC	THEFT	CTCCCTCTCT	AGGCATTOGG	CATGTGCCTC	7200
	CITATIATO	Character	ammagaa ama	CICCCICICI	ACCOUNTION	man a manage	7260
	TTCTTAGCCT	GIGATTITIGC	CITGGGACIG	AIGAIAAAII	ATTICCAGAT	TCANTCAGCC	
	CTGGTCCTAC	CCCAGTCCAA	TCAGAAGTAT	GTTCGTCGGG	AATCAACCTG	ATCCTGGCCC	7320
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	TARRONAGEC	ACATTOTACC	TOTAL	TTABACAGAA	TTGCDAAGCC	CTTYCCAAATYC	7980
	TANDONAUCC	AGALIGIAGO	1011441114	**********	110CA7010CC	CTTGGGGGTTG	8040
70	TCACTGCTTG	GCAATACCAT	ATGGCATGCC	AAAATTTACA	AIGACITTIC	TTTATAMGTT	8040
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	AAAATGGAAA	CAGCCCACCC	TTTCTGCCCT	ATAGCTGTAG	TTAGAATTGA	GTACCTGTAG	8340
75	CARACTOC	CTA ATTYCOM	CALCASCAL	TAGAGGTGTT	ACCTTCCTAC	TGACTAGCTO	8400
,,	TATAGCTCAT CCTTTTTAGT GAGGARAAAAT GTGCCCATAA GTCACTTGTT ATTAAACCCT ATTACACCA TAAAGAGCA TCACTGCTTG TAAAAGAGC TCACTGCTTG GTAAATATAT TTTATTGAT TTTATTGAT TTAATGAT TTAATGAT TTAATGAT TGGGGGGTAA GAAAACAGCT TGGGGGGTAAA GAAAACAT	- AMITOGIG	G. IGINGIGI	*wangaratt		CONCINCIT	
	1GGAGAGTAA	MIGCATGGTA	TIGTACATCA	CAPTICITAA	CICGITITAA	CCICIGAAAA	8460
	GAATATATTC	TTCTTTGTAG	TECTTETTEE	CACCCCCTTG	CCCTCTCCCCT	CTCCCTGCTC CCAAGTAAAG ATCTCTCAGC TACGTAAAAA	8520
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80	ACTTATTORT	CATTTCTTAA	GGAACAGCAT	TGTGATCAAA	GACTCAACTT	TACGTAAAA	8700
	TCACTCCT**	Ammorrogramo	TATTGGCCAT	TOATTACA TO	CAGGATTCAS	TACTTTTTCAC	8760
	- AGIGGIAA	ni 1000017G	TUTTOUCCUT	TIMOMIT	CHOQUE TOWN		3,60
	AATCACATGT	MATCCAAAGA	CAGTAGGTAG	IGATGTCCCT	TATCCCTGCA	GCIGITITAA	8820
	GATAGAGACC	TCAGAAGACT	CTGCTTGACC	GATGACCAAT	AATTATTTGA	AAAAAAAAGA	8880
~ =	AAAAATGAGA	GAAATAAAAC	AGATATTTAA	GAACTTTAGC	CACCTATTTA	GAATAGTTAT	8940
85	AGCCAGAAAA	AAAAACAAGG	GCATGAGTTC	AAATGCATTA	CTATCAGTGT	CCTAGGCAAT	9000
	ACCTARCTA	CTCTCAAATT	GTGATTCAAA	AGCAGTATTT	CAAGAGGCAT	TCTCCTTTTT	9060
	TO CARROLLIA	POCCOUNTIL	CACTROCTACO	TTTGGTGRGG	CCCCCATAAA	CCAGCTGGAG	9120
	1001110010	CCCAC11G	CTCTCGT400			TAGTTTTCAG GCTGTTTTAA AAAAAAAAGA GAATAGTTAT CCTAGGCAAT TCTCCTTTTT CCAGCTGGAG	2120

TCCATCTTAC TITTAÁTCGA GTATAAGGAA ATGTTTCTTT ATGGCCATTT TGGAGGGAGC 3960

	WO 02/	086443 TCATCTCCTG TTCTTGGGTC TGAACTGTGA	TGCCTGTAAC	ACCCCTCTTC	CCCCACCCC	TCCGCAATTC	9180 9240
5	AGCTGCTCTT	TGAACTGTGA GCAATTATTT CAAGATGTGT	TGGCTCTCAA	GCTCTGTTCT	TCATCGCATT	CTCATTTCTG	9300 9360
10		214 Proteir ession #: }					
	,	11	21	31	41	51	
15	GDRYFKGIVY BGESYVCSSD LVTIIRSGVK	RDKTSRNMRG AVSSDRFRSP NFFKKVEYTK PRKAVRVILIN ACGPEKFRYA ANGTSSSQLS	SRMNGLPSPT DALLADLTRS NVNPNWSVNV KKTAHSPEOV	HSAHCSFYRT LSDNINLPQG KTSANMKAPQ LTDITEAIKL	RTLQALSNEK VRYIYTIDGS SLASSNSAQA BTGVVKKLYT	KAKKVRFYRN RKIGSMDELE RENKDFVRPK LDGKOVTCLH	60 120 180 240 300
20	MKKSKSPADS	ANGTESSQLS	TPKSKQSPIS	TPISPGSLAK	REDUTERLSE	DOSDSTRUSM	
	Nucleic Ac:	215 DNA sec id Accession mence: 312.	1 #: NM_1304	67			
25	1	11	21	31	41	51	
30	GTCTTCCAACA GTCTTCCTGG TCCTGTGGCA CCCAGGTCGT	AGAGCTCTGC TCTTCGTTCT TAATTTAGTT CAGTCGTGG GATGCAGGCG TATGAGTGAG	AAGGAGAGGT TTCTCACTGA GTGAGTGAAT CTTTGAGGGA CCATGGGCCG	TGTGTCTTCG CCGAGACTCA GTGTGGAGGA AAAGGGCCTC GTAATCGTGG GATCCCAATC	TTCTTTCCGC GCCGGTAGGT GCCAGCGGC GCGGTGGTCC CTGGGCTGGA CTCAGAAAGA	CATCTTCGTT CTGCAGAGTG TTAGGACAGG TCCGCCTTCC ACGAGGGAGG GGAAATGACC	60 120 180 240 300 360
35		CCAGCCAGTT ACCACCAACT TGCTGTTCAA GGATGCACCT TAAAGTGCTG AAACCAAGAA					420 480 540 600 660
40	ATGAAGACTG	AAACCAAGAA TTACAGTTTT	CIGCAAAAA	ATGCTGGAAA	TTTGACTGCT	AACATTCTCT	720
45	Seq ID NO: Protein Acc	216 Protein	n sequence: NP_569734	31	41	51	
	MSERVIRSOS	SERGNIDQESS	ī	Ĭ .	ĺ	1	60
50	AVQGTDVEAF	QQELALLKIE	DAPGDGPDVR	EGTLPTFDPT	KVLEAGEGQL		
55	Nucleic Ac	217 DNA sec id Accession mence: 82	1 #: NM_0014			51	
	ì	11	21 	31 	41	Ī	
60	TGAGATTCAT CCAAGGCGCT GATGAAGTGG GCAGCTGCTC GCTGATAGCC	TGTGAGGCAG CTGTGTGAAA ATGTACAGCC AACCAGCAAC AGGAGGGAGA AGGAACAGGG	TATGAGTTGG TCCTGAAGTG ACCTGAAGAA GGATGAGGGA TCACCCACAG	CGAGGAAGAT ATTGGGCCTA GGGGAACCAG GCATCTGCAG ACTGGGTGTG	CGACCTATTA TGCGGCCCGA CAACTCAACG GTCAAGGGCC AGTGTGAAGA	TTGGCCTAGA GCAGTTCAGT TCAGGATCCT GAAGCCTGAA TGGTCCTGAT	120 180 240 300 360
65	GGGCAGGAGG	TGGACCCGCC GTTAAAAGAA AAATTCTCCC	GACACGTTGA	GAGGTGAAAA AATGATGCAG	GCTGCTCCTA	AGGTGAAAAG	420 480
70	Seq ID NO: Protein Ac	218 Protein cession #: 1	NP_001467.1	31	41	51	
	1	 WPRPRRYVQP	21 -	i	i	1	60
75	DEGASAGQGP	KPEADSQEQG	HPQTGCECED	GPDGQEVDPP	NPEEVKTPEE	GEKÖSÖC.	90
	Nucleic Ac	219 DNA seid Accession uence: 90-3	n #: NM_001	476			
80	1 ACAGCGGAGC	11 GCAGAGTGAG TGAGCGGCCC	21 AACCACCAAC	31 CGAGGCGCCG	41 GGCAGCGACC	51 CCTGCAGCGG	60
85	ATGGGAAGTC TOGCTGCCT	TGAGCGGCCC CCTCCTGCCC CAGGCAGTGT CAACTGCAAT GCACAGAGAA	GCAGCCOGGG ATCTTTGATC GACAACACTG	GGGAACTTCA ATGGCATTCA	CAGACAAACT CTGCGAGAAA	GGTAATGGAT TGCAAGAATG	120 180 240 300 360

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	CCAGATGCGA	COGATGTCTG	CCAGGCTTCC	ACATGCTCAC	GGATGCGGGG	TGCACCCAAG	480
							540
	*CCCCCCCCCCC	CHARLELLING	AAGCCAGCTG	TTACTGGAGA	ACCCTGTGAT	AGGTGTCGAT	600
5	CRCCCCCCCCCC	TAATCTCCAT	CCCCCCAACC	CTGAGGGGTG	TACCCAGTGT	TTCTGCTATG	660
_	CCCATTCACC	CAGCTGCCGC	ACCTCTCCAG	AATACAGTGT	CCATAAGATC	AGGTGTCGAT TTCTGCTATG ACCTCTACCT	720
	OGCALITANGE	TGTTGATGGC	TOCA ACCOUNT	TOCABOGABA	TOGGTOTOCT	GCAAAGCTCC	780
							040
	AATGGTCACA	GCGCCATCAA	CATGIGITIA	BACACCTCAC	CTATOGGGAA	AGCCTGTCCT ATTCTGGAAG CCTTGTGGGC AGCCCCCAGC	900
10	TIGIGGCICC	TGCCGGGTTT	CTIGGGAATC	MCMGGIGMG	CINIGOGCAN	ATTCTCCAAG	960
10	TTGACTACCG	TGTGGACAGA	GGAGGCAGAC	ACCCATCIGC	CONTONIOR	COMPORTOCO	1020
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25	ACCAGTGCAA	AGCAGGCTAC	TTCGGGGACC	CATTGGCTCC	***********	CARCOCACOT	1860
25	GAGCTTGCAA	CTGTAACCCC GCCAGGATTT	ATGGGCTCAG	AGCCTGTAGG	ATGTCGAAGT	an reserved	1920
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	AGTICOGGG	* * CTCCCACA	CACABATCAC	ATCACCTCCT	TTCCCGTGCC	ANTCTTGCTA	2880
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65	ACTATIGCCI	CATATIGICC	TCIGCAMGCI	A A CONCORDO	NACTOR COL	TOTTOGRACITO	4260
03	ACCCAGGGTC	TGAACATGTT	CTCCATTTTC	A MOCTOGRAM	- And and cho	CCACCENCAA	4320
	AGGACCTGT	AGGCAGGCCC	ATTCAGAGCT	AIGGIGCIIG	CIGGIGCCIG	TACACATTCC	4380
	GTTCTGGAC	TGGGCATGAC	ATCCTTTCTT	TIMATGATGO	CHIGGCHACI	TAGAGATIGC	4440
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	CACACTTCAC	CIGGGICACA	TCCATCCCTC	CATTCATCCI	TCCATCCATC	TTTCCATCCA	4680
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80	TOCTOCTO		ATTTCCTTC	ATTTTCCTG	AAGTGTTTT	TGAGTTATGA GGGAAGACTA AAATAAAGAA	5160
00	CAATTGTTA	. Tracticiat					
	CHATTOTIM						

Seq ID NO: 220 Protein sequence: Protein Accession #:NP_005553

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1 11 21 31 41 51

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	MPALWIGCCL	CESILLI PAAR	ATSRREVCDC	NGKSRQCIFD	RELHROTGNG	FRCLNCNDNT	60
	DGTHCEKCKN ·	GFYRHRERDR	CLPCHCNSKG	SLSARCDNSG	RCSCKPGVIG	ARCDRCLPGF	120
	HMLTDAGCTQ	DORLLDSKCD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYYNLDGGN	180 240
5	PEGCTQCFCY	GHSASCRSSA PVAPAKFLGN	EYSVHKITST	FHODVDGWKA	VORNGSPARE	CACLETTARI	300
,	MDIACKEDIA I	LTKTYTFRLN	ERDSNINSBO	LSYPEYERLL	RNLTALRIRA	TYGEYSTGYI	360
	DNUTT.TSARP	VSGAPAPWVE	OCTCPVGYKG	OFCODCASGY	KRDSARLGPF	GTCIPCNCQG	420
	CCACTIONTCI	CACCUENBUL	ECAUCHIGRY	NDPHDPRSCK	PCPCHNGPSC	SVMPETEEVV	480
	CNNCPPGVTG	ARCELCADGY	FGDPFGEHGP	VRPCQPCQCN	NNVDPSASON	CDRLTGRCLK	540
10	CIHNTAGIYC	DOCKAGYFOD	PLAPNPADKC	RACNONPMGS	EPVGCRSDGT	CVCKPGFGGP	600
	NCBHGAFSCP	ACYNOVKIOM	DOFMOQLORM	EALISKAQGG	DGVVPDTELE	GRMQQAEQAL	660 720
	QDILRDAQIS	EGASRSLGLQ AESEASLGNT	LAKVRSQENS	YOSKLODLKM	TVERVRALGS	GAGNKAKDIH	780
	REITOMOLSE	SLVRKALHEG	VCCCCCCCCCC	NUMBER STREET	WYTEST BOOT	TREATMENT	840
15	ADDONOUS	LLDSVSRLQG	VSDOSFOVER	AKRIKOKADS	LSTLVTRHMD	EFKRTOKNLG	900
13	NWKEEPUOLT.	ONGREGREKS	DOLLSRANLA	KSRAOEALSM	CNATFYEVES	ILKNLREPDL	960
	OUDNEKARAR	EAMKRLSYIS	OKVSDASDKT	OOAERALGSA	AADAORAKNG	AGEALEISSE	1020
	IEOEIGSLNL	BANVTADGAL	AMEKGLASLK	SEMREVEGEL	ERKELEPDTN	MDAVQMVITE	1080
20	AQKVDTRAKN	AGVTIQDTLN	TLDGLLHLMD	QPLSVDEEGL	VLLEQKLSRA	KTQINSQLRP	1140
20	MMSELEERAR	QQRGHLHLLE	TSIDGILADV	KNLENIRDNL	PPGCYNTQAL	EQQ	
	a 110						
	Sed in No:	221 DNA sec d Accession	uence	29			
	Coding sem	ence: 13-16	1 #: MM_0103	2.5			
25	courses out						
	1	11	21	31	41	51	
	1	1	1	1	1	L	60
	GTCAAGAAAA	GAATGTCTGT	AATTGTTCGA	ACTOCTTCAG	GACGACTTCG	GCTTTACTGT	120
30	AAAGGGGCTG	ATAATGTGAT ATCTGGAATA	TTTTGAGAGA	CHICAAAAG	CONCECTO	TOTOGOGOGAA	180
30	ACATTATGCC	CYGAGAATGA	CTTTGCCACG	DCCCTCC 3 3 C	TOTATCAGGA	ACCCACCACC	240
	ATATOTCA	ACAGAGCTCA	ACCOUNTS	GACTETTACE	AGATCATTGA	GAAGAATTTG	300
	CTGCTACTTG	GAGCCACAGC	CATAGAAGAT	CGCCTTCAAG	CAGGAGTTCC	AGAAACCATC	360
	GCAACACTGT	TGAAGGCAGA	AATTAAAATA	TGGGTGTTGA	CAGGAGACAA	ACAAGAAACT	420
35	GCGATTAATA	TAGGGTATTC	CTGCCGATTG	GTATCGCAGA	ATATGGCCCT	TATCCTATTG	480
	AAGGAGGACT	CTTTGGATGC	CACAAGGGCA	GCCATTACTC	AGCACTGCAC	TGACCTTGGG	540
	AATTTGCTGG	GCAAGGAAAA	TGACGTGGCC	CTCATCATCG	ATGGCCACAC	CCTGAAGTAC	600
	GCGCTCTCCT	TOGAAGTCCG	GAGGAGTTTC	CTGGATTTGG	CACTCTCGTG	CAAAGCGGTC	660
40	ATATGCTGCA	GAGTGTCTCC	TCTGCAGAAG	TCTGAGATAG	TGGATGTGGT	GAAGAAGCGG.	720 780
40	GTGAAGGCCA	TCACCCTCGC	CATCGGAGAC	GGCGCCAACG	ATGTCGGGAT	GATCCAGACA	840
	GCCCACGTGG	GTGTGGGAAT CACAGTTTTC	CAGTGGGAAT	DAAGGCATGC	MOGCCACCAA	MACTOGOAT	900
	TACGCCATCG	TGACCAAGTG	CATCTTGTAG	TECTTCTATA	AGAACGTGGT	CCTGTATATT	960
	ATTOMCCOOG	GGTTCGCCTT	TOTTOTAL	TTTTCTGGGC	AGATTTTATT	TGAACGTTGG	1020
45	TOCATOGGCC	TOTACABTOT	CATTTTCACC	GCTTTGCCGC	CCTTCACTCT	GGGAATCTTT	1080
	CACACCTCTT	CCACTCACCA	GACCATCCTC	ACCEPTECCCC	AGCTCTACAA	AATCACCCAG	1140
	AATGGCGAAG	GCTTCAACAC TCTTCTGGTT	AAAGGTTTTC	TGGGGTCACT	GCATCAACGC	CTTGGTCCAC	1200
	TCCCTCATCC	TCTTCTGGTT	TCCCATGAAA	GCTCTGGAGC	ATGATACTGT	GTTTGACAGT	1260
	GGTCATGCTA	CCGACTATTT	ATTTGTTGGA	AATATTGTTT	ACACATATGT	TGTTGTTACT	1320
50	GTTTGTCTGA	AAGCTGGTTT	GGAGACCACA	GCTTGGACTA	AATTCAGTCA	TOTOGGCTGTC	1380 1440
	TGGGGAAGCA	TGCTGACCTG	GCTGGTGTTT	COLLOWATER	MCTCGACCAT	COCCACACTEC	1500
	ATTCCCATTG	TATTTCTGGT	TOTTACTOCC	TOTTTGATTG	AAGATGTGGC	ATGGAGAGCA	1560
	GCCBAGCACA	CCTGCAAAAA	GACATTGCTG	GAGGAGGTGC	AGGAGCTGGA	AACCAAGTCT	1620
55	CGAGTCCTGG	GAAAAGCGGT	GCTGCGGGAT	AGCAATGGAA	AGAGGCTGAA	CGAGCGCGAC	1680
	CGCCTGATCA	AGAGGCTGGG	CCGGAAGACG	CCCCCGACGC	TGTTCCGGGG	CAGCTCCCTG	1740
	CAGCAGGGCG	TCCCGCATGG	GTATGCTTTT	TCTCAAGAAG	AACACGGAGC	TGTTAGTCAG	1800
	GAAGAAGTCA	TCCGTGCTTA	TGACACCACC	AAAAAGAAAT	CCAGGAAGAA	ATAAGACATG	1860
60	AATTTTCCTG	ACTGATCTTA	GGAAAGAGAT	TCAGTTTGTT	GCACCCAGTG	TTAACACATC	1920
oo	TTTGTCAGAG	AAGACTGGCG TTTGTTAGTT	TCCAAGGCCA	TOTORANOCT	CCACTCCACT	CLGLGGGGG	2040
	AGTTAAGCAG	GCCCTCCCAA	CTCCTCTCCA	GTGCTTAGCC	TARCTTTTGT	TTATGTCGTT	2100
	ATGRAGCATT	CAACTGTGCT	CTGTGAGGTC	TCAAATTAAA	AACATTATGT	TTCACCAATA	2160
	AGARARARA	AAAAAAA					
65							
	Seg ID NO:	222 Protei	n sequence:				
	Protein Acc	cession #: 1	NP_057613				
	_	11	21	31	41	51	
70	1	11	21	31	7.	1	
70	Harring Co.	RLRLYCKGAD	MUTDEDLOVA	CKAMBELLUR	LEVENTECIA	TICVAYADIS	60
	EMPARAMITAN	YQEASTILKD	PAORLEECYE	TTEKNILLIG	ATAIEDRIOA	GVPETIATLL	120
	KARIKIMULT	GDKQETAINI	GYSCRLVSON	MALILLKEDS	LDATRAALTO	HCTDLGNLLG	180
	KENDUALITED	GHTLKYALSE	EVRRSFLDLA	LSCKAVICCR	VSPLOKSBIV	DVVKKRVKAI	240
75	TLAIGDGAND	VGMIQTAHVG NVVLYIIELW	VGISGNEGMQ	ATNINSDYAIA	QFSYLEKLLL	VHGAWSYNRV	300
	TKCILYCFYK	NAAPA I IEIW	PAPVNGFSGQ	ILPERWCIGL	YNVIPTALPP	PTLGIFERSC	360
	TQESMLRFPQ	LYKITONGEG	PNTKVFWGHC	INALVHSLIL	PWPPMKALEH	DTVFDSGRAT	420
	DYLFVGNIVY	TYVVVTVCLK LESAHFWLGL	AGLETTAWTK	FSHLAVWGSM	LIWLVFFGIY	SILMETIFIA	480 540
80	PDMRGQATMV	RINERDRLIK	PLVPTACLIE	DVAWROUGHT	DUCKABLEEVQ	PUBLICATION	600
00	RAYDTTKKKS		KINKKIPPIL	ENGOSIN/VOV	* HO LAF SULL	HOLL SQUEVY	
	MIDITARKS	nnn.					
	Sea In No.	223 DNA se	quence				
	Nuclaic Ac	id Accessio	n #: BC0170	01			
85	Coding sea	uence: 1-39	4				
	1	11	21	31	41	51	

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	AACGCTGGGC	l l	COCCTCCCCC	acacacacas a	gggcccgggc	CGAGCGGCGG	60
	CGCGCAGGC C	COCACCATCC	ACTOGGGGG	CATCGCCGCG	GTGCACAACG	TGCCGCTGAG	120
							180
5	CACGATCOGG CCAGGGAGGT ACTGCAGCGA	GAGGACCCAG	ACAGCGTGCC	CCCCATCGAT	GTCCTCTGGA	TCAAAGGGGC	240
	CCAGGGAGGT	GACTACTTCT	ACTCCTTTGG	GGGCTGCCAC	CGCTACGCGG	CCTACCAGCA	300
	ACTGCAGCGA	GAGACCATCC	CCGCCAAGCT	TGTCCAGTCC	ACTCTCTCAG	ACCTAAGGGT	360 420
							480
10	TTCAAGAGCC AGGGGTGCAT	CAGAAGACAC	ACCTGGCCTC	CAGCAGGCTG	GGCCATGCAG	ARGGIATAGC	540
10	CTACAAGGCC	TCTCTTTGCA	CCTGGCGAGA	CCCACCCCCA	CTTCCCACCT	CTCTCACCOG	600
	CTACAAGGCC	COPEN COCET	CARCCATTAC	DADDAGADOO	AACAGAGATG	GGCTTGAAGA	660
	AGGATCATGG GCCACGTGCT	CCCCCCCCC	AATTCCCAAG	GACAAGGATC	CCTCTGCATT	TTTGTCTATG	720
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15	TAACCACATA TATTGGTTCA	GAAGATTGTT	TTTCCACATA	GCATGGATTC	TGGAGATGGG	TGGCTAATGG	840
	TATTGGTTCA	ACAACTCCAC	GGAGGTAGGG	GTCACGTCTT	GGATCCTTTT	GCCTTAATCT	900
							960
	TTCAAGGAAG	GAGGGGTGGA	GGAAGAGGAA	GGGCCAAACT	AGCTGGACCC	GTCACCTTCT	1020
	ATCAGAAAGT CTTAGATGCC	AAAACCTCGT	CAGAAGTCTG	TTTCCTGCTC	Terceerere	CATATOTICA	1140
20	CTTAGATGCC	CTTGGCCCGA	GCCAGCTACC	ATTGCACCTC	TAGCTGCAAA	TACTCACACT	1200
	ACAGCAGGGA GGCACACTGC	ACAGAATIGT	CATGGCTGAA	TAGACCAATC	GTGTTCCATC	TACIGAGACI	1260
	GGCACACTGC	CTCCTGCAAT	COCCEANCAN	CCATCCCCAA	ACTTGGCAGC	TAGAAACAAA	1320
	TGTACCAGTT	MGCTTTTGCT	CTATCCCTTC	CCAATTTCCC	ACTTGGCAGC CTGGGCTCAA	CAGGGCAGTT	1380
25							1440
23	TOGATOGTCT	AGGATAGCCT	TACTCACTTG	CCTGGCAGGT	GACAGGCTGT	TGGCTGGAAT	1500
	TGCTTGGTTC	TCCTCCATGT	GGCCTCTCCA	GCAGGCTAGC	GACAGGCTGT TCAGGCTTAT	TCACATGATG	1560
	GCTTCAGGAT	TCCAAAGAGA	GTGAGAGTAG	AAGCTGAAAG	ACTTCTTGAG TTGGTCAGAG	TTCTTGGCCT	1620
	GGAACTGGGA	CTAGGACAGT	GTCACTTCTG	CTAAGTTCTT	TTGGTCAGAG	CAAATCACAA	1680
30	GGCTTTACCC	AGATTCAAGG	GATGAGAAAC	AGACTACATG	TCTTGATGAG	GGGAACCACA	1800
	AAGAGCTTGT	GGCCATTTTT	CACCTATCAC	AAATAATTTT	GGATGGGTAT GGCCTCACTC GAAGAGGTGT	TTATTTGGAT	1860
	AAAGGTATTT	CCCTCTTCCC	CCTTTCTCTC	TGTCTCATGG	GGCCTCACTC	TOCCOMBILE	1920
	GAAGGCACTA	AGACATTGTC	CIGGCCCICA	TAGTAGGAGT	GCCTCCTTGT	CTGCACTGCT	1980
35	AGTGAGTCTC	TOCKIGGGCI	AGGACATTCC	AGAGGGGGCTT	CTGAAAACCA	AGAGTCCCTG	2040
33	CCCNANCCCA	ACAGAGTAAG	CCACCCCTTG	TTCTCACTGC	CTGAAAACCA CCTCTAAGGG	AACTTGGTCA	2100
							2160
	GCATTCTCTT	TCCCCGGGAA	AGTTGACTGA	GGTGACCAGT	AATAGAATTG AACAAAAACA	AAAAGGGAGA	2220
	GTGTCTTCAG	TGCAATGTGG	CATCCTGGAT	TGGGTCTTGG	AACAAAAACA	GGACATTAGT	2280
40							2400
	TGGTTTTGAC	AGATGTACCA	TGGTGATGTA	AGATGTTGAC	CTTGGGGTAG TGTAAATCTA	GCTGGGTGAA	2460
	GGGTATACAG	GAACTCTTTG	TACTATCTCT	GCAACTTCTC	TGT/GGTCTA	GIAICATICC	2400
	AAAATAAAAG	TTTATTTAAT	TTAAAAAAAA	AAAAAAAA	AA	•	
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45	AAAATAAAAG	TTTATTTAAT	TTAAAAAAAA	AAAAAAAAA	AA	•	
45	Seq ID NO:	224 Proteinession #:	TTAAAAAAAA n sequence:	AAAAAAAAA	AA		
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	Seq ID NO: Protein Acc	224 Proteinession #:	n sequence: AAH17001.1	31	41 VLIRPLPSVL	51 DPAKVQSLVD	60 120
	Seq ID NO: Protein Acc	224 Proteinession #:	n sequence: AAH17001.1	31	41 VLIRPLPSVL	51 1	
	Seq ID NO: Protein Acc	224 Proteinession #:	n sequence: AAH17001.1	31	41 VLIRPLPSVL	51 DPAKVQSLVD	
50	Seq ID NO: Protein Acc	224 Proteicession #: 11	n sequence: AAH17001.1 21 AQGGSIHSGR QGGDYFYSFG	31	41 VLIRPLPSVL	51 DPAKVQSLVD	
	Seq ID NO: Protein Acc 1 1 TLGRAGAGRG TIREDPDSVP YLGASTPDLQ Seg ID NO:	224 Proteinession #:	TTAAAAAAAA n Bequence: AAH17001.1 21	31 IAAVKNVPLS GCHRYAAYQQ	41 VLIRPLPSVL	51 DPAKVQSLVD	
50	Seq ID NO: Protein Acc I I I TLGRAGAGRG TIREDPDSVP YLGASTPDLQ Seq ID NO: Nucleic Ac:	224 Proteicession #: 11	TTARARARAAA n sequence: AAH17001.1 21 AQGGSIHSGR AQGGSYFYSFG QUENCE n #: NM_021	31 IAAVKNVPLS GCHRYAAYQQ	41 VLIRPLPSVL	51 DPAKVQSLVD	
50	Seq ID NO: Protein Acc I I I TLGRAGAGRG TIREDPDSVP YLGASTPDLQ Seq ID NO: Nucleic Ac:	224 Protei cession #: 11 APEGPGPSGG PIDVLWIKGA 225 DNA Se	TTARARARAAA n sequence: AAH17001.1 21 AQGGSIHSGR AQGGSYFYSFG QUENCE n #: NM_021	31 IAAVKNVPLS GCHRYAAYQQ	41 VLIRPLPSVL	51 DPAKVQSLVD	
50	Seq ID NO: Protein Acc I I I TLGRAGAGRG TIREDPDSVP YLGASTPDLQ Seq ID NO: Nucleic Ac:	224 Proteinession #: 11 Apecipopsco pidviwica 225 DNA se id Accessionence: 11	n sequence: AAH17001.1 21	31 LAAVKNVPLS GCHRYAAYQQ	41 VLIRPLPSVL LQRETIPAKL	51 DPAKVQSLVD VQSTLSDLRV	
50	Seq ID NO: Protein Acc I I I TLGRAGAGRG TIREDPDSVP YLGASTPDLQ Seq ID NO: Nucleic Ac:	224 Proteicession #: 11	TTARARARAAA n sequence: AAH17001.1 21 AQGGSIHSGR AQGGSYFYSFG QUENCE n #: NM_021	31 IAAVKNVPLS GCHRYAAYQQ	41 VLIRPLPSVL	51 DPAKVQSLVD	
50	Seq ID NO: Protein Acc I I I ITLGRAGAGRG TIREDPOSVF TIGASTIPLIQ Seq ID NO: Nucleic Ac: Coding sequ	224 Proteinession #:	n sequence: AAH17001.1 21 {	31 IAAVKNVPLS GCHRYAAYQQ	41 VLIRPLPSVL LQRETIPAKL	51 DPAKVQSLVD VQSTLSDLRV	120
50	Seq ID NO: Protein Act I I I TIGRAGAGRG TIREDPDSVP YIGASTPDIQ Seq ID NO: Nucleic Ac: Coding sequ	224 Proteicession #: 11 Apecapersos PidvlwikgA 225 DNA seid Accession uence: 11	n sequence: AAH17001.1 21 AQGGSIHSGR QGGDYFYSFG quence n #: NM_021	31 IAAVENVELS GCHRYAAYOO	41 VLIRPLPSVL LQRETIPAKL	51 DPAKVQSLVD VQSTLSDLRV 51 ATCCCAAAGT	120
50	Seq ID NO: Protein Act I I I TLGRAGAGRG TIREDPDSVP YLGASTPDIQ Seq ID NO: Nucleic Ac: Coding sequ	224 Protest cession #: 11	n sequence: AAH17001.1 21 1 AGGGSIHSGR QGGDYFYSFG quence n #: NM_021 110 21 1 TCAGGGCTGC TGCAGAGGCT	31 IAAVENVPLS GCHRYAAYOO 248 31 IATGCTGAAG CCCCTGGCTG	41 VLIRPLPSVL LQRETIPAKL AGANCTICA TODAGGAGGA	51 J DPAKVQSLVD VQSTLSDLRV	60 120 180
50 55 60	Seq ID NO: Protein Act I I I TLGRAGAGRG TIREDPDSVP YLGASTPDIQ Seq ID NO: Nucleic Ac: Coding sequ	224 Protest cession #: 11	n sequence: AAH17001.1 21 1 AGGGSIHSGR QUENCE n #: NM_021 110 21 1 TCAGGGCTGC TGCAGAGGCT	31 IAAVENVPLS GCHRYAAYOO 248 31 IATGCTGAAG CCCCTGGCTG	41 VLIRPLPSVL LQRETIPAKL AGANCTICA TODAGGAGGA	51 J DPAKVQSLVD VQSTLSDLRV	60 120 180
50	Seq ID NO: Protein Act I I I TLGRAGAGRG TIREDPDSVP YLGASTPDIQ Seq ID NO: Nucleic Ac: Coding sequ	224 Protest cession #: 11	n sequence: AAH17001.1 21 1 AGGGSIHSGR QUENCE n #: NM_021 110 21 1 TCAGGGCTGC TGCAGAGGCT	31 IAAVENVPLS GCHRYAAYOO 248 31 IATGCTGAAG CCCCTGGCTG	41 VLIRPLPSVL LQRETIPAKL AGANCTICA TODAGGAGGA	51 J DPAKVQSLVD VQSTLSDLRV	60 120 180
50 55 60	Seq ID NO: Protein Act I ILGRAGAGRG TIREDPDSVP YLGASTPDLQ Seq ID NO: Nucleic Ac: Coding sequence I ATGCTTCGAG GRGACACAGG TCCACTTCCA TCCTCCTGCT TCCACATCCA	224 Protei: cession #: 11 Apedperses Pidvinika 225 DNA se id Accessio uence: 11 1: Tranhacce GCCTGGAGGG CCAGCTCCT ATCANACCE CAGCTCCT ATCANACCT CAGCTCCT ATCANACCT CAGCTCCT ATCANACCT CAGCTCCT ATCANACCT CAGCTCT ATCANACCT CAGCTCT ATCANACCT CAGCTCT ATCANACCT CAGCTCT	n sequence: AAH17001.1 21 AQGGSIHSGR QGGSYFYSFG Quence n #: NM_021: 110 21 TARGCGCTGC TGCACAGGCT TTTTCCACC TCTAGAGGCT TCT	31 LAVKNVPLS GCHRYAAYQQ 048 31 ATGCTGANG COXCTGGCTG TOTTTTCCTC CCAGAGGAGG TGTTCCTCC AGCCANAAGG	41 VLIRPLPSVL LQRETIPAKL 41 ANGARCTICA TOGAGGAGGA CCTCTCCTCA TITTCTGCTGA CCTCGGTCGAT	S1 DPARVQSLVD VQSTLSDLRV VQSTLSDLRV I ATCCAAAGT TGCTTCACTC TGATGAGACA TGCTTCCCTTC AAGCACCCTA AAGCACCCTA	60 120 180 240 300 360
50 55 60	Seq ID NO: Protein Act I IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	224 Proteinession W: 11 APEGBGPSGG PIDVLWIKGA 225 DNA seid Accession uence: 11 CTCCAAAGCG GCCTCGAGGGCCAGGTCCTC ATCCTCTAAT CCCAGGGTCAAATCGAGAGAGAAATCGAAAAGAGAAATCGAAAAGAGAGAG	m sequence: AMHITOO1.1 21 1 AgogsIHSGR QGGDYPYSFG Quence n 8: NM_021 110 21 1 TCAGCGCTGC TGCACAGGCT ACCAAGACT ACCAAGACT TCTAGACACT CACCAAGACACT TCTAGATAGCC TCTAGATAGCC TCGAGATAGCC TCGAGATAGCC TCGAGATAGCC TCGAGATAGCC	31 LAVKNVPLS GCHRYAAYOO	41 ULIRPLPSVL LGRETIPAKL ANGACCITCA TIGGAGGAGGA CCTCCTCCTC TTICTACTAG CCTCGGTCGT	51 DPAKVQSLVD VQSTLSDLRV 51 ATCCCAAAGT TGCTTCATCA TTCCTCTCTC TGATGAGACA TGCTTCCCTTT	60 120 180 240 300 360
50 55 60 65	Seq ID NO: Protein Act I IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	224 Proteinession W: 11 APEGBGPSGG PIDVLWIKGA 225 DNA seid Accession uence: 11 CTCCAAAGCG GCCTCGAGGGCCAGGTCCTC ATCCTCTAAT CCCAGGGTCAAATCGAGAGAGAAATCGAAAAGAGAAATCGAAAAGAGAGAG	m sequence: AMHITOO1.1 21 1 AgogsIHSGR QGGDYPYSFG Quence n 8: NM_021 110 21 1 TCAGCGCTGC TGCACAGGCT ACCAAGACT ACCAAGACT TCTAGACACT CACCAAGACACT TCTAGATAGCC TCTAGATAGCC TCGAGATAGCC TCGAGATAGCC TCGAGATAGCC TCGAGATAGCC	31 LAVKNVPLS GCHRYAAYOO	41 ULIRPLPSVL LGRETIPAKL ANGACCITCA TIGGAGGAGGA CCTCCTCCTC TTICTACTAG CCTCGGTCGT	51 DPAKVQSLVD VQSTLSDLRV 51 ATCCCAAAGT TGCTTCATCA TTCCTCTCTC TGATGAGACA TGCTTCCCTTT	60 120 180 240 300 360
50 55 60	Seq ID NO: Protein Act I IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	224 Proteinession W: 11 APEGBGPSGG PIDVLWIKGA 225 DNA seid Accession uence: 11 CTCCAAAGCG GCCTCGAGGGCCAGGTCCTC ATCCTCTAAT CCCAGGGTCAAATCGAGAGAGAAATCGAAAAGAGAAATCGAAAAGAGAGAG	m sequence: AMHITOO1.1 21 1 AgogsIHSGR QGGDYPYSFG Quence n 8: NM_021 110 21 1 TCAGCGCTGC TGCACAGGCT ACCAAGACT ACCAAGACT TCTAGACACT CACCAAGACACT TCTAGATAGCC TCTAGATAGCC TCGAGATAGCC TCGAGATAGCC TCGAGATAGCC TCGAGATAGCC	31 LAVKNVPLS GCHRYAAYOO	41 ULIRPLPSVL LGRETIPAKL ANGACCITCA TIGGAGGAGGA CCTCCTCCTC TTICTACTAG CCTCGGTCGT	51 DPAKVQSLVD VQSTLSDLRV 51 ATCCCAAAGT TGCTTCATCA TTCCTCTCTC TGATGAGACA TGCTTCCCTTT	60 120 180 240 300 360
50 55 60 65	Seq ID NO: Protein Act I LIGRAGAGRG TIEEDPSVP YLGASTPIDL Seq ID NO: Nucleic Ac: Coding seq ATGCTTGGAG GAGACAGG TCACTTGAT CCCTGCT CCTATTGATC COMMITTED TTGGAGGTTT	224 Protei: cession %: 11 1	n sequence: AAMIT7001.1 21 AQGGSIHSGR QGGDYFYSPA quence n #: RM_021: 110 21 TCAGCGCTGC TGCACAGGCT TTTTCCATTC ACCAAGGACC CAAGGACC CAAGCACC CAAGGACC CAAGCACC CAAGGACC CAAGCACC CAAGGACC CAAGGACC CAAGGACC CAAGCACC CAAGC	31 LAVENVPLS GCHRYANYOO 248 31 NTGCTGAMG CCCCTGGCTG TCTTTTCCCT TCTTTTCCT AGCCAAAAGC AGCCAAAAGC AGCCAAAAGC AGCCAAAAGC CCATTCCTT CTATTCCTT CCATTCCTT CCATTCCTT CTATTCCTT CCATTCCTT CTATTCCTT CTATTCTT CTATTC	41 VLIRPLPSVL LQRETIPAKL LQRETIPAKL LQRETIPAKL AAGATCITCA TGGAGGAGGA CCTCCTCTCTTTTTTTTTTTTTTTT	S1 DARKYGSLYD VOSTLSDLKV S1 ATCCCAAAGT TGCTTCATCA TGCTTCATCA GGCAGAAGT TGAGCAGTGAT GGCAGAGAT TGAGCAGTGAT TGAGCAGTGAT TGAGCAGTGAT TGAGCAGTGAT TGAGCAGTGAT TGAGCAGTTAT TGAGCAGTTAT TGAGCAGTTAT TGAGCAGTTAT TGAGCAGTTAT	60 120 180 240 300 360 480 540
50 55 60 65	Seq ID NO. Protein Act Interpolation Act	224 Proteiression #: - 11 Apegggggggggggggggggggggggggggggggggggg	n sequence: Adliana Alliana Al	31 LANIENVPLS GCHRYAAYOO	41 ULTRIPSVL LQRETIPAKL 41 INCRETIPAKL 41	S1 S1 ATCCCAAAGT TGCTTCAYCA TGCTTCCTCC TGCTTCCCTCC TGGTTCCCTT TGATGAGGCCTCC TGCTTCCCTT TGATGAGCCTCC TGCTTCCCTTCC	60 120 180 240 360 420 540 600
50 55 60 65	Seq ID NO. Protein Act Interpolation Act	224 Proteiression #: - 11 Apegggggggggggggggggggggggggggggggggggg	n sequence: Adliana Alliana Al	31 LANIENVPLS GCHRYAAYOO	41 ULTRIPSVL LQRETIPAKL 41 INCRETIPAKL 41	S1 S1 ATCCCAAAGT TGCTTCAYCA TGCTTCCTCC TGCTTCCCTCC TGGTTCCCTT TGATGAGGCCTCC TGCTTCCCTT TGATGAGCCTCC TGCTTCCCTTCC	60 120 180 240 360 420 540 600
50 55 60 65 70	RANATAMANG Beq ID NO: Protein Acc. ILRAGAGAGG ILRAGAGAGG Seq ID NO: Nuclaic Acc. Coding seq: ATGCCTCGAG ATGCCTCGAG ATGCCTCGAG ATGCCTCGAG TCGAGTCTGG TCGAGTCTGG TCGAGTCTGG TCGAGTCTGG TCGAGTCTGG TCGAGTCTGG TCGAGTGGG TCGAGTGGGG TCGAGTGGGGG TCGAGTGGGGGG TCGAGTGGGGGGGGGG	224 Proteiression #: 224 Proteiression #: 11 1	n sequence: AMH17001.1 21 1	31 LAVIGUYELS GEIRYAAYOO	41 VLIEPLPSVL LQRETIPAKL 41 I AMARCTICA TIGGAGGAGGA CCTCCTCCT TICTGCTGATG TICTGCTGATG TICTGCTGATG TICTGCTGATG TICTGCTGATG TICTGCTGATG TICTGCTGATG TICTGCTGATG TICTGCTGATG TICTGCTGATG TICTGCTGATG	S1 DPARVIGSLVD VQSTLSDLRV S1 ATCCCAAAGT ATCCTCATCA TCCTCCATCA TCCTCCATCA GGCGAAATA TGCTCAAAGCCTA GGCCAAAGT GGCCAAATA TGCTCCAAGCCTA GGCCAAATA TGCTCCAAGCC TGGCCACTCC	60 120 180 240 480 540 660 6720 780
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10	Nucleic Act	227 DNA sec ld Accession sence: 82-1	#: NM 0050	025.1			
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20	TATAATCGTC GCTCTTGCAA CACTCAATGG	TTAGAGCCAC TGGGAATGAT GATATGACAG	TTTCCCTGAG TGGTGAAGAT GGAACTTGGG CCTAAAAAAT AGAGAGCCAA	GAAAATATTC GCCCAAGGAT GGTGAAGAAT	TCTTCTCTCC CTACCCAGAA TTTCTTTCTT	ATTGAGTATT AGAAATCCGC GAAGGAGTTT	240 300 360 420
	GTGCAAAATG GCAGCAGTAA TGGGTGGAGA GCTGCCACTT	GATTTCATGT ATCATGTGGA ATAACACAAA ATCTGGCCCT	CAATGAGGAG CITCAGTCAA CAATCTGGTG CATTAATGCT	TTTTTGCAAA AATGTAGCCG AAAGATTTGG GTCTATTTCA	TGATGAAAA TGGCCAACTA TATCCCCAAG AGGGGAACTG	ATATTTTAAT CATCAATAAG GGATTTTGAT GAAGTCGCAG	480 540 600 660
25	ATTCCAATGA GAAGCTGGTG ATGCTGGTTG	TGTATCAGCA GTATCTACCA TGTCCAGACA AAGAATGGGC	AACCTTTCT AGGAGAATTT AGTCCTAGAA GGAAGTTCCT AAACTCTGTG	TATTATGGGG ATACCATATG CTTGCTACTC AAGAAGCAAA	AATTTAGTGA AAGGAGATGA TGGAGCCATT AAGTAGAAGT	AGTCAAAGCA AGTCAAAGCA ATACCTGCCC	720 780 840 900 960
30	AGGTTCACAG GAAATTTTCA TCCAAAGCAA GTCTCAGGAA	TGGAACAGGA TCAAAGATGC TTCACAAGTC TGATTGCAAT	AATTGATTA AAATTTGACA CTTCCTAGAG TAGTAGGATG	AAAGATGTTT GGCCTCTCTG GTTAATGAAG GCTGTGCTGT	TGAAGGCTCT ATAATAAGGA AAGGCTCAGA ATCCTCAAGT	TGGAATAACT GATTTTTCTT AGCTGCTGCT TATTGTCGAC	1020 1080 1140 1200 1260
35	GTCATGCATC TTATTTGAAT TAGGATTTGT AATATATGTA	CTGAAACAAT AACAAGGAAA GTTTTACAGT AATTATAAGT	CAGAAACAGG GAACACAAGT ACAGTAACTA ATATCTTAAG AACTTGTCAA	GGACATGATT AGCACATTAT ATAATATTTA GGAATGTTAT	TCGAAGAACT GTTTGCAACT AAATAGTTCC CAGTATTAAG	TTAAGTTACT GGTATATATT AGATAAAAC CTAATGGTCC	1320 1380 1440 1500
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45	MAPLGLPSLL ELGAOGSTOK	11 VLQSMATGAT BIRHSMGYDS	21 PPEEAIADLS LKNGEEPSFL	31 VNMYNRLRAT KEPSNMVTAK	41 GEDENILFSP ESQYVMKIAN	51 LSIALAMGMM SLFVQNGFHV	60 120
50	ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDB IDLKDVLKAL	VLQSMATGAT EIRHSMGYDS YFNAAVNHVD KSQFRPENTR ISMMLVLSRQ GITEIFIKDA	1	VNMYNRLRAT KEPSMMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS	GEDENILPSP ESQYVMKIAN NLVKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE	LSIALAMGMM SLFVQNGFHV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQE	
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_	AGGGGCGCAG	GAATTCTGAT GGATATCGAC	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCACTCAG	120
5	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCCT	GGGTATAGAA	180 240
	GENERACTOS	GAGAACCAGC	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
	TCTCTCTTGA	ACCOTTGGAA TGCCTCCATG	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
10		TCATGGCTTG CAATGCTGGG					420 480
10	ACCCAGTGGA	CAATGCTGGG CCACAAGAAG	COCCACCOCT	CANTGGARGA	CGTGTGGGTCT	CTGTCCAAGC	540
	ACGAGTETTE	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660 720
15	TTCAGGATGG	CATCGTGTGC	CCCTCAGAAT	GAGAGAGTCA	AGCTGGGCAG	AATCTCTCGC	780
13	Chacaconica	CCCTTCCTTT	GGAGACTGCT	CCATCAGTGC	CGAGGTGTGT	GGGAACAGGC	840
	TTCACTGCAC	CGCCATCTTA	CTGAGTTGCT	TCACGTGAGG	AAAAGGGGGC	TTTGGCCCTG	900 960
	TGACTCAGTT	CCACATTTTG	GATTGCATAC	TGGAAAAGAA	GCCAATCTTC	TABABATCTG	1020
20	AGGGAGGGGA	CGGCTGTATA GAGGTGGAAT	ACAGTAGTTC	TTGGAATCTG	AAGTCTCCTA	TTTGATCAGG	1080
	TTATTTCCTG	GGACTTGGCA	AAAATCTGAT	TGGTGGGGAT	CTCCTAGGAC	CTAGTGGACA	1140
	TCTGGTATTA	ATTTAATCTC GTAGCTACCT	AGGAAAAACA	AGAAATTAAC	CCAGAGAGAG	TCTGGGTTTT	1200 1260
	ACCTCTGACT	TACAGCTGCA	GTCACCTTTG	CTATAAGGCA	CCTGGGTAGA	AGGGTGGATG	1320
25							1380
	GTGGTTTTTT	GITTTATTTT	TGTCAAGATT	GATTTTTAGA	TGCAAGGACT	TGAAAAGACC	1440
	CAGAAGGATG	CACAACTTAG	TGCACCAGTA	GCACCAGCCA	TTTTGAGCAG	AGTACCTCTT	1560
	TGGGGAGCTT	TTCGTTTTGT	TTTGTTTTTA	ATTCTCTTTC	CTTAGCAGCA	AGGTCTTTTT	1620
30	TCCTAGAGAA	TCTACTCCGT	TGCAGAATCA	TTGCAACCTC	AGGAGCCCTC	ACTGATTGAG	1680 1740
	TGCTGTCAGC	CTGATATACT TGTCGTTAAA	CAACCGTCGG	AGACCAGATG	ACCTOTTAGA	TGGCTAGTCC	1800
	TGTATAACTC	GACTCTGTAT	GTTTCAATGT	ATCTTACTCC	AATGCTTCAC	CTGCTGTACA	1860
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50	LSIVCLMITQ Seq ID NO: Nucleic Ac TTTTTANGGT CACAACATGA TGTTTGTTACCA TGTTTATAGGT TGTTATGAGT TGTTATGAGT TAGTATATATA	LAGFSGPNFQ 233 DNA sei id Accession 11	DGCLIRSE THERE THE THE THE THE THE THE THE THE THE TH	31 TIGGTGTTA TTGTTGTTTA TTGTTGTTGTC CCAATAACTC CCATAGTC TTAATTTTCA TATTTTGACTA TATTTTGACTA TATTTTTTTTTT	41 GITTTACTTA TTACTCCC TAAACTTTM TTAACCTGGA TAAGCTACT AGCTTTACT AGGTTACT ATGTTTTCC ATGTCTGGAT ATACCTGATT ATACCTGAT ATACTGGTC ATTATATAGT TATATATGTT ATAGATACA ATGATTTTTC	51 I TORGAGTOT AMATTATICA AGTTATAACA AGTTATAACA TOTTAGTATAT TAATATACA ATAAACATAA ATAACCTAAA TTATTTCAAAC TAATTATAA ATTCAAACA AGCTCACA AGGTCTCCAT	120 180 240 300 360 420 480 540 660 720 780 840 960
50 55 60	LSIVCLMITQ Seq ID NO: Nucleic Ac 1	LAGFSGPNFQ 233 DNA sei id Accession 11 GCTCATATAT ATCACATAAT ATCACATAAT ATCACATAAT ANGCACAAT ANGCACAAT ANGCACAT ATACTATTAT AATCATCAGA ATTACTATTA ATTATATATA CATTITAAT CAGTITATA CAGTITATA ATGTTCTAG TTGTTCTAG ACTCTTACTA A	DGCLIRSE THERCE ##: CAT cl' 21 ACTOMATTIT CATGRATTIT TGAGAAGTC TTIGGOTAG TGAATTATT TATGGAAAAT ATTATATAT CANGTTACAT ATTATATATA CANGTTACAT ATTATATATA CANGTTACAT ATTATATATA CANGTTACAT TATGGATAAA TOTTATATAT TGAGATAAAT TGAGATAAAT GAGATTATT GGTTCCCTAR GCAAGCACTG	31 TIGITIGITIA TIGITIGITA TITTITIACI CCANTANCIC CICITAGATA CICITAGATA ANATIACITA ANATIACITA ANATIACITA ANATIACITA ANATICIAN TANATAGGIC GGATCIGCCA ANATICCAN ANTICCAN	41 GTTTTACTTA TTTACTCCCC TARACTITTO TTARACTGGA TARACCACTA AAGCTITCAT TGCATTITCA TGCATTITCA TGCATTITCA TGCATTITCA TATACTGGAT TATACTGGAT TATATATATAT TATATATATAT TATATATATA	51 I TTGAGAGTGT AMATTATICA AGGTTATAACG TITTAATTTT AATTTGATTTT TCTTGGATATT AAAATATTTG TATATATGGA ATTTAAAAA TTTTTTTT	120 180 240 300 360 420 480 540 660 720 780 840 900 900 960 1020
50 55 60	SEQUEMITO Seq ID NO: Nucleic Ac ITTERATOR TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TAG TAG TAG TAG TAG TAG TAG TAG TAG TAG	LAGESGPNFQ 233 DNA set id Accession 11 jGCTCATATAT ATCACATAAT ATCACATAAT ATCACATAAT ATCACATAAT ATCACATAAT ATACCAGAA ATTACCAGAA ATTACCAGAA ATTACCAGAA ATTACCAGA ATTACAGA ATTACCAGA ATTACCAGA ATTACTTTTAAAA CAGGTTACAA AGATTTAAAA AGATTTAAAAA AGATTTACAGAA AGATTACAGAA AGATTACAGAA AGATTACAGAA AGATTTACAGAA AGATTACAGAA AGATTACAGAA AGATTACAGAA AGATTACAGAA AGATTACAGAA AGATTACAGAA AGATTACAGAA AGA	DGCILRSE TUNGICS TUNGICS TO # #: CAT G1 21 ACTOSTATTS CATGATTTT TTGGAGAGG TTTGGTAGG TTTGGTAGG TTTGGTAGG TTGGTAGG AAGGTGACAG AATGATTATT TATGGAAAAC AATGATATT TATGGAAAAC AATGATTATT TATGGAAAAC AATGATTATT TATGGAAAAC AATGATTATT TATGGAAAAC AATGATTATT TATGGAAAAC AATGATTATT TAGGATAACT AATGATTATT TAGGATAACT AATGATTATT TAGATTATTATT TAGATTATTATT TAGATTATTATT TAGATTATTATTATTATTATTATTATTATGATTATTATTA	31 TROTTOTTA TITOTTOTTA TITOTTA TITOTTA TITOTTA TITOTTA TITOTTA TITOTTA TITOTTA TITOTTA TITOTTA TATTITICA TITOTTA TATTITICA TATTITICA TITOTTA TATTITICA TA	41 GTTTTACTTA TTTACTCACTA TTTACTCACTCA TAACTTTTO TTAACCTGA AACACTACT AACCTATCA AACACTACT AACCTATTTC AACCTATTTTC AACCTATTTTC AACTTTTTC TAACTATATTTTC TAATATATTTT TAATATATTT TAATATATTT TAATATATTT TAATATATTT TAATATATTT TAATATATCT TAATATTTTT GAATATTTTC CTTAGGTTAT	SI TIQAGAGTOT AMATTATACA AGTIATATACA GTITTAATITI AATTOATITI AATATATTO ATATATAGCA ATAAAAGATA ATATTICATAA ATATTICATAA ATATTICATAAA ATTICATAAA ATTICATAAA ATTICATAAA ATTICATAAA ATTICATAAA ATTICATAAA ATTICATAAA TOAAAAACA TOAATAACA TOATTICATAAA TOATTICATAAA TOATTICATAAA TOATTICATAAA TOATTICATAAA TOATTICATAAA TOATTICATAAA TOATTICATAAA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1080
50 55 60	LSTVCLMITQ Seq ID NO: Nucleic Ac TITTHANGGT CACACATGA TAGTITCHANGGT TAGTITCHACA TAGTITCHACA TAGTITCHACA TAGTITCHACA TAGTITCHACA TAGTITAHACA TAGTITAHACA TATATITAHAG TATATITHAG TAGTITHAG TATATITHAG T	LAGESGINING 233 DIA Ge did Accession 11	DOCLINES TURNOS TO STATE TO ST	31 TOTTOTTA TITITIACT COCATRACT TITATITACT COCATRACT TITATITACA TATTITACA TATTICA	41 THIRCTORY THACCTOR THACCTOR TANCETTOR ANCACTACT ANCACTACT ANCACTACT ANCACTACT ANCACTACT ANCACTACT ANCACTACT ANCACTACT ANCACTACT TOCATTACC ANCACTACT ANC	51 I TIGAGAGTOT AMATTATACA AGTATATACA AGTATATACA TITTAATTIT AATTATACACTACA ATTATATACA ATTATATACA ATTATATACA ATTATATACA AACCTGAAA ATTATATACA AACCTGAAA ATTATATACA AACCTGAAA ATTATATACA AACCTGAAA ATTATATACA AACCTGAAA ATTATATACA TOTATATACACA TOTATATACACA TOTATATACACACA TOTATATACACACACACACACACACACACACACACACACA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140
50 55 60 65	LSTVCLMITQ Seq ID NO: Nucleic Ac 1 TITALINGST CACALACHINA TOTITICATA TOTITICATA TOTITICATA TOTITICATA TOTITICATA TOTITICATA TATALINATI TATALITATO TATAL	LAGISSONNO 233 DNA GE 464 ACCESSION 11 11 (CICATATAT ATTORNATAT ATTORNATAT ATTORNATAT ATTORNATAT ATTORNATAT ATTORNATAT ATTORNATAT ANACCARA ATTACCACAT ANACCARA ATTACCACAT ATTACCACAT ATTACCACAT TATACTACT ATTACTACT ATTACTACT TATACTACT TATACTACT TATACTACT TATACTACT TATACTACT TATACTACT TATACTACT TATACTACT TATACT T	DOCLINES THENCE TO THE TOTAL THE TOT	INTERPRETARION OF THE PROPERTY	41 GETTACTTA TITACTCOC TRANCITTO TITACCTCOG AGCITTCAT TGCATTTCC ATGCTTCAT AGCATTACAT ATACCTGAT ATACCTGAT ATACCTGAT ATACATCAT ATACATGAT ATACATGAT ATACATGAT ATACATCAT ATACATGAT ATACATCAT ATACATGAT ATACATCAT ATA	51 1 TRUMGMATTOT AMATTATAGA TITTHAMTTAGA TITTHAMTTT AMTTGATTC TCTTMATTATT AMATTATTOT AMATTATTO AMATTATTO AMATTATTO AMAGGRA AMA	120 180 240 300 360 420 480 540 660 660 720 720 780 840 900 960 1020 1080 1140 1260
50 55 60 65	LSTVCLMITQ Seq ID NO: Nucleic Ac 1 1 TITTANIGGT CACAACNTA TOTTITACT TAGTANACT TAGTANA	LAGESGINTQ 11 11 1 GETCATATAT ATCORPANTA ANDOTORPANTA	DUCLIESE TUNNEL THE CAT CL 21 INTERPRETATION ACTIONATION ACTIONATION TOTAL CANALITATION TOTAL CANALITATION AND CANALITATION THE CANALITATION AND CANALITATION AND CANALITATION AND CANALITATION CONDUCTION AND CANALITATION AND CA	31 TOUTOUTTA TITTITIACT CCAATACTC CCTOTAGE THANTICACT THANTICACT TATTITIACTC TATTITIACTC TATTITIACTC TATTITIACTC TATTITIACTC ACTICACTA ACTICACT GUARTICACT TAATTICACT TAATTICACT GUARTICACT ACTICACT GUARTICACT GUARTICACT ACTICACT	41 GHITACTIA TITACTIA TITACTICA TITACTICA TITACCTOCA TAAACTITTO TITACCTOCA TAAACCACATA TAAACCACATA AACACTACT GGCAAATT AACACTACT TAATACATACT TAATACATACT TAATACATAC	51 TRUNGAGGTOT ANATTATICA AGTIVATAAGG TITTAATTIT ANTIGAT TOTTOTATIT ANTIGAT TATATAGG TATATAGG TATATAGG TATATAGG TATATAGG TATATAGG TATATAGG TATATAGG TATATAGAG TOTTOTAGT TATTETTTTT TOTTOTAGT TOTTOTAGT TOTTOTAGT TOTTOTAGT TOTTOTAGT TOTTOTAGT TOTTOTAGT GTGAGGAG GTTAAAAGCA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140
50 55 60 65 70	LSTVCLMITQ Seq ID NO: Nucleic Ac 1 ITTIMATOR CRCAACATMA TOTITICATA LAGESGINNO 11 11 11 11 11 11 11 11 11 11 11 11 1	DOCLINES TUNNING TUNNING THE CAT CI 21 INTERPRETATION CATASTIT TIGAGASTC TITTGOTATA TITTGOTATA TATGAGASTC TITTGOTATA TATGAGASTC TITTGOTATA TATGAGASTC TITTGOTATA TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGAGASTC TATGATTAGASTC TATGATT TATGAT	31 TROTTOTTA TITITITAC CCANTAGET CCCTOTAGE TRAGET TRAGETACT TRAGETACT TATATEGET ANATTACTA TATATEGET ATACTANT ATACTANT ATACTANT ATACTANT GGATTCTAC GGATTCTAC GGATTCTAC GAAGTTACAG AATTCAGT GAAGTTACAG AATTCAGT GAAGTTACAG AATTCAGT AAATTACTAC AAATTACAT AAATTACTAC AAATTACAT AAATTACTAC AAATTACAT AAATTACTAC AAATTACAT AAATTACAT AAATTACTAC AAATTACAT AAATTACTAC AAATTACAT AAATTACTAC AAATTACAT AAATTACAT AAATTACAT AAATTACAT AAATTACAT AAATTACTAC AAATTACAT AAATTACTAC AAATTACAT AAATTACTAC AAATTACAT AAATTACTAC	41 GETTACTTA TTTACTCO TTACTCO TAAACTTTO TTAACCTCO TAAACTTTO TTAACCTCO TAAACTTTO TTAACCTCO TAAACTTTO TAACCTCO TAAACTTAA ACGTTACT TAACTTAA ACGTTACT TAATTAAATT TAATTAAATT TAAATTAAAT	51 TRANSACTOT AMATTATECA AGTTATACA AGTTATACA AGTTATACA ATTACATATT AAATCATTC TCTCATATATT AAAATCATTC TATATTATA AAATCATTC TATATTCTT TATATTATA ATTCCAAAAC TCTAAAAC TCTAAAAC TCTAAAAC TCTAAAC TCTAAC	120 180 240 300 420 480 540 660 720 780 840 960 1020 1080 1140 1200 1320 1320	
50 55 60 65	LSTVCLMITQ Seq ID NO: Nucleic Ac I ITTIANIGGT CACAACATAA TOTTCTTAG TAGTATACT TITGTTAGGT AAGCATATT TAGTATACT TCCAGATAA TCCAGAT	LAGESGINTO LAGESGINTO LAGESGINTO LI I I I GETCATATAT ATTOCATATAT ATTOCATATAT ATTOCATATAT ATTOCATATAT ATTOCATATAT ATTOCATATAT ATTOCATATAT ATTOCATATAT ATTOCATATAT ATTACATATA ATTOCATATAT ATTACATATAT ATTACATATAT ATTACATATAT ATTACATATAT ATTACATATATAT	DUCLIESE TURNES TURNES TURNES TO TO TO TO TO THE TO	31 TROTROTTIA TRITTACT COARTANCTC COCTORAGE COCCOTAGE TRITTITACT COARTANCTC TRITTITACT TRATTITACT TRATTITACT ARATTACTAT TRATTACTAT TRATTACTAT TRATTACTAT TRATTACTAT TRATTACTAT ARATTACTAT ARATTACTAT ARATTACTAT ARATTACTAT ARATTACTAT ARATTACTAT ARATTACTAT ARATTACTAT TRATTACTAT TRATTACT T	41 GITTACTTA TITACTCCCC TARACTTTTI TITACCTCCC TARACTTTTI TITACCTCCC TARACTTTTI TARACTCCCC TARACTTTTI TARACTCCCC TARACTTTIC TARACTCCCC TARACTTTIC TARACTCCCC TARACTTTIC TARACTCCC TARACTTTIC TARACTCCC ARACTCCC TARACTCC ARACTCC	51 ITMAGAGTOT AMATHATTICA AGTTATAGA AGTTATAGA ATTATAGA ATTAGAGTAT AAATTATTICA AAATTAGATTICA AAATTAGATTICA AAATTAGATTICA AAATTAGATTICATTICA AAATTAGATTICATTICATICA AAAATTAGATTICATICATICATICATICATICATICATICATICATI	120 180 240 300 420 480 540 600 660 840 960 960 1020 1080 1140 1260 1380 1440
50 55 60 65 70	LSTVCLMITQ SVCILMITQ INCLEIC AC ITTIANIGGT COCCAGACATA TOTTICTTAG TOTTICTTAG TOTTICTTAG TOTTICTTAG TATTIATITGT ADGCTATT TATTIATITGT TATTIATITGT TATTIATITGT TATTIATITGT TATTIATITGT TATTIATITAT TATTIATITT TATCAGAGACCT TITTITTAGAG TATTIATITT TATCAGAGACCT TITTITTAGAGAGCCT COCTAGATATA COCTAGATA COCTAGATATA COCTAGATA COCTAGATA COCTAGATA COCTAGATA COCTAGATA COCTAGATA COCTAGAT	LAGISSIPNIO 233 DNA Sect de Accessión de Control de Con	DGCLIRES TURENCE TO THE CATT CIN 21 1 ACTUANTITY TORONAMA ATTANTAMA ACTUANAMA ATTANTAMA ATTANT	11 TOSTIGITAR TOTAL TOTA	41	51 TUMOGOTOT THUNGOGOTOT THUTTITITITI THUTTICH GOCTOTOGOT THUTTICH GOCTOTOGOT THUTTICH GOCTOTOGOT GOCTOTOGOT THUTTICH TOTOGOTOT THUTTICH GOCTOTOGOT GOTOTOGOT GOT	120 180 240 300 360 420 480 660 720 780 840 960 1020 1080 1140 1260 1320 1380 1440 1560
50 55 60 65 70	LSTVCHITQ Seq ID NO, Nucleic Ac I IIITIANISOT CACAGANTAA TAGTITATTI TAGTITCHACT AATRAGTI TAGTITAGCT AATRAGCT TATTITAGCT AATRAGCT TATTITAGCT AATRAGCT TATTITAGCT AATRAGCT TATTITAGCT TATTIT	233 DNA 99 Edd Accession 11 [COTCATATAT ATCATATAT ATCATATAT ATCATATAT ATCATATAT ANACCAGA ATTATATATATATATATATATATATATATATATATA	DUCLIERS TURNING TURNING TO THE TOTAL THE TOTA	31 TOUTION TO A THE TOUTION TO A THE THE THE THE THE THE THE THE THE THE	41	51 TUMAGATOT AMATHATTOA AGTTATAGA AGTTATAGA AGTTATAGA ATTAGATTTT AMATHATTT AMATHATTT AMATHATTT AMATHATTT AMATHATTT AMATHATTT AMACONAMA ATTAGATATTT TATATATTG AMACONAMA ATTAGATAGAT AMACONAMA ATTAGATAGAT AMACONAMA ATTAGATAGAT AMACONAMA ATTAGATAGAT AGTTAGAT A	120 180 240 360 420 480 540 660 720 960 960 1020 1020 1140 1200 1120 1320 1380 1440 1560 1680
50 55 60 65 70	LSTVCLMITQ Note of the control of th	LAGISSIPNIO 233 DNA Se dd Accessio 11 11 GCTOATATAN ACCACANA ACTOCACANA ANACCANA ANA	JUNIOLE NE L'ACT CHE L'ACT	31 TOUTIONTAN TOUTION TO THE TOUTION	41	S1 1 TOUGGGTOT AMATTATICA AMATTATICA AMATTATICA AMATTATICA TATTOTAM TATTOTAM TATTOTAM AMATTATICA AMATTATICA AMATTATICA TATTOTAMA AMACTIGNA AMACTIGNA AMACTIGNA AMACTIGNA AMACTIGNA AMACTIGNA AMACTIGNA AMACTIGNA AMACTIGNA AMACTICA TITTOTAMAT AMACTICA AMACTICA TITTOTAMAT AMACTICA	120 180 240 360 420 480 540 660 720 960 1020 1020 1140 1200 1200 1320 1320 1320 1560 1560 1560 1560 1740
50 55 60 65 70	SEQ ID NO. NUCLEIC NUCLEIC NO. NUCLEIC NUCLEIC NO. NUCLEIC	233 DNA 98 Ed ACCESSIONO 11 11 12 13 13 14 15 15 15 16 17 17 17 17 17 17 17 17 17 17 17 17 17	DGCLIRES JUENCE B F CAT CIN 21 1 CONTRATTI CATGATATT TOGAGAGAT TTTGAGAGAT TTTGAGAGAT TTTGAGAGAT TTTGAGAGAT TTTGAGAGAT TTTGAGAGAT TTTGAGAGAT ANGUTAGAGA ATGATTAGAGA ATGATTAGAGA ATGATTAGAGA ATGATTAGAGA ATGATTAGAGA AATGATTAGAGAA TGAGAGAGA	INTERPRETATION OF THE PROPERTY	41 OFFITACITA TTIACITACITA TTIACICOC TAAACCITYOT TAAACCITYOT TAAACCITYOT TAAACCITYOT TAAACCITYOT TAAACCITYOT TAAACCITYOT TAAACCITYOT TATACITYOT TATACITY TA	51 1 TUMBGAGTOT AMATTATICA AMATTA	120 180 240 360 420 480 540 660 720 720 960 960 1020 1020 1140 1200 1140 1260 1140 11560 1680 1740
50 55 60 65 70	SET UNITY OF THE SET O	231 DNA 98 164 ACCEPTATOR ACCEPTATION ACCE	DGCILESS NUMBER A F. CAT SIN LCRUTATITY ACTORITY AND ACCOUNTS ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AC	111 THOTTOTTA THITTITACT COASTANCTO THAT THAT THE THAT THAT THAT THAT THAT THAT THAT THAT THAT THAT THAT THAT THAT	41 GHITTACTTA TTIACTCACTTA TANCETTURA TANCET	S1 1 TOMAGATOT AMATTHATICA AMATTHATICA AMATTHATICA AMATTHATICA AMATTHATICA AMATTHATICA AMATTHATICA THANNINGO THANNIN	120 180 240 360 420 480 540 660 720 960 1020 1020 1140 1200 1200 1320 1320 1320 1560 1560 1560 1560 1740
50 55 60 65 70	Seq ID NO. Nucleic Ac Seq ID NO. Nucleic Ac TITITANIOGE CACAGATGA TOTTICACA	2.31 DMA 98 ed dd Accession ed	DGCLIRES Quence B #: CAT cli 21 1 CTUTATATT CATGATATT TGAGAAGATT TTTGAGAAGATT TTTGAGATATAT TATGAGAAGAT ATTATGAGAAA ATTGATACAT ATTATGAGAAAA TTTGAGAAAAA TTTGAGAAAAA TTGAGAAAAAA TTGAGAAAAAAAA	INTERPRETATION OF THE PROPERTY	41 OFFITTACTTA TTTACTCACTTA TTTACTCACTTA TTTACCACTTA TAACCTTTACT TAACCTTACT TAACCTTACA ACCTTTCAT TACCACTTACA TACCACTTACA TACCACTTACA TACCACTTACA TACCACTTACA TACCACTTACA TACCACTTACA TACCACTTACACTTACA TACCACTTACACTTACA TACCACTTACACTTACACTTACACTTACACTTACACCACTTACACTACACTTACACTTACACTTACACTTACACTTACACTTACACTTACACTTACACTTACACTTACACTACACTTACACTTACACTACACTTACACACACACACACACACACACACACACACACACACACAC	51 I TURNINGTOT AMATTATICA CONTROL CO	120 180 240 300 360 420 540 660 660 660 720 780 840 900 1020 1080 1140 1120 11320 1140 11500 11500 11500 11500 11500 11500 11500 11740 11500
50 55 60 65 70 75 80	SET UNION NUCLEAR OF THE SET OF T	2.31 DMA SE 1.31	DGCLLESS NUMBES NUMB	THOTTOTTAN THE THE THE THE THE THE THE THE THE THE	41 GRITTACTTA TTTACTCACTTA TTTACTCACTTA TTTACTCACTTA TTTACCTCACTTA TTTACCTCACTTACACTTACA AGCTTACAT AGCTTTCAT TACACTTCAC ATTACTTGAT AACTTGAT AACTTGAT TACACTTCAT TACACTCAT TA	SI TRUGGGTOT AMATTATICA AMATTATICA AMATTATICA TITTATICA TITTATICA TITTATICA AMATTATICA ATAMANGEN ATTAMANGEN ATTAMANGEN ATTAMANGEN ATTAMANGEN ATTAMANGEN AGGITTOMANGEN AGGI	120 180 240 360 420 480 540 660 720 780 840 900 1020 1020 1140 1220 1380 1440 1550 1620 1740 1680 1740 1880 1880
50 55 60 65 70	SEQUENTING SEQUENTS SEQUENTS THINKINGS THINKIN	2.31 DNA 98 et de de la consession de la	DGCLLESS NUMBER B : CAT div 21 21 12 13 14 15 16 17 17 17 17 17 17 17 17 17	11 11 11 11 11 11 11 11 11 11 11 11 11	41 GHTTTACTTA TTTACTCA TTTACTCA TTTACTCA TTTACTCA TTTACTCA TAAGCTTAC AACACTAAC AACACTAC AA	51 1 TOMOGRATION AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA AMATTATICA COCCUTTORIA COCCUTTO	120 180 240 300 360 420 540 660 660 660 720 780 840 900 1020 1080 1140 1120 11320 1140 11500 11500 11500 11500 11500 11500 11500 11740 11500
50 55 60 65 70 75 80	LestvickHing Seq ID NO. Nucleic Ac The Management of the Control o	2.33 DMA 98 1d Accession 11 11 11 11 11 11 11 11 11 11 11 11 11	DGCLLESS JUMESS B F: CAT G1: 21 1 CTOTATTT CATGATTTT CATGATTTT TTGAGAAGTTT TTGAGAAGTTT TTGAGAAGTTT TTGAGAAGTTT TTGAGAAGTTT ATTAAATAT ATTAAATAT ATTAAATAT TATGAGAAAA ATTOTACAT AGAGCTTAAA TCCTGGGGAT AGAGCACT AGCACATGT CTTCTTGAGAA ATTOTTTAAA ATTATTTAA TTAATATAT TTAATATAT TAGGAAAAA TTAAAATAT TAGGAAAAA TTAAAATAT TAGGAAAAA TTAATATAT TAGGAAAAA TTAATATATAT	TOTAL TOTAL	41 THIRACTIA THIRACTIA THIRACTIA THIRACTICA	SI TRUGGGTOT AMATTATICA AMATTATICA AMATTATICA TITTATICA TITTATICA TITTATICA AMATTATICA ATAMANGEN ATTAMANGEN ATTAMANGEN ATTAMANGEN ATTAMANGEN ATTAMANGEN AGGITTOMANGEN AGGI	120 180 240 360 420 480 540 660 660 720 780 840 900 1020 1140 11200 11200 1140 1140 11500 1140 11500 1

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		AGTTTTCTGA					2280
		TTTGTTTACT					2340
	AAAACCTCAT	GCCTTTTCAT	TACATCTAAT	TTGAACTCTC	AACTTCAGTG	CCAGAAGTGC	2400
	TTTAAAGATG	CTTTAATGAA	AAGTATTAAG	AAAATATATA	GATTTGTATG	TCAGTTTATA	2460
5	CTTCAGAAAT	CCATATATTT	GTCATATTTA	TTTTTTTAGA	AACCTCCTAA	TTGGATAACT	2520
-	AGATGGTATT	TAAAATGAAT	GCCCAAAAAT	ATCTTGTACC	TTTGTCCAAA	AGTTTATCTG	2580
		CCAGCCATTC					2640
	ATTTTATATT	ACTATGGTAT	CTGTGTACCA	TATTTCTAAG	TATTCATTAT	TAAATTGGTA	2700
		CCATAACCTG					2760
10	ATAGAGATTC	TTCTTTTATG	AAGAAGAGCT	GACGTAATTT	ATTACCAGTG	CATCTGCACA	2820
	AAGACATTAA	CATAAGTCTC	TGAGCAGTGA	TACATTTTCA	AACATGAAGA	GTGACAACCA	2880
		CAACCACGGC					2940
	TOTALCTROT	ATCGCCTCTG	GCATAACTTA	CACGAATCGT	CCTCCCTACT	TGTCTACGCT	3000
		GCACTTGCCA					3060
15		CAACTCTACC					3120
		AAAACCACTA					3180
						ACCACAAACA	3240
		CACATACACT					

20 Seq ID NO: 234 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 27-281

	1	11	21	31	41	51	
25	1	1	1	1	1	1	
	AGCAGGAGGA	GAGCTGGCGG	GAAGACATGC	ACCCCTTGAA	GACCCAGAGA	GAGGCCGTCT	60
	GTCTACCGCG	TAGCAGTTAC	ATCAGACTGA	GACACTTCCT	GTTTACAGGA	GACTATAAAA	120
	TTCCTGCCCC	GTGCTCATTT	GGGGCTGACG	CCATTTTAGG	CCTCAGCCCA	TCTGCACCCA	180
	GGCGCTCACT	GAAACAGTGT	GTTGCTCCAC	ACCGCCTTGT	TTTGCTTGTT	GGCGCGCTCT	240
30	CAGGGTTCCG	ACCAATCCAA	GAGCCTTGCA	GAAAGCATTA	ACGTGCTTTT	CTCTTTGGCA	300
	GAGTTTTTCT	TTGCTCTGAT	CTTGGAGACA	TCCCTCTGCC	TAGTGGAAAC	ATAAGGAATA	360
	CAGAAAGAAT	GCAAGGAGAT	AGACCAACGT	GAGATTCTCC	TTCATGCACT	CAAGAGAAAG	420
	ATGTTGCAGG	AAGAGCTAGT	CTTTCAGGCT	GGGCTGGTGA	CCTGAGAAAG	AATGTCCAGC	480
	TTTTCTTCTC	CACTTGGCAT	ATCAAGAGCC	AGGCGTGGAA	GACTANAACA	GGAAATGTTT	540
35	ATAAAAACTG	TTCAGCGGTT	CGCCAACAAG	AAGTGGTAAA	GTAGCAAAAA	TGGGGATGGA	600
	GATGCCAGGA	GGAAAGATGC	CAGGGGTAAA	GTGGGAAAAT	GGGAACCTGA	AGCCAGGAGG	660
	TCAAGCCAAG	CCAACAGGTG	TTCTGTTTTT	CATCACAGAA	CTAATAAGTG	GTGCTGAGGA	720
	CTCAAACCCG	GGGAAGCCCA	CTCTAGAACC	CATGCTGGTC	ATCCATATCC	CCAAGGCCCT	780
	GGTCAGAACA	CAGCTAAGCA	GATGGCTTGG	GTCATCAGGA	CGTCCATTAC	ATCCAAAGGA	840
40	AGACAGCCTG	TGACGTTTCA	AAAGCAAAAG	TCCCCTACCA	GCCAGTGAAG	CTACCTGATT	900
		TTACGCCCAG					960
	CATABACACA	TAACAGCAGC	AGCAATAATT	AAAGATGAGA	TGAGAACAAT	TAAGAAAAA	1020
	GGAAAGGTCT	CCTGTGACTG	TTTTATTTT	AGGGAAACAG	AGAGGAAGAA	GAATGATTTT	1080
	TOTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ACTCTATATC	CAACTCTGAG	GTTTGATTAA	AGAAATGACC	TTGAACCACA	1140
45	CCAAACAAAA	ATAAAAGACA	ATTTCCAGTA	AGTATGCCAG	TTCGAATTAA	TGATTTACTT	1200
	TTTATTTTA	AACTGAATTC	AGCAGAGATT	TACATGCATT	ACGATGATTA	ACATCTGAAA	1260
	THYDROCTEG	AAATAATCTT	TACATIGTAA	ATTCTTAATG	ATCARARCAA	GGTTCTCAGT	1320
	CATTABASCA	TATTAGTAAT	TAATTATTAA	AGGAGAATAA	TTGCAAATAC	AACATTCCTA	1380
	BARTOTOBAG	GCTTTTAAAG	CATTTGTACA	AATGACTGGA	CATTTTTTAA	ATTTGAAAAA	1440
50		CCTCCATCTG					150
	CACTTOTO	TCTCATTTTC	CACTGTCTCG	CARGCTAGAA	ATTCTCACGA	CTACCTTTGA	1560
	TOCCATCAGA	CCCABAGAAA	GAAAAGAAAA	TTGTTCTGTA	CAGATATATG	ACATTAAAAA	1626
	ATAATCCC	-					

Seq ID NO: 235 Protein sequence: Protein Accession #: Eos sequence

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- Seq ID NO: 236 DNA sequence Nucleic Acid Accession \$: NM_002075 Coding sequence: 406..1428

	1	11	21	31	41	51	
	1	ı	I	1	1	1	
70				TCTGTGGGTC			60
	ACAGGATCAG	ACCCAGAGGC	AGCTGGTTGG	GGTTTGTCGA	GAAGAAGGAT	TATCCAGATC	120
	AGTCCTTTCT	AATCTCAGCT	CCTGCCTGTA	CCCTCCCATA	CTCACCAAAC	CCTCTTCCCC	180
	ACCACCCTGA	GCTGAGGAGC	ACAGTTTGAG	GCCCCCCAA	CCCCCCGCCG	GTCGGGGCCA	240
				GAGCCTGGGC			300
75	COTCGCAGCT	GAGGGAGTAA	GGAGGCTCCC	AGGNACCGGA	GCTGGAAACC	CGGCCGAGGT	360
	CCAGCCAGAG	CCCAAGAGCC	AGAGTGACCC	CTCGACCTGT	CAGCCATGGG	GGAGATGGAG	420
				AAGCAGATTG			480
	CONCROTTA	CTCTGGCAGA	CONCONCION	GGCCTAGAGG	TGGTGGGACG	AGTCCAGATG	540
	COLORGO	GGROGTTANG	GGGACACCTG	GCCAAGATTT	ACGCCATGCA	CTGGGCCACT	600
80	CAMPOCEARCO	TOTOTTANO	TOCOTOGOAA	GATGGGAAGC	TGATCGTGTG	GGACAGCTAC	660
00	ACCACCAACA	ACCTOGIANG	CATCCCACTG	CCCTCCTCCT	GGGTCATGAC	CTGTGCCTAT	720
	GGGGGGARGA G	CONTOCHOO	CCCATCTCCC	GGGCTGGACA	ACATGTGTTC	CATCTACAAC	780
	GCCCCATCAG	CORACITIOI	momen access	AGCCGGGAGC	TOTAL	CACACCTTAT	840
				AATATTGTGA			900
85	Crerecreer	GCCGCTTCCT	GGATGACAAC	CAGAAGACTG	WAS TREET CARGO	A CA CA COGGG	960
92			GACTGGGCIG	TTCAATCTCT	TATTIGIOGG	CCCCCCCCC	1020
		GCCTGGCTGT					1080
	GCCAGTGCCA	AGCTCTGGGA	TGTGCGAGAG	GGGACCTGCC	GICHGACTIT	CACTOGCCAC	1080

	WO 02	/086443					
5 10 15	GATGACGCTT CACGAGAGCA TTCGCTGGCT GGCATCCTCT GCTGTGGCCA AAGGGAAGTG GGTGTTCTCT GGGAGCATGG CCATCTCCTC GGCAACCTG GCCCTAGGAT	TCAACGCCAT CCTGCCCCT TCATCTGGG ACGACGACT CTGGCCACG ACGACGACT CTGGCACG CAGGTTCCTG GAAGGCACTG GAAGGCACTG CCCTCCCCCA TCCTCCCCCA GACTATGGCT TCTACTTTT TCACCTTTT	GTTTGACCTG CATCACTGCAAT TAACAGGGTG GGACAGCTTC AACACACTCA GGGTGCCATT TTGGGAGGCA CCCTCCCCAC GCCCTTTGCA GAGCCACTAC CTGGCACCAC	OGGCAGACC GTGGCCTTCT GCTGGGACT AGCTGCCTGG CTCAAAATCT GCAGCCCCCT CCCACTAAGC GCATCAGGGA AGTCCTCACA GGCCCAGCAG CTTTGTCCAG TAGGGTCCTG	AGGAGCTGAT CCCTCAGTGG CCATGAAGTC GAGTCACAGC GGAACTGAGG GCCCGACCCC TTTCTCCTTT CACAGGGGCA GCCTCTCCCT ACTTGAGTCT GCCTGGGTGG GCCCTCTCT	CTGCTTCTCC CCGCCTACTA TGAGCGTGTG TGACGGGATG AGGCTGGAGA ATCTCATTCA GAGGGCAGTG AAGAACTGCC TAATGAGCCAA GAGGCCCCAG TATAGGGCGT TATTCATGCT	1140 1200 1260 1320 1380 1440 1500 1660 1620 1640 1840 1860 1920
	Seq ID NO: Protein Ac	237 Protein cession #: 1	n sequence: NP_002066				
20	1 -	11	21 ARKACADUTL	31 } ARLVSGLEVV	41 GRVOMRTRRT	51 LRGHLAKIYA	60

20	1	11	21	31	41	51 1	
	MGEMEQLEQE	AEQLKKQIAD	ARKACADVTL	AELVSGLEVV	GRVQMRTRRT	LRGHLAKIYA PVACGGLDNM	60 120
25	CCTVNT.EQDE	CNUKUSRELS	AHTGYLSCCR	FLDDNNIVTS	SGDTTCALWD	IETGQQKTVF AICPFPNGEA	160
23	ICTGSDDASC	RLFDLRADQE	LICESHESII TADGMAVATO	CGITSVAFSL	SGRLLFAGYD	DFNCNVWDSM	300

Seq ID NO: 236 DNA sequence Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51 	
	TCCCAATGTG	THIGAACCTAC	CATAAATTCT	TTTCTTACNG	GACAATCTTA	TNCTAANCAA	120
35	ACTUATOTO	TYPARTTATYA	GATAATCCTC AATCTGAAAA	GGAATTGGAA	GTTGCTAAAA	ATCTATCATT	180
	TOCATTOACC	AGTGTGAAGC	ACAGTGGAAT GAATCACCGG	GAGAATGCGT	GCCCTGACAC	CAAAGAAAAA	300
40	TTTTCACCAC	TATOGGGGGA	CTTTGAGGTG GCAACCAAAG	GTCAAGAAAC	CACACTTTAA	GAACAATGTC	360 420
40	ANGARAGARA	DATABABTAC	ACAATATGGA	CGATGGAGAA	AAACAGTTAC	ATTTCTTTAT	480
	CACAACTGAA	TCAAAATATT	TCAAAATGCT	CTCTTATGAA	ACTACAATAT	TTTTGTCTTT	600
45	CARCTACTCA	ACTITICCTAC	TGTAGCACAA	GAGTAGCTGT	GGTACTGTGC	GTGTCTTTTG AAATAAATTG	720
45	CHARGERATURE	AATAAAGCTT	CATTTACAAA	AACATGCCAT	GGGCCATATT	TGGCCTGTAC ATTTGAGGAA	780
	CACATGABAG	TTCATTGGGT	TGCTAAAAAG	TATGTAGAAA	TTCAAAGGAA	AATTAAAATT TTTACAAATA	906
50	TAGGCTAAGT		TGTTTTAACA	ATTOTAMA	GIMONONON		

Seq ID NO: 239 DNA sequence Nucleic Acid Accession #: NM_001786.1 Coding sequence: 130-1023

Seq ID NO: 240 Protein sequence: Protein Accession #: NP_001777.1

MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH PNIVSLODVL MODSRLYLIF EFLSMDLKKY LDSIPPGOYM DSSLVKSYLY QILQGIVFCH

		/080443					
	SRRVLHRDLK	PQNLLIDDKG GTIFAELATK	TIKLADFGLA	RAFGIPIRVY	THEVVTLWYR	SPEVLLGSAR	180 240
	PPKWKPGSLA	SHVKNLDENG	LDLLSKMLIY	DPAKRISGKM	ALNHPYFNDL	DNOIKKM	. 40
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5							
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	Coding sequ	ence: 132-8	54				
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10	i	11	1	11	1	î.	
	ceccecece	CGGGCTCAAC	TTTGTAGAGC	GAGGGGCCAA	CTTGGCAGAG	CGCGCGGCCA	60
	GCTTTGCAGA	GAGCGCCCTC	CAGGGACTAT	GCGTGCGGGG	ACACGGGATC	TACCCATACC	120
15	ATTGACTAAC	TATGGAAGAT GGGTAGACAC	DADACTACAG	GTCAAGTGGT	AGCCATGAAA	AAAATCAGAC	240
	TAGAAAGTGA	AGAGGAAGGG	GTTCCTAGTA	CTGCAATTCG	GGAAATTTCT	CTATTAAAGG	300
	AACTTCGTCA	TCCAAATATA	GTCAGTCTTC	AGGATGTGCT	TATGCAGGAT	TCCAGGTTAT	360 420
	ATCTCATCTT	TGAGTTTCTT GGATTCTTCA	TCCATGGATC	TAGTABCACT	CTIGGATICI	TCTCCAGAAG	480
20	TATTGCTGGG	GTCAGCTCGT	TACTCAACTC	CAGTTGACAT	TTGGAGTATA	GGCACCATAT	540
	TTGCTGAACT	AGCAACTAAG	AAACCACTTT	TCCATGGGGA	TTCAGAAATT	GATCAACTCT	600
	TCAGGATTTT	CAGAGCTTTG	GGCACTCCCA	ATAATGAAGT	GTGGCCAGAA	GTGGAATCTT	660 720
	TACAGGACTA	TAAGAATACA TGAAAATGGC	TTTCCCAAAT	TOTOGRADAT	GTTBATCTAT	GATCCAGCCA	780
25	BACCASTTTC	TOTOTALANTA	CCACTGBATC	ATCCATATTT	TAATGATTTG	GACAATCAGA	840
	TTAAGAAGAT	GTAGCTTTCT	GACAAAAAGT	TTCCATATGT	TATGTCAACA	GATAGTTGTG	900
	TTTTTATTGT	TAACTCTTGT	CTATTTTTGT	CTTATATATA	TTTCTTTGTT	ATCAAACTTC	960 1020
	AGCTGTACTT	AATTCTGTAA	ATTENADAT	ADADADADA	AAAAAA	TICIAIAIGA	1020
30	ALLIAMIA	AATTCTGTAA	A.0.0.				
	Seq ID NO:	242 Protein	sequence:				
	Protein Acc	cession #: 1	NP_203698.1				
	1	11	21	31	41	51	
35	Ī	Ī	Ī	1	ł	1	
	MEDYTKIEKI	GEGTYGVVYK	GRHKTTGQVV	AMKKIRLESE	EEGVPSTAIR	EISLLKELRH	60 120
	PNIVSLQDVL	MODSRLYLIF WSIGTIFAEL	ATKKDI.PHCD	SETDOLPRIP	RALGTPHNEV	WPEVESLODY	180
	KNTFPKWKPG	SLASHVKNLD	ENGLDLLSKM	LIYDPAKRIS	GKMALNHPYP	NDLDNQIKKM	
40							
	Seq ID NO:	243 DNA sec id Accession	quence	161 1			
	Coding seq	ience: 221-	856				
15							
45	1	11	21	31 1	41	51 	
45	1 GAGCAACCTC	11 AGCTTCTAGT	21 ATCCAGACTC	CAGCGCCGCC	COGGGGGGGG	ACCCCAACCC	60
45	1 GAGCAACCTC	11 AGCITCTAGT	21 ATCCAGACTC GGCGGCGCAG	CAGCGCCGCC CGAGCAGGGC	CCGGGCGCGG	ACCCCAACCC AACTTCCTCC	120
	1 GAGCAACCTC CGACCCAGAG GCGGGGCCCA	11 AGCITCTAGT CTTCTCCAGC GCCACCTTCG	21 ATCCAGACTC GGCGGCGCAG GGAGTCCGGG	CAGOGOGGCC CGAGCAGGGC TTGCCCACCT	CCGGGCGCGG TCCCCGCCTT GCAAACTCTC	ACCCCAACCC AACTTCCTCC CGCCTTCTGC	120 180
45 50	1 GAGCAACCTC CGACCCAGAG GCGGGGCCCA	11 AGCTTCTAGT CTTCTCCAGC GCCACCTTCG	21 ATCCAGACTC GGCGGCGCAG GGAGTCCGGG	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC	CCGGGCGCGG TCCCCGCCTT GCAAACTCTC ATGGCCAACG	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA	120
	1 	11 AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG	21 ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CGCGGGCGCC CCTTCCTGGG	CAGCGCCGCC CGAGCAGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC	CCGGGCGCGG TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA GCACTGCCCT AGGCCATGTA	120 180 240 300 360
	1 	11 AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT	21 ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CCTTCCTGGG CCTATGCCGG GCGTGTCGCA	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACATC GAGCACCGGG	CCGGGCGCGG TCCCCGCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGCGGCTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT	120 180 240 300 360 420
50	1 GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCT TGACTCCTTG	11 AGCTTCTAGT CTTCTCCAGC GCCACCTTCG GCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTGA	21 ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CCCTTCCTGGG CCTTCCTGGG CCTTCCTGGG CCTTCCTGGG CCTTCCTGGG CCAGCACATT	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACATC CGAGCACCGGG GCAGCACACAC	CCGGGCGCGG TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT CGTGCCTTGA	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGCGGCTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG	120 180 240 300 360
	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGTTG TGACTCCTTG	11 AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT AGGATGTCATAGGAGTGATAG	21 ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CCTTCCTGGG CCTATGCCGG GCGTGTCGCA GCAGCACATT CAATCTTTGT	CAGCGCCGCC CAGCAGGGC TTGCCCACCT TCGCCACCT CAGCGAGGTC ATGGATCGGC CGACAACATC GAGCACCGGG GCAAGCAACC GGCACCGGTT	CCGGGCGCGC TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT CGTGCCTTGA GGCATGAAGT	ACCCCAACCC AACTTCCTCC CGCGTCTCTCC CGCGGCTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG	120 180 240 300 360 420 480
50	1 GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCCTAGTGG GCCCAGTGG CGACCCTCTG CATCCTCTG CTTGGAAGAG TCTTGGAAGAG	11	21 ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CCTATGCCGG GCAGTATGCCAG GCAGCACATT CAATCTTTGT AGAAGATGAG	CAGCGCCGCC CCGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACACATC GAGCACCGGG GCAACCACCGTG GCCACCGTT GATGGCTGTC AGCATGGTTAT	CCGGGGGGGG TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCC CAGATCCAGT CGTGCCTTGA GGCATGAAGT ATTGGGGGT GGCATAGAA	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAGA	120 180 240 300 360 420 480 540 600
50	AGGENACTIC GAGCACCAGAG GCGGGGCCA ACCTGCCACC GCTTTTGGAG GCCCAGTGG CATCCCTGG CATCTCCTGG CTTGGAAGAC TCTTGCAGGT	11	21 ATCCAGACTC GGCGCGCGCAGGGGCGCC CCTTCCTGGG GCAGTCCCGG GCAGCACATT AGAAGATGAG TAGTTGCCAG CAGTCTAGACAGACACACACACACACACACACACACACAC	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACATC GAGCACCGGG GCAAGCAACC GGCCACCGTT GATGGCTGTC AGCATGGAT	COGGGGGGGG TCCCOGGCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCC CAGATCCAGT CGTGCCTTGA GGCATGAAGT ATTGGGGGTG GGCAATAGAA TTTGGTCAGG	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGCGGCTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAGC CTCTTCAAC CTCTTCAAC	120 180 240 300 360 420 480 540 600
50	1 GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGCCCAC TGACTCCTTG CATCCTCTG CATCCTCTG CATCCTCTGAACAC TCTTGCAGGT ATTCTATGAC TGGCTGGGGTTGGGCT GGCTGGGGTTGGGTT	11 AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCCT CTGAATCTGA GATGAGTGG CTGGCTATTT CCTATGACCC GCTGCTTCTCC	21 ATCCAGACTC GGCGGCGCG GGAGTCCGGG GCTTCCTGGG CCTTCCTGGG CCAGCACATT CAATCTTTT AGAAGATCAG TAGTTGCCAC CAGTCAATGC CAGTCAATGC CTTCCTAGTGCAC CTTCCTTCTT	CAGCSCCGCC CCAGCAGGGG TTGCCCACCT TCGACCACTC ATGCATCGGC CGACACATC GACCACCGGG GCAAGCACCGGG GCAAGCACCGTT AGCATGGTACAC AGCATGGTACACACGGGGGGGGGG	CCGGGCGCGG TCCCCGGCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCC CAGATCCAGT CGTGCCTTGA GGCATGAAGT ATTGGGGGTG GGCAATAGAA TTTGGTCAGG CTACTTTGCT	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA GCACTGCCCT AGGCCATOTA GCAAGATCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAGA CTTCCTTCACC GTTCCTGTCC	120 180 240 300 360 420 480 540 660 720 780
50	1 GAGCANCCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCACGTGG GCACCAGTG CAACCTCCTG CATCCTCCTG CATCCTCCTG CATCTCCTG CATCTCCTG CATCTCTCTGAAGAC TCTTCAAGGT ATCTTCTATGAC TGGCTGGGCT CCGAAAAACA GBAAGACCAC	11 AGCTTCTAGT CTTCTCCAGC GCCACCTTCG GCCACCTTCG AGGATTACT TOGATGTCCT CTGAATCTCA GGAGTGATAG CTGGATATT CCTAATGACCC GCTGCTTCTC ACCTCTTACC CTTGTATACACCA	21 ATCCAGACTC GGCGGCGCAG GGAGTCCGGG GCCTTCCTGGG CCTTCCTGGG CCTATCCCGG GCGCACATT CAATCTTGT AGAACATCAATGC CAGTCAATGC CTCGCCTTC CACCAAAG AGACAAAAG AGACAAAAG AGACAAAAG AGACAAAAG AGACAAAAG	CAGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCGGGCGCG CCGGCCTT CCCCGCCTT CCAAACTCTC ATGGCCAACG GCATCGTCA GTGACGCCC CAGATCCAAT GGCATGAAG GTGCCTTGA GGCATGAAG GTGCTCAG GCAATAGAA ATTGGGTGAG GCAATAGAA CTACTTTGCT AAACCTGCAA	ACCCAACC AACTTCCTC GGCGTTCTGC GGGGGTGCA GCACTGCCCT AGGCCATGTA GGCAAGTCTT TGCTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAGGA CTCTCTCACCG GTTCCTGCC CTTCCACCGA	120 180 240 360 420 480 540 600 -660 720 780 840
50	1 GAGCANCCTC CGACCCAGAG GCGGGCCCA ACCTGCCACCG GCCTATTGGG CCCACTGG CATCCCTG CATCCACCTCTTGCAGGT TCTTGCAGGT TCTTGCAGGT TGGAGGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGACATAGACTAGAGACTAGACATAGACTAGAGACTAGACATAGACATAGACTAGACATAGAATAGACATAGAATAGACATAGAATAGACATAGAATAGACATAGAATAGACATAGAATAGACATAGAATAGACATAGAATAGAATAGACATAGAATAGAATAGACATAGAATAGACATAGAAT	11 AGCTTCTAGT CTTCTCCAGC GCACCTTCG GCACCTTCG AGGATTTACT TGGATGTCCT TGGATGTCCT TGGATGTCT CTGATATGACC GCTGGCTATT CCTATGACC GCTGGTTCTC GCTGTTCTC GTGTACACC GTGTACACAC	21 ATCCAGACTC GGCGGCGCAG GGAGTCCGGG GCGGGCGCC CCTTCCTGGG CCTATGCCGG GCAGTCTTTT AGAAGATCAG TAOTTGCCAC CAGTCAATGC CAGCCAATT CTAGCCATCC CAGCCAATGC CAGCCAATGC CAGCCAATGC CAGCCAATGC CAGCCAATGC CAGCCAATGC CAACACCAAG GAGGCAAAAG	CAGCSCCCC CGAGCAGGG CTGCCCACCT CGAGCAGGG TTGCCACCT CGAGCACT CGACAACATC CGACAACATC GGCCACCGT GATGGCTGCT GATGGCTGTC AGGTACGAC GGCACCGTT CAGGTACGAC GGCAGGTACCA GGGAAGGTACCA GGCAGGTACCA AGGTACGAA AGCTATCCA AGGAAAATCA ACCTTAGAAT	COGGGGGGGG TCCCGGCTT GCAAACTCTC GCAAACTCTC GCATCGTCA GCCATCGTCA GTGACCGCCC CAGATCCAAT ATTGGGGTG GGCATAGAA TTTGGTCAGG CTACTTTGGT AAACCTTTGGT AAACCTTGGACT TTTGGACTG	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGCTGGTTGG GTATGAAGA CTCTCTAAGA CTCTCTAAGA CTCCTCCAC GTTCCACGA AACGGAAAAT	120 180 240 300 360 420 480 540 600 - 660 720 780 840 900
50	1 GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTCTTGGGG GCCCCAGTGG GCCCCAGTGG CTAGCAGGT CTTCTACAGG ATTCTATCAG TGGCTGGGCT CCGAAAAACA GAAAGACTAC GGACATTCAG GGACATTCAG GGACATTCAG GGACATTCAG GGACATTCAG GGACATTCAG GGACATTCAG	11 AGCTTCTAGT CTTCTCCAGC GCCACCTTCG GCCACCTTCG GCCACTTCG TTCATTCTCG AGGATTTACT TOGATGTCT TOGATGTCT CTGATATCAG GATGAGTGC GCTGCTATT CCTATGACCC GCTGCTTTCT ACCTCTTACC TGTGTGACACA ATACTATCAT ACAAAACAAA	21	CAGGGCCGCC CGAGCAGGGC CGAGCAGGGC TTGCCACCT CGAGCAGTC ATGGATCGGC GGACACATC AGGAACCAGG GGAACAACATC AGGATGGCT GATGGCTGTC AGCATGGTAT AGCATGGTAT AGCATGGTAT AGCATTACGAA AGGAAGAACA ACCTTAGAAT AAAAACCAT AAAAACCAT	COGGGGGGGG TCCCCGGCTT GCAAACTCTC GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT GGCATGAAT ATTGGGGTG GGCAATAGAA ATTGGTCAGG CTACATTGCT AAACCTGCAC TGTTGAAACT TTTGGGTATT TTGTTGAAACT	ACCCAACC AACTTOCTOC CGCGTTCTCC CGCGTCTCCC GCACTGCCCT GCACTGCCCT TGGTGGTTGG GTATGAAGTCTT TCGTTCAACG CTTCCACCG GTCCTCCC CTTCCACCG AACCGAAAAT GTAATCTGAA ACTCAGTGCT	120 180 240 300 360 420 480 540 600 - 660 720 780 840 900 900
50 55 60	agcanecte carecage Accidence Accidence Accidence Accidence Controlle Control	11	21 ATCCAGACTC GGGGGGGGGGGGGGGGGGGCGCAGC CCTTCCTGGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCAGCACATT CAATCTTTGT CAGCCTCT CAGCCAATG CAGCCAATG GAGGCAAAG GAGGCAAAG GAGCAAAAC AACAACAACAACAACAACAACAACAACAACAAC	CAGCUCCCC CGAGCAGGG CTGCCCACCT CGAGCAGGG TTGCCACCT CGAGCAGTC CGACAACATC GAGCAACCAC GGCCACCGT GATGGCTACCA GGCAGCAGT CGGGCACCGT GATGGTACGAA GGGAGGTACCA GGGAGGAGCAACC GAGAAAATCA AAAAACCCAT TCCTCAATAT TCCTCAATAT	COGGGGGGGG TCCCGGCTT GCAAACTCTC GCAAACTCTC GCATCGTCA GTGACTCGTCA GTGACTCGTCA GTGACTCAGT ATTGGGGGTG GCATTAGAA ATTGGTCAGG CTACTTTGCT AAACCTGCAC TGTTGAAACT TTTGGGGTAT GTGTTGAAACT ATTGGGATT TTTGGATTAAACT ATTGGATAGA TTTGGATAGA	ACCCCAACCC AACTTCTCC CGCGTCTCTGC CGCGGCTGCA AGGCCATGTA GCAAGGCCT AGGCCATGTA GCAAGTCTT TGGTGGTTTGG GTATGAAGTCT TCGTTTCAAGG CTCCTCTCCAC GTTCCAGGG AACGGAAAAT CTTCAGGGA ACTGAAAAT ACTCAGTGGA ACTCAGTGGA ACTGAGAAAT ACTCAGTGGA ACTCAGTGGA ACTCAGTGGA ACTCAGTGGA ATTTTACCAT	120 180 240 300 360 420 480 540 600 720 780 840 960 1080
50	GAGCAACCTC GAGCAACCTC GAGCACCACAG GCGGGGCCCA ACTGCCACC GCCCACTGC GCCCACTGC GCCCACTGC GCCCACTGC GCCCACTGC GATCCTCTG CATCCTCTG CATCCTCTTG CATCTCTTGCAGGT TTTGCAGGT TTTGCAGGT TTGGTAGGT TTGGTAGGT TAGTATTAGGT TAGTATTAGGT TATATATA	11	21 ATCCAGACTC GGGGGGGGGGGGGGGGCGCAGG CCTTCCTGGG CCTTCCTGGG CCTAGCTGGG CCAGCACATT CAATCTTGT AGAAGATTAGCAG CAGCCAATT CAGCCTTCT CAACACCAAG GAGGCAAAAG AGAGCAAAAC AACAACAA TAACTTTGT TAACATTTGCTTCT TAACATTTGCTTCT TAACATTTAGCT	CAGCOCCGC COAGCAGGG COAGCAGGG TTGCCCACCT COAGCAACTC CAGCAACATC CAGCAACATC GACCACCGT AGCAACATC GACCACCGT AGCAATGGTAC AGCAAGCAAC GGCAAGGTAC GCCCTATCCA GAGAAAATCA AAAAACCCAT TCCTCAATAT ACTCAAATAT ACTCAAATAT	COGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ACCCCAACCC AACTICTOCC CGCGTCTOAC CGCGGCTGCA GCACTGCCC AGGCCATGTA GCAACGTTA GCAACGTTA GCATATTTC TGGTTGGTTGG GTATTTCT TCGTTCAGG TTCCTGTTCAG ACCGATATTTC CTTCCAGCG AACCGAACAT ACTCCAGCG AACCGAACAT ATTTTACCAT GCTCCTTAAC GCTCCTTAAA ACTCCTTAAC	120 180 240 360 420 480 540 600 - 660 720 780 840 900 1020 1080 1140 1200
50 55 60	1 GARGEARCETC COARCOCAGA COTTO CARCOCAGA GCOTTO CARCOCAGA COARCOCAGA COARCOCAGA COARCOCAGA CATCACAGA ATCACAGA ATCACAGA ATCACAGA CAACATGAC COARAAAACA GAACATGACA GAACATGATA AAACATGACT TATATATACAA ATCATATATACAA CTCATTATAT	11 AGCTTCTAGT CTTCTCCAGG GCACCTTCG GCCACCTTCG CCTAGCCAG TCATTCTCTCAGG AGGATTTACT TOGATGTCAT GGATGTCAT GGATGTCAT GGATGTCAT CCTATGACCA ATACTATCA ATACTATCAT ACATACAAT TAATCTATCAT TATUTATATAT TATUTATATAT TATUTATATAT TATUTATATAT TATUTATATATA	21 ATCCAGACTC GGCGGCGAG GGAGTCCGGG GCGGGGCGCAG CCTTCCTGGG CCTTCCTGGG CCAGTCATCC CAGTCATCC C	CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	COGGGGGGGG TOCCCGCTT GCAAACTCTC GCAACTGTC GCATCGTCA GTGACCGCC CAGATCACA GTGACCGCC CAGATCACA TTTGGTCAAC CTACTTTGCT AAACCTGCAC TTTGGGTATT TTTGGGTATT TTTGGGTATT TTTGGTAACA TTTGGTAACA GGAAGGGAAA GGAAGGGGAA GGAAGGGGAA GGAAGGGGAA	ACCCAACCC AACTTCTCCC CGCCTTCTGC CGCGGCTCTGC CGGGGTCGCA AGGCCATGTT TGGTGGTTGG GAAAAGTT TGGTTCAAGA CTCTCTCACCG CTCCCACGG AACCGAAAAT GTAATCTGT AACCGAAAAAT GTAATCTGTA AATTTTACCAT TGTTTCACCTT ATTTTACCAT TGTTTCACTTAAAAAATTACTATT	120 180 240 300 360 420 480 540 600 720 780 840 960 960 1020 1140 1260
50 55 60	1 GAGCAACCTC CUACCCAGAG GCGCGGCCA ACCTGCCACC GCTCTTGGGC GCCCAGTGG GCACCAGTGG CATCCTCCTG CATCCTCCTG CATCCTCCTG CATCCTCCTG CATCGAGAAAACA ACCTCATGGAAAACA ACCTCATGAAAACA TGGCTGGGCT TGAAAACACTCATGACT TGAATACT TATATATACA TATATATACA CCAATTATAT	11 AGCITICTAGI CITICTOCAGE GCCACCITICG GCCACCITICG CCTAGACCAG AGGAITTACT TUGANTCICT TUGANTCICT TUGANTCICT TUGANTCICT GCATATCHICA GCTGCTICT ACCICTIACC TUGANTCICT ACCICTIACC TUGANTCICT ACCICTIACC TUGANTCICT ACCICTIACC TUGANTCICT TU	21	CAGCOCCCC CAACCACCCC CAACCACCCC CAACCACCCCC CAACCACC	COGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ACCCAACCC AACTICTOCC CGCGTCTTGG CGGGGTGCA GGCACTGCC AGGCCATGTA GGCATGTA GGAAGTCT TGGTGGTTGG GTATGAAGT CTCGTTCAAGA CTCCTTCAC GTTCCTTCAC GTTCCTTCAC GTTCCTTCAC GTTCCTTCAC GTTCCTTCAC GTTCCTTCAC GTTCCTTCAC GTTCCTTCAC ACTCCTTCAC ACTCCTTCAC GTTCCTTTAC GTTTATTCTTAT GTTTTATCTTT GTATTTATTTT GTATTTATTT GTATTTATTT GTATTTATT	120 180 240 300 360 420 480 540 600 - 660 720 960 1020 1080 1140 1260 11320
50 55 60	1 GAGCANCCTC CGACCCAGAG GGGGGGCCCA ACCTGCCAGAG GCGCCAGTG GCCCCAGTG GCCCAGTG CTGACTCCTCT CTTGAAGAC TCTTGCAGGG ATTCTATAGAC TGGCTGGGC CCCAGAGGGCT TGACTCCTTC CTTGGAAGAC TTTTGATTATAC TGGCTGGGC TGGAAGACCT TGGATGGGCT TGATTATATACAG CGACATTGAG GGACATTGAG GGACATTGAG TATGTATTATATACAG CTCATTATATA	11 AGGTTCTAGT AGGTTCTAGT CTTCTCCAGC GCAGCTTGC CCTGAGCAG TTCATTCTGC TCGAGTGCAG TTCATTCTGG AGGATTTACT TCGAGTGTCC TCGAATCTAG GATGAACC GGAGTGATAG ACTGTTACC TGGAGTGTCT ACCTGTTACC TGGAGTGTTTACT TCGATGTCCT ACCTGTTACC TGGAGTGTTTACT TCGATGTACT TCGATGTACT TCGATGTACC GGAGGAGTTTACT TATGTATATAT	21 ATTCAGACTC GGCGGCGCAG GGCGGCCAG GGCGGCCC CCTTCCTGGG CCCTTCCTGGG CCAATCTTGT AGAAGATGA TAGTTGCCAG GGAGCCAAT CAATCTTTGT CAACACCAG GGGGCAATC CAACAATCT CAACACCAG GGGGCAATC TATCTTCTT TACAGTTTT ACAGTTTT TACAGTTTT TACAGTTTT TACAGTTT TACAGTTT TACAGTTT TACAGTTT TACAGTTT TACAGTTT TACAGTT CAGGGGCGGC CAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	COGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ACCCAACCE AACTTCTCC CGCGTCTTGC CGCGGCTCCA GGCCATGTC GGGGGTGCA GGCCATGTC GGAAGGTCT TGGTGGTTGG GTATGAAGA CTCTTCAC GTTCCTAAGA CTCTTCAC GTTCCTAGAG ACTCAAGA AATTTCTGAA AATTTCTGAA AATTTCTGAA AATTTCACAT TTACCAT TTACCAT TTACCAT TTACCAT TTACCAT TTACTTAAA AATACTATT ACATATGTAAA AATACTATT ACATATGTAAA AAGACCTAGC	120 180 240 300 360 420 480 540 600 720 780 840 960 960 1020 1140 1260	
50 55 60 65	1 GAGCAACCTCC CRACCAGAG GGGGGGCCCACA ACCTGCCACAC GGGGGGGCCCCAC GGGGGGCCCCCAC GGGGGGCCCCC GGGGGGCCCCC GGGGGGCCCCC GGGGGG	11 AGCTICTAGE CTICTCOAGE GCOACTITICG CCTGGGCAG CTGGGCAG TICATCTCTG CCTGGGCAG TICATCTCTG CCTGGATCTAG CGGATGTGCC CTGGATCTAG GGATGATAG GGATGATAG GGATGATAG GGATGAGT CCTGGGCATTT CCTGGCCATT TANTTAGTAG TGATGACGA TANTTAGTAG CGTCCCATT TANTTAGTAG CGTCCCATT TANTTAGTAG CGTCCCATT TANTTAGTAGT CGATGATGAG CAATAGTAGT AAGGAAGAAA CCAATAGTACT AAGGAAGAAA CCAATAGTACT AAGGAAGAAA CCAATAGTACT CAAGGAAGAAA CCAATAGTACT CCAAT	21 ATTCAGACTC GGCGGGCAGA GGGGGCAGA GGGGGCAGA GGGGGCAGA GGGGCAGACATC CAACACCAGA GAGACACAG GAGCACATT CAACACTTG CAACACCAGA GAGCAAAAA TAACATTG AACATTG A	CHACATORATA	COGGGCOCGG COGGCCOCGC TOCCGGCACA TOCCGGCACA GCAAACCCTC GCAAACCCCC GCAACCCACA GCACCACAC GCACCACAC GCACCACAC TOCCGCAC TOCCGCAC TOCCCTCA GCAACCCAC TOCCCTCA GCACCACAC TOCCCTCA TOCCCTCA TOCCCTCA TOCCCTCA TOCCCTCA TOCCCTCA TOCCCTCA TOCCCTCA TOCCCTCA TOCCCTCACTTCCC TOCCCTCACTTCCC TOCCCTCACTTCCC TOCCCTCACTTCCC TOCCCTCACTTCCC TOCCCTCACTTCCC TOCCCTCACTTCCC TOCCCTCACTTCCC TOCCCTCACTTCCC TOCCCCCCTCTCCA TOCCCTCTCCCC TOCCCTCCCCC TOCCCCCCCCC TOCCCCCCCC	ACCCCAACCC AACTTCTCCC CGCCTTCTGC CGCGGCTCTTGC CGGGGCTCAG GCACTGCCT AGGCCATTGT TGGTGGTTTGC GTATGAAGTG GTATGAAGTG CTCCTCTCAC GTTCCAGGG AACCGAAAAT TCTCTCTCAC GTATCTGAC GTATCTGAC GTATCTGAC GTATCTGAC GTATCTGAC GTATCTGAC GTATCTGAC GTATCTGAC GCTCCTTAAA ACTCATTATCAC ACTTATTAAT ACATTATTAA AAGACCTAGC TATGTTATTT	120 180 240 300 420 480 540 600 720 780 840 960 1020 11200 11200 11320 1340 1140 11500
50 55 60 65	1 GAGCAACCTC COACCAGA A COACCAGA A COTTOCAGA COACCAGA A COTTOCAGA COACCAGA COACCACACACACACACACACACACACACACACACACA	11 AGCTICCTAGE AGCTICCTAGE CTTOCCCAGE CTTOCCCAGE CCTTOCCCAGE	21 ATCOMACTIC GORDANIA CONTROL CONT	CAGGUECGEC CAGGCAGGE CAGGCAGGE CAGGCAGGE CAGGCAGGE CAGGCAGGE CAGCAGGAGT CAGGAGGE CAGCAGGE G CAGCAGGAGG CAGCAGGAGG CACCAGGAGG CAGCAGGAGG GG CAGCAGGAGG CAGCAGGAGG CAGCAGGAGG CAGCAGGAGG CAGCAGGAGG CAGCAGGAGG CAGCAGGAGG CAGCAGGAGG CAGCAGGAGG CAGCAGGAGGAGGAGG CAGCAGG	COGGGCTOGCTT COCGGCTT COCGGCTT COCGGCTT COCGGCTT COCGGCTT COCGGCTT COCGCTT COCGCCTT COCGCCTT COCGCCTT COCGCCTT COCGCCTT COCGCCTT COCGCCT COCGCCTT COCGCCT OCGCCT COCGCCT COCGCCT COCGCCT COCGCC COCGCCT COCGCC COCGCCT COCGCC COCGC COCGC COCGC COCGCC COCGC COCC COCGC C	ACCCCAACCC AACTTCATCC COCOGCTTCATC COCOGCTTCATC COCOGCTTCATC COCOGCTTCATC COCOGCTTCATC AGGICCATOTA GCAAAGTCTT TGGTGGTTGGG GTATGAAGTGG CTCCTTCACA GTTCCATCC GTTCCATCC GTTCCATCC GTTCATCAC GTTCATCC GTTCATCAC GTTCATCAC GTTCATCAC GTTCATCAC GTTCATTCACAC TTATTCACAT AACTCATTCACAT AATTTACCAT ACTCATTACAT AAATACCATT ACTCATTAAT AAATACCATT TGTTTTACCT TGTTTTTACCT TGTTTTTACT TGTTTTTTACT TGTTTTTTACT TGTTTTTTTTTT	120 180 240 360 420 480 540 600 720 780 960 1020 1140 1260 1320 1340 1440 1560
50 55 60 65	1 Idealactic Constitution	11 CONTINUENCE OF THE PROPERTY OF THE PROPER	21 ATTCAGACTC GGCGGGCGCAG GGCGGCGCAG GGCGGCAGCACTC CCTTCCCAGC GGCGGCCACC CCTTCCCAGC GGCGCACCACT CAACCCCAG GGGGCAAAG TAGCTAGCA GGGGCAAAG TAGCTAGCA GAGCACACT TACCTCT ACCTC TACCT TACCTC TACCTC TACCTC TACCTC TACCTC TACCT	CAGGOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	COGGGCTGCTTTCCCGCTTTCCCGCTTTCCCGCTTTCCCGCTTTCCGCTTTCCGTTCCTTCTTCCTTCTC	ACCCAACCC AACTTCCTCC CGGGGCTGCA CGGGTGCAC CGGGGCTGCAC CGGGGCTGCAC CGGGGCTGCAC CGGGGCTGCAC CGGAAGTCT AGGCAAGTCT CGGTACCAC CTCCTCCAC CTCCTCCAC CTCCTCCAC CTCCCTCC	120 180 240 300 420 480 540 600 720 960 1020 1140 11200 11320 11320 11320 11320 1140 11500 11500 11500
50 55 60 65 70	1 GARLANCTIC GARLANC	11 CONTINUENCE OF THE PROPERTY OF THE PROPER	21	CAGGREGAGGE CAGGRE	COGGOCTOC COGGOCTO COGGOCTO COGGOCTO COCACO COMPANION CONTROL	ACCCAACCC AACTTCOTCC COCCTTCTCCC COCCTTCCCC COCCTTCCCCC COCCTTCCCCC CTCCCCCC CTCCCCCC CTCCCCCC CTCCCCCC	120 180 240 300 420 480 540 600 600 720 960 960 900 960 11200 11200 11200 11320 11320 1140 11500 11500 11620 11620 11620 11620 11620
50 55 60 65	1 GACANACTIC GACCAGAGA GACCAGAA GACCAGAGA GACCAGAGA GACCAGAGA GACCAGAGA GACCAGAGA GACCAGAGA GACAGAGA GACAGAGA GACAAGAA GACAA	11 CONTROL OF THE PROPERTY O	21 TOTAL STATE OF THE PROPERTY OF THE PROPER	CAGGUEGGE COAGCAGGE COACCAGGE COACCA	COSGOCIOCA CONTROLLA CONTR	ACCOMACCE ACCITIONA ACCITI	120 180 240 360 420 540 540 540 760 780 840 960 1020 1140 1260 1380 1440 1560 1450 1560 1680 1740
50 55 60 65 70	1 GAGCAACCTEC GAGCAACCAGA GCGGGGGCCA ACCTGCCACC GCTGTTUGGG GCCCACTGC GCCCACTGC GCCCACTGC GCCCACTGC GCCCACTGC GCCCACTGC GCCCACTGC GCCCACTGC GCCCACTGC GCCACTG	11 INCIDENT AND THE PROPERTY OF THE PROPERTY O	21 ATCAGGACTTC ATCAGGACTTC ATCAGGACTTC ATCAGGACTTC ATCAGGACTTC ATCAGGACTTC ATCAGGACTTC ATCATCTTC ATCATCTC ATCATCTTC ATCATCTC ATCATCTTC ATCATCT ATCATCATC ATCATCT ATCATCATC ATCATCAT ATCATCATC ATCATCATC ATCATCATC ATCATCATC ATCATCATC ATCATCATC ATCATCATC ATCATCATC ATCATCATC ATCATCATC ATCATCATC ATCATCATC ATCATC ATCATCATC A	CAGCAGAGAGA CAGCAGAGAGAGAGAGAGAGAGAGAGA	COGGCOCCACATOR CONTROL	ACCOMACCE AACTICACA AACTICACA AACTICACA AACTICACA AACTICACA AACTICACA GOAGATCT GOGGACTICA GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT GOAGATCT AACTICACA A	120 180 300 420 360 480 540 780 720 780 960 1020 1140 1240 1240 1250 1380 1140 1500 1500 1620 1620 1620 1620 1620 1630 1630 1630 1630 1630 1630 1630 163
50 55 60 65 70	1 GAGCAAACTTC GAGCAAGAG GCGGGGCCA ACCTGCAGG GCGCTTGGGG GCGCTTGGGG GCGCTTGGGG GCGCTTGGGG GCATCCTCTG GAAGGGGCT CATCCTGG GAAGGGGCT CCTGGAAGAG GAACGACTT TGGATTGGGCT CCGAAAAAC TTGTATTGA TTGTATTGA TTGTATTGA CATCAACTA CATCAACTA CATCAACTA TATCTTATTGA TATCTTATTGA TATCTTATTGA TATCTTATTGA TATCTTATTGA TATCTTATTGA CATCAACTA CATCAACTA CATCAACTA CATCAACTA CATCAACTA CATCAACTA CATCAACTA TATCTTATTGA CATCAACTA CATCAACTA TATCTTATTGA CATCAACTA CATCAACTA TATCTTATTGA TATCTTATTATTGA TATCTTATTG	11 ROCTICTAGE GCCACCTTCG CCTTAGCCAGE GCCACCTTCG CCTTAGCCAGE TCCATTTGCC TCGATTTGCT TCGATTTGCT TCGATTTGCT TCGATTTGCT CTGAATCTAG GATTGACT GATTGACT GCTATGACC GCTGCTTCCC GCTGCTCCC GCTGCTCCC GCTGCTCCC GCTGCTCCC GCTGCTCCC GCTGCTCCC GCTGCTCCC GCTGCTCCC GCTGCTCCC GCTGCTCC CTGCTC GCTGCTC GCTGCTC GCTGCTC GCTGCTC GCTGCTC GCTGCTC GCTGCT GCT	21 TOTAL STATE OF THE PROPERTY OF THE PROPER	CAGGOCCGCC CAGGCAGGGC CAGGCAGGCC CAGGCAGGCC CAGGCAGG	COGGGCCCGGCTT COCCGGCCTT COCCGGCTT OCCGGCTT COCCGGCTT COCCGGCT COCCGGCT COCCGGCT COCCGCT COCCGGCT COCCGGCT COCCGGCT COCCGGCT COCCGGCT COCCGGCT COCCGGCT COCCGGCT COCCGGCT COCCGCT COCCGCT COCCGCT COCCGGCT COCCGGCT COCCGCT COCC	ACCOMANCE ACCOMA	120 180 240 360 420 540 540 540 760 780 840 960 1020 1140 1260 1380 1440 1560 1560 1560 1680 1740 1860 1860 1860
50 55 60 65 70	1 GAGCAACCTEC GAGCAACCAG GCGGGGGCCA ACCTGCCAG GCGTTTUGGG GCGTTTUGGG GCGCAGGGGCT TGACTCCTTG CATCCTCTT CATCCTTG CATCCTCTT CATCGAGGGC TGACACCAG GAAAGACAC GAAAGACAC GAAAGACAC TGACACCTT TGACACCAC TGACACCAC TATCTTCACAG TGACACCAC TATCTTCACAG TGACACCAC TATCTTTACAG TGACACCAC TATCTTTACA TGACACCAC TATCTTTACA TGACACCAC TATCTTTACA TCACACCAC TATCTTTACA TCACACCAC TATCTTTACA TCACACCAC TATCTTTACA TCACACCAC TATCTTTACA TCACACCAC TATCTTTACA TCACACCAC TACACCAC TATCTTTACA TCACACCAC TACACCACAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCACAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCACAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACCAC TACACACAC	11 RECTICATE TO THE PROPERTY OF THE PROPERTY O	21 ATCAGACTCA GOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ENGOGECIGIC CONGENICACIÓN CONCENICACIÓN CONC	COGGGCTCGC TOCCGGCTT GCGGCTT GCGGCTT GCGGCTT GCGCTT GTGCCTAT GGCATGAT GGCATGAT ATTGCGCT GGCATGAT ATTGCGCT ATTGCGCT GGCATGAT ATTGCGCT GGCATTGAT ATTGCGGCT ATTGCGCAT GGCATTGAT ATTGCGCT ATTGCGCAT GGCATTGAT ATTGCGCAT GCCATTTGCAT ATTGCGCAT GCCATTTGCAT ATTGCGCAT GCCATTTGCAT ATTGCGCAT GCCATTTGCAT ATTGCCAT GCCATTTGCAT ATTGCCAT GCCATTTGCAT ATTGCCAT AGCCCTTAT ATTGCCAT GCCATTTGCAT AGCCCTTAT CCTGCCATTGCAT AGCCCTTAT AGCCCCTTAT AGCCCTTAT AGCCCCTTAT AGCCCTTAT AGCCCCTTAT AGCCCTTA	ACCOUNTY OF THE PROPERTY OF TH	120 180 240 360 420 360 420 600 780 840 900 1020 11200 11200 11320
50 55 60 65 70	1 GAGCAAACTCC COACCAGAGGGCCCAACCAGAGGGCCCAACCAGAGGGCCCAACCAGGGCCCCAACCAGGGCCCCAACCAGGGCCCCAACCAGGGCCCCCAACCAGGGCCCCCAACCAGGGCCCCCAACCAGGGCCCCCC	AGENTATION OF THE PROPERTY OF	21 ATTCAGAGTTC GGGGGGGGGGGGGGGGGGGGGGGGGGG	ENGINEER CONTROLL CONTROL CONTROLL CONTROL CONTR	COGGCCCCG COGGCCCCG COGGCCCCC COGGCCCCCCCC	I CONTROLLARIO DE LA CONTROLLARIO DELLA CONTROLLARIO DE LA CONTROLLARI	120 180 240 360 360 360 360 540 660 720 960 960 900 960 1020 1020 1020 1030 1240 1250 1320 1440 1260 1320 1460 1500 1620 1620 1620 1620 1620 1620 1620 16
50 55 60 65 70	1 GARCANACTIC COACCOUNTS OF THE PROPERTY OF TH	11 AGCTTCTAGT AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CTTCTCCAGC GCCACCTTCG CTTCATTCTCA TCGATTTCC TTGATTTCCA TCGATTTCC TTGATTTCCA GGATTTAC TTGATTTCCA GGATTAGC GTGATCAGC GTGATCAGC GTGATCAGC GTGATCAGC GTTGACCAGT TAGTTTAC TGATTAGCAG AGATTAGT TGATTAGT AGGATGAGT AGGATGAGT TAGTTAGT	21 ATCCAGACTC GGCGGCCCAG GGCGGCCCAG GGCGGCCCAG GGCGGCCAG GGCGCCAG GCAGCACT GCAGCAG GCAGCACT TAGCCGG GCAGCACT TAGCCGG GCAGCACT TAGCCGG GCAGCACT TAGCCGG GCAGCACT TAGCCGG GCAGCACT TAGCCGG GAGCACAT TAGCCAG GAGCACAG TAGCTCAT TAGCCAC GAGCACAG TAGCTCAT TAGCCACT GAGCCACT TAGCCACT TAGCCACT TAGCACT TAGC	CAGCINGCA CONTRACTOR C	COGGGCCCCG COGGCCCCCGCCCCCCCCCCCCCCCCCC	ACCOMMENT AND ACCOMMENTATION ACCOMMENT.	120 180 240 360 420 360 420 600 780 840 900 1020 11200 11200 11200 11320
50 55 60 65 70	1 SARCANCTIC GARCAGAGA GARCAGA GARCAGAGA GARCAGAAGA GARCAGAGA GARC	11 AGCTTCTAGT CTTCTCCAGC GCOLCTTCG G	21 I ATTOCAGA TO CONTROL OF THE ATTOCAGA TO CONTROL OF THE ATTOCAGA CONTROL OF	CAGOSTOCIONE CAGOSTOCIO CAGOSTOCI	COGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	NACOMMENT	120 180 240 360 360 360 360 540 660 720 960 960 900 960 1020 1020 1020 1030 1240 1250 1320 1440 1260 1320 1460 1500 1620 1620 1620 1620 1620 1620 1620 16
50 55 60 65 70 75	1 GROCANCTIC COLORDO CONTROL C	11 AGCTICTAGE CONCENTION TO AND THE ACT OF T	21 ATCCAGACTC GOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CAGGUEGGE CAGGUE	COGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ACCEPANCE AGENTATION A	120 180 240 360 360 360 360 480 600 720 840 600 720 840 1020 1020 1140 1260 1260 1260 1260 1260 1260 1260 126
50 55 60 65 70	1 GARCAMACTEC COACCAGAGA GOOGGACACAGAGA GOOGGACACAGAGA GOOGGACACAGAGAGACACACACACACACACACACACACA	11 REGITCHART REGITCHART REGITCHART REGITCHART REGITCHART REGITTHART REGITTHA	21 ATTOCAGA CONTROL AND AND AND AND AND AND AND AND AND AND	CAGGUAGO CONTROL CONTR	COOSGOOCACE TOCCOCCIONE TOCCOCIONE TOCCOCIONE TOCCOCIONE TOCCOCCIONE TOCCOCCIONE TOCCOCIONE TOCCOCIONE TOCCOCIONE	I CONTROLLARIO DE LA CONTROLLARI	120 240 360 480 420 480 600 600 720 780 840 1020 1120 1120 1120 1120 1120 1120 11
50 55 60 65 70 75	1 GARCAMACTEC COACCAGAGA GOOGGACACAGAGA GOOGGACACAGAGA GOOGGACACAGAGAGACACACACACACACACACACACACA	11 REGITCHART REGITCHART REGITCHART REGITCHART REGITCHART REGITTHART REGITTHA	21 ATTOCAGA CONTROL AND AND AND AND AND AND AND AND AND AND	CAGGUAGO CONTROL CONTR	COOSGOOCACE TOCCOCCIONE TOCCOCIONE TOCCOCIONE TOCCOCIONE TOCCOCCIONE TOCCOCCIONE TOCCOCIONE TOCCOCIONE TOCCOCIONE	ACCEPANCE AGENTATION A	120 180 240 360 360 360 360 480 600 720 840 600 720 840 1020 1020 1140 1260 1260 1260 1260 1260 1260 1260 126

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	AGCANGGCAT '	TTGGCTGCTG	TAAGCTTATT	GCTTCATCTG	TAAGCGGTGG	TTTGTAATTC	2580
	CTGATCTTCC	CACCTCACAG	TGATGTTGTG	GGGATCCAGT	GAGATAGAAT	ACATGTAAGT	2640
5	GTGGTTTTGT .	AATTTGAAAA	GTGCTATACT	AAGGGAAAGA	TOTTANGAAA	TAACIGCATA	2760
,	CCCTTA A CCA	OTOTOTO AG	TCATCACACA	GTGAAGTAAA	ATTGAGTGCA	CTAAACGAAT	2820
	AAGATTCTGA	GGAAGTCTTA	TCTTCTGCAG	TGAGTATGGC	CCAATGCTTT	CTGTGGCTAA	2880
	ACAGATGTAA '	TOCODACABA	TARABGCCTA	CCTCTTCCTA	AATCCAACAG	CAAGGGAGAT	2940 3000
10	TTTTGAATCA TGTTAGCTGG	CACCTCACCC	TARGGIGGTA	GTTAGTTGG	DATEGUCTACT	TCATAATAAA	3060
10	CTACACAAGG	DODGETTAGEC	ACCOTGTCTT	ATGAGGAATT	GGACCTAATA	AATTTTAGTG	3120
	TGCCTTCCAA	ACCTGAGAAT	ATATGCTTTT	GGAAGTTAAA	ATTTAAATGG	CTTTTGCCAC	3180
							3240 3300
15	ACAAAAAAAT	TTTATGGCCC	AAAATGACCA	ACGAAATTGT	TACAATAGAA	TTTATCCAAT	3360
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25	Managlollo QIQCKVFDSL	FILAFLGWIG	AIVSTALPOW	RIYSYAGDNI	VTAQAMYEGL	WMSCVSQSTG	60
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	IGGAIFLLAG LLCCSCPRKT	LAILVATAWY	CNRIVQEPYD	PMTPVNARYE	PGQALFTGWA	AASICULGGA	180
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35	TTTTTTTTT	TITTTTTTT	TTTTTCAAGG ACCAAGTGAC	AGAGCACAAG	GAACTTTATT	AATGACTTTC	60 120
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40	CAGTTGTTAT	GAAGAATGCA	TATATTAGAA	TGCCTGTAGT	CTCAGCTACT	CAGGAGGCTA	300 360
40	AGGTGGGGAG	GTCGCTCAAG	CCCAGGAATT	CAAAGCTGCA	ATGCATTATG	ATTACAGCTG	360 420
	TTAATAGCCA			TGTAGTAAGA	TCCCATCTCT	GGCTCGGAGG	420
	OTCOTACGCC	CACCCACTCT	CGCTGATTGC	TAGCACAGCA	GTCTGAGATC	AAACTGCA	
			GCCTGGGCAA	TAGCACAGCA	GTCTGAGATC	AAACTGCA	
45	Seg ID NO:	246 DNA 86	quence		GTCTGAGATC	AAACTGCA	
45	Seq ID NO: Nucleic Aci	246 DNA se	guence n.#: XM_058		GTCTGAGATC	AAACTGCA	
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50 55 60	Seq ID NO: Nucleic Acif Coding sequ 1 ANTITICAGA TANANUTATT GRIANACCAT TOGRATGAGG ANTIGAGGAA ACTGGTAACC TTANTTCAG TTOGRATGAGG GCCTTGGCT TAGTCTTAG TTOTCAGGG GCCTTTGCT TAGTCTTAG TAGAGGAA ACGAGAACTTA ACCACCAAAACTAA	246 DNA seid Accession cencer 897- 11 AGTITICATAT TAGTATCAGAT TAGATATTAGAGAGTATAA AAGAAAAAGT TACTOTATTATATATATAGAGAGTATATAGAGAGTATAGAGAGAGTAG	QUELCE n #: XM_05i 1400 21 GGGGATGGTT GCTCAATAGA ATGTTCACA AGTTCTTGAGA AGTTCTTGAGA AGTTCTTGAGA AGTGTTCTTGAGA AGTGTTCTTGAGA ATGAGAATGT CAAAAATGT CAAAAATGT CAAAAATGT CAAGAATGT AGGAGATTACA AGGAGATTACA ATTACAGCACA AGTTTCTTGAGA AGTAGTTTTGA AGTAGTTTTGA AGTAGTTTGAGAGCACA AGGTTTCTTGAGAGCACA AGGTTTCTTGAGAGCACA AGGTTTCTTGAGAGCACA AGGTTTCTTGAGAGCACA AGGTTTCTTGAGAGCACA AGGTTTCTTTGAGAGCACA AGGTTTCTTTTGAGAGCACA AGGTTTCTTTTGAGAGAGAGAGAA AGGTTTCTTTTGAGAGAA AGGTTTCTTTTGAGAGAAA AGGTTTCTTTTGAGAGAAA AGGTTTCTTTTGAGAGAAA AGGTTTCTTTGAGAGAAA AGGTTTCTTTGAGAGAAA AGGTTTCTTTGAGAGAAA AGGTTTCTTTGAGAGAAA AGGTTTCTTTGAGAGAAA AGGTTTCTTTGAGAGAAAA AGGTTTCTTTGAGAGAAAAAA AGGTTTCTTTGAGAGAAAAAAAAAA	31 TTATATAAAT AGAGATTICT TTCCTGTTAC TCCTAACATT AAAAGGACA TGAACATT AAAAGGACA GAACCAGGAA TTCAAGCTCC GGCATAAACC GGCAGGATCA AACTCCTCA TTCAACATT TCATAACCTC TTGAATTCA AGAACCATTA	41 TCAGGITTIT AATAGAAANG GATTOOTIT GACACTTAG AAGACTTAG TTTCCAAGCA AGGICCTAG AAGACCTAG CCCATGCCAG TTTAGTTTT TTTCATGCT TTTAGTTTT TTCAAGTCCCC CCAGTGCAG TTTTGTTTTT TTCAAGTGCCC CCAGTGCCAG TTTTGTTCATT TTCAAGTGCCC CCAGTGCCAG	51 CCCACAATAA GATTCAAACT TCTTOTGACT CACTTAGTGC CACTTAGTGC CACTTAGTGG GGCCTTCCT TATTOGAAGA TAATAGAACA TCTCACTCC TGATTGGAAGA TAATAGAACA TCTCACTCC TGCTAAGTTTG TGTAGAGAGC TCTCACTCC TCCAACATGG TATGGAAAA AAGAATCACCT TCCAACATGG TATGGCAAAA AAGAATCACCT TCCCAACATGG TATGGCAAAA AAGAATCACCT TCCCACCCCCCCCCC	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020 1080
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	1	CCGGGCTGCT	1	<u></u>	1	macca composition	60
	TTAAGGAAAT	CCGGGCTGCT	A TOTAL A TOTAL	CONCERCAT	TTCCCAGCTG	GGCACTCTCG	120
10	AACTGATTAT	CCCCCCCCCCCC	CCCCCCCAC	CCCCTGCCCT	TCCCTCCCGC	GGCACTCTCG GTCCTGCCCC GGCAGCGCGC	180
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23	mmmaaaaaaa	COCKOCCACA	TAGGCAGCCG	COMMANGEMENT	TTCACATACG	CCGTGAGCGC	1140
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30	GCGCATCCAC	GCCAAGGGCT	CCTACGAGAG	TGCTCGCATC	CCCCCCCAACC		1440
						GCCATGGGGT GCAAGGTGGG	1500
	TO TO COCTO	AAGGAGAAGT	ACGACAGOGO	GGCGGCCATG	CGGCTCAACA	GCCGGGGCAA	1560
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00	TATCACIGI	A ADACTOTTO	CACTGTACT	T GAACAGTTG	CATTTATAAG	T TGTACTGCAG G GGGGAAATGT	3240
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	omore coore	T ATCTCTCTC	TAGDAGCAT	T GTTGTCCTT	C ACTGCAGTC	C AGTIGGGATI	3420
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75						T AATTTATTGC C TTGAAAGCAA	
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	AATGGAAGA	T AGAATATAA	A ATAAAACGI	T ACTIGIAAA	A AAAAAAA		
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Seq ID NO: 249 Protein sequence: Protein Accession #: NP_003383

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5	MAGSAMSSKF SQGQKKLCHL AFTYAVSAAG FVDARERERI LADERKYGDA	FLVALAIFFS YQDHMQYIGE VVNAMSRACR HAKGSYESAR LKEKYDSAAA NKTSEGMDGC	GAKTGIKECQ EGELSTCGCS ILMNLHNNEA MRINSRGKLV	YOFRHRRWIC RAARPKOLPR GRRTVYNLAD OVNSRFINSPT	STVDNTSVFG DWLWGGCGDN VACKCHGVSG TODLVYIDPS	RVMQIGSRET IDYGYRFAKE SCSLKTCWLQ PDYCVRNEST	60 120 180 240 300 360
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	1	11	21	31	41	51	
15	TGACTTGGAT	GTAGACCTCG	ACCTTCACAG	GACTETTCAT	TGCTGGTTGG	CAATGATGTA	60
	MOCCOCRGS TAT	CTCCTCACCC	CTAGGAAAAG	ACTIVITIES	GRACCCTGGG	TTATCGGCCT	120
	CGTCATCTTC	ATATCCCTGA	TTGTCCTGGC	AGTGTGCATT	GGACTCACTG	CAACTGACAA	180 240
	ACTATATGCT	GAGTTTGGCA	GAGAGGCTTC	TAACAATTTT	ACAGAAATGA	GCCAGAGACT	300
20	TGAATCAATG	CAAAAGAAGA GAGTTTGGCA GTGAAAAATG AAGTTCAGTC	CATTTTATAA	ATCTCCATTA	AGGGAAGAAT	TTGTCAAGTC	360 420
	TAGATTTCAC	TCTACTGAGG	ATCCTGAAAC	TGTAGATAAA	ATTGTTCAAC	TTGTTTTACA	480
	TGAAAAGCTG	CAAGATGCTG AAGACAGAAA GGTCAGAGTC	TAGGACCCCC	TAAAGTAGAT	CCTCACTCAG	TTAAAATTAA	540 600
25	TABARCTCTA	GGTCAGAGTC	TCAGGATCGT	TGGTGGGACA	GAAGTAGAAG	AGGGTGAATG	660
	GCCCTGGCAG	GCTAGCCTGC CTTGTGAGTG TTTGGAGTAA	AGTGGGATGG	GAGTCATCGC	TGTGGAGCAA	CCTTAATTAA	720 780
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30	AATTGTCCAT	GAAAAATACA	AACACCCATC	ACATGACTAT	GATATTTCTC	TTGCAGAGCT ATGCATCCTA AAAATGATGG	900
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-	MYRPDVVRAR DKLYAEFGRE ICRPHSTEDP RSKTLGQSLR	KRVCWEPWVI ASNNFTEMSQ ETVDKIVQLV IVGGTEVEEG	GLVIPISLIV RLESMVKNAF LHEKLQDAVG EWPWQASLQW	LAVCIGLTVH YKSPLREEPV PPKVDPHSVK DGSHRCGATL DSHDVDISLA	YVRYNQKKTY KSQVIKFSQQ IKKINKTETD INATWLVSAA ELSSPVPYTM	NYYSTLSPTT KHGVLAHMLL SYLNHCCGTR HCPTTYKNPA AVHRVCLPDA	120 180 240 300
-	MYRPDVVRAR DKLYAEFGRE ICRPHSTEDP RSKTLGQSLR RWTASFGVTI SYEFQPGDVM LEGKTDACQG	KRVCWEPWVI ASNNFTEMSQ ETVDKIVQLV IVGGTEVEEG	GLVIPISLIV RLESMVKNAF LHEKLQDAVG EWPWQASLQW	LAVCIGLTVH YKSPLREEPV PPKVDPHSVK DGSHRCGATL DSHDVDISLA	YVRYNQKKTY KSQVIKFSQQ IKKINKTETD INATWLVSAA ELSSPVPYTM	NYYSTLSFTT KHGVLAHMLL SYLNHCCGTR HCFTTYKNPA	120 180 240 300
50	MYRPDVVRAR DKLYAEFGRE ICRPHSTEDP RSKTLGQSLR	KRVCWEPWVI ASNNFTEMSQ ETVDKIVQLV IVGGTEVEEG	GLVIPISLIV RLESMVKNAF LHEKLQDAVG EWPWQASLQW	LAVCIGLTVH YKSPLREEPV PPKVDPHSVK DGSHRCGATL DSHDVDISLA	YVRYNQKKTY KSQVIKFSQQ IKKINKTETD INATWLVSAA ELSSPVPYTM	NYYSTLSPTT KHGVLAHMLL SYLNHCCGTR HCPTTYKNPA AVHRVCLPDA	120 180 240 300
-	MYRPDVVRAR DKLYAEFGRE ICRPHSTEDP RSKTLGQSLR RWTASFGVTI SYEFQPGDVM LEGKTDACQG GI Seq ID NO: Nucleic Ac	KRVCWEPWVI ASNNFTEMSQ ETVDKIVQLV IVGGTEVEEG	GLVIPISLIV RLESMVKNAF RLESMVKNAF LHEKLODAVG EWPWQASLOW RIIVHEKYKE DGYSONHLRQ ARDIWYLAGI QUENCE D#: NM 00:	LAVCIGLTVH YKSPLRBEFV PPKVDPHSVK DGSHRCGATL PSHDYDISLA AQVTLIDATT VSWGDECAKP	YVRYNQKKTY KSQVIKFSQQ IKKINKTETD INATWLVSAA ELSSPVPYTM	NYYSTLSPTT KHGVLAHMLL SYLNHCCGTR HCPTTYKNPA AVHRVCLPDA	120 180 240 300
50	MYRPDVVRAR DKLYAEFGRE ICRPHSTEDP RSKTLGQSLR RWTASFGVTI SYEFQPGDVM LEGKTDACQG GI Seq ID NO: Nucleic Ac	KRVCMEPWVI ASNNFTEMSQ ETVDKIVQLV IVGGTEVEEG KPSKMKRGLR FVTGFGALKN DSGGPLVSSD 252 DNA Bee id Accessio	GLVIPISLIV RLESMVKNAF RLESMVKNAF LHEKLODAVG EWPWQASLOW RIIVHEKYKE DGYSONHLRQ ARDIWYLAGI QUENCE D#: NM 00:	LAVCIGLTVH YKSPLRBEFV PPKVDPHSVK DGSHRCGATL PSHDYDISLA AQVTLIDATT VSWGDECAKP	YVRYNQKKTY KSQVIKFSQQ IKKINKTETD INATWLVSAA ELSSPVPYTM	NYYSTLSPTT KHGVLAHMLL SYLNHCCGTR HCPTTYKNPA AVHRVCLPDA	120 180 240 300
50	MYRPDVVRAR MYRPDVVRAR MYRPGRE ICRPHSTEDP RSKTLGQSLR RKTASEGVTI SYEFOPGDVM LEGKTDACQG GI Seq ID NO: Nucleic Ac Coding seq	KRVCWEPWVI ASNNFTEMSQ ETVDKIVQLV IVGGTEVENGK KPSIOKKGLR FVTGFGALKN DSGGPLVSSD 252 DNA seid Accessio uence: 71-1:	GLVIFISLIV RLESMVRNAF LHEKLQDAVG EMPMQASLQM RIIVHEKYKE DGYSQNHLRQ ARDIWYLAGI Quence n #: NM_00: 771	LAVCIGLTVH YKSPLREEPV PKVDPHSYK DGSHRCGATL PSHDYDISLA AQVTLIDATT VSWGDECAKP	VNRYNQKKTY YVRYNQKKTY YVRYNQKKTY YVRYNQKKTY YVRYNQKKTY INATWLYSA INATWLYSA INATWLYN INTO INTO INTO INTO INTO INTO INTO INT	NYYSTLSFTT KHGVLAEMLL SYINHCCOTR HCFTTYKNPA AVHRVCLPDA ITPRMLCAGS ALROWITSKT	120 180 240 300 360 420
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50 55 60	MYRPDVVRAR DKLYAEFGRE ICRPHSTEDP SKTIGGSLR RHTASSGVTI SYEFORGOW LEGKTDACOG GI Seq ID NO: Nucleic Ac Coding seq 1	RVCMEPHVI ASNNFTEMSQ ETVDKIVQLV IVGGTEVEEG KPSKNKRGLR FVTGFGALKN DSGGPLVSSD 252 DNA seid Accessiouence: 71-1 11 CTGGTGCCCC	GLVIFISLIV RLESMVKNAF LHEKLODAVG EMPHQASLQM RIIVHEKYKE DGYSGNHURQ ARDIWYLAGI Quence n #: NM_00: 7771 21 CGGGCTCTTG	LAVCIGLTVH YKSPLREEFV PPKVDPHSVK DGSHRCGATL PSHDYDISIA AQVTLIDATT VSWGDECAKP 3504.2 31	VNRYNQKKTY YVRYNQKKTY	NYYSTLSPIT NYYSTLSPIT NHOULARMLL SYLWHOCGTR HCPTTYKNPA AVHRVCLPDA VIEWCLPDA AVHRVCLPDA A	120 180 240 300 360 420
50	MYRPDVVRAR DKLYAEFGRE ICRPHISTEDP RSKTLGGSLR RNTASSGVTI SYEFGPGDVM LEGKTDACQG GI Seq ID NO: Nucleic Ac Coding seq 1 GGCACGAGGC GG	REVEMENTAL SAME TEACH OF THE PART OF THE P	GINTFISLIV RLESHVINAR LHEKLODAVG EMPMOASLOM RITVHEKYKE DGYSGNIHRO ARDIWYLAGI Quence n #: NM_00: 771 21 casscrttma cccarttccs cctcasacat Acctacata	LAVCIGLTVH YKSPLREEPV PPKVDPHSVK PSHDYDISLA AQVTLIDATT VSNGDECAKP 3504.2 31 GTACCTCAGC GAAAGAGTTC GGATGCTCTG TACGCTGGTT	VVRYNOKKTY KSQVIKPSQO IKKINKTETD INATWLVSNA ELSSFVPYTM CNEPQAYNDA NKPGVYTRVT 41 GCGAGGGGCA TACGAGGTGG TGTGCGTGCA CCAGTTTCTG	NYYSTLSPIT KRGVLAERCLL SYLMHCCGTR ECPTTYSNPA AVHRVCLPDA ITPRMLCAPA ALRDWITSKT 51.	120 180 240 300 360 420 60 120 180 240 300
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50 55 60 65	MYRPDVVRAR DKLYAEFGRE ICRPHISTEDP RSKTLGGSLR RNTASSGVTI SYEFGPGDVM LEGKTDACQG GI Seq ID NO: Nucleic Ac Coding seq 1 GGCACGAGGC GG	REVEMENTAL SAME TEACH OF THE PART OF THE P	GINTFISLIV RLESHVINAR LHEKLODAVG EMPMOASLOM RITVHEKYKE DGYSGNIHRO ARDIWYLAGI Quence n #: NM_00: 771 21 casscrttma cccarttccs cctcasacat Acctacata	LAVCIGLTVH YKSPLREEPV PPKVDPHSVK PSHDYDISLA AQVTLIDATT VSNGDECAKP 3504.2 31 GTACCTCAGC GAAAGAGTTC GGATGCTCTG TACGCTGGTT	VVRYNOKKTY KSQVIKPSQO IKKINKTETD INATWLVSNA ELSSFVPYTM CNEPQAYNDA NKPGVYTRVT 41 GCGAGGGGCA TACGAGGTGG TGTGCGTGCA CCAGTTTCTG	NYYSTLSPIT KRGVLAERCLL SYLMHCCGTR ECPTTYSNPA AVHRVCLPDA ITPRMLCAPA ALRDWITSKT 51.	120 180 240 300 360 420 60 120 180 240 360 420
50 55 60	MYRPDVVRAR DKLYAFFGRE ICRPHSTEDP RSKTLGGSLR RNTASFGVTI SYEFOFDVM LEGKTDACQG GI Seq ID NO: Nucleic Ac Coding seq 1 GCCACGAGGC CGCCGTGGCT GAGGGTCCTT TGGAGCTCATT TGGAGCTATT TGGAGCTATT TGGAGCTATT GGTGTTGACACC ACTCATTAAA	RVCMEPWVI ASNIFTEMSQ ETVDKIVQLV IVGGTEVEES RPSIONKRGLR FVTGFGALKN DSGGFLVSSD 252 DNA se- id Accessio- uence: 71-1 CTCGTGCCGC ATGTTCGTG CATGTTCGTG GCATTTCTTG GCATTTT	GLVIPISLIV RLESHVINAR LHEKLQDAVG EMPMQASLQM	LAVCIGLTVH YKSPLREEFV PRYDPHSYK DGSHRCGATL PSHDYD1 SLA AQVTLIDATT VSWGDECAKP 3504.2 31 GTACCTCAGC CAAAGAGTTC GGATOCTCTG GGATOCTCTG TACGCTGGT ACAACCTGAT ACAACCTGAT ACAACCTGAT ACAACCTGAT TACACCTCGAT ACAACCTGAT ACAACCTGAT TACACCTGAT TACACCTCGAT TACACCTCGAT TACACCTGAT TACACCTCGAT TACACCTCCAT TACACCTCAT TACACCTCCAT TACA	VVRYNQKKTY KSQVIKF8QQ IKKINKTETD INATHIVSRA ELISSPUPTIN CNEPQAYNDA NKPGVYTRVT 41 GCGAGCGCA TACGAGGTOG TGTACGTOG GAAGAACTT GAAGACACTT GAAGACACTT TCAGAGCCT GAAGACACTT TCAGAGCCT TCAGAGCCC TCAGAGCCC TCAGAGCCC TCAGAGCC TCAGA	NYISTLSPIT KHGULARMLI KHGULARMLI SYIMHCGOTR HCPTTYMPA AVHRVCLPDA ITPRMLCAGS ALRDWITSKT 51 GCCTCCGGC GCCAGACCCA AGATCGTCA AGATCGTCA AGATCGTCA TCATAACT TCATGAACT TCATGAACT TCATGAACT TCAGGGATGA TCTGGGAAGA CTGGGAAGA CTGGGAAGA	120 180 240 300 360 420 180 240 360 420 480 540
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50 55 60 65 70 75	WYPPDVVRAR DRLYAFGREE DRLYAFGREE BRITLGSBIR BRITLGSBIR BRITLGSBIR BRITLGSBIR GI Seq ID NO: Nucleic Ac Coding seq I GGCACGAGGIC GGCOTTGGT GGAGGICAC ACCTGGTT GTGAACCTAT GTGAACC	KRYOMERWYI ARRHITTRINGO ARRITTRINGO A	I I I I I I I I I I	LAVCIGITYM YASPIAREPY PERVINNISTA DESIREOUTL A OFFICIAL STATE STAT	YNYINGKITY KSQVIKIPSQQ IIKIMITETH IIRITYIPSQA GURQAYING GURQAYING AGGAGCICCA TACGAGGTGG TOTGCTTCA TACGAGGTGG GAAGACATCA AACGAAACAC TACAGAGCTCC TACAGAGCTTC AACGAGCACC TACAGAGCTTC TACTTTTATTTATTATAC ACGAGCACC TACAGAGCTC TCCTTTGAGT TCCTAGAGCTC TCCTTTGAGT TCCTAGAGCT TCCTTTGAGT TCCTAGAGCC TCCTTTGAGT TCCTAGAGCC TCCTTGAGT TCCTAGAGCC TCCTTGAGT TCCTAGAGCC TCCTTGAGT TCCTAGGAGCC TCCTTGAGT TCCTAGGAGCC TCCTTGAGT TCCTAGGAGCC TCCTTGAGT TCCTAGGAGC TCCTTGAGT TCCTAGGAGC TCCTTGAGT TCCTAGGAGC TCCTTGAGT TCCTAGGAGC TCCTTGAGT TCCTAGGAGC TCCTTGAGT TCCTAGGAGC TCCTCTGAGT TCCTAGGAGC TCCTTGAGT TCCTAGGAGC TCCTCTGAGT TCCTAGGAGC TCCTCTGAGT TCCTAGGAGC TCCTCTGAGT TCCTAGGACC TCCTCTGAGT TCCTAGGACC TCCTAGGAGC TCCTCTGAGT TCCTAGGACC TCCTAGGAC TCCTCTCTCT TCCTAGGACC TCCTAGGAC TCCTCTCT TCCTAGGAC TCCTCTCT TCCTAGGAC TCCTCTCT TCCTAGGAC TCCTCTCT TCCTAGGAC TCCTCTCT TCCTAGGAC TCCTCTCT TCCTAGT TCCTAGC TCCTCT TCCTAGT TCCT	NYSTLSPTT REGULANCIA NYSTLSPTT REGULANCIA RECUTTONIN RECUTTONIN NYSTLSPTT REGULANCIA NISVCLAPA N	120 180 240 300 420 420 420 420 420 480 600 650 650 720 720 720 720 720 720 720 720 720 72
50 55 60 65 70 75	WYPEDVVRAR DRLYAPFGRE BRITLGGSRE	I	I DESPRIENT SERVICE SE	LAVCIGLTWR YESPLENERY YESPLENERY YESPLENERY YESPLENERY POSSIBLEONT	VNETNOIGNTY ASSOLITATION COCCASITICT ASSOLITATION ASSOLITATION ASSOLITATION COCCASITICT COCCAS	NYTSTLSFTT REGULANCIA REGULA REGULANCIA REGULA REGULANCIA REGULA REGULANCIA REGULA REGULANCIA REGULA REGULANCIA REGULA REGULA REGULA REGULA REGULA REGULA REGULA REGU	120 180 240 300 420 420 600 120 130 360 420 480 650 660 660 660 660 600 610 120 1080 1020 1080 1020 1080 1020 102
50 55 60 65 70 75	MYPPOVVRAR DIRLARGEMEN DIRLARGEMEN DIRLARGEMEN ENTIAGRAM ENTAGRAM ENTIAGRAM	I CONTROLLED TO THE CONTROLLED	LINETERLY ELESHYOLDE LHESKLODNO RIJVHENYE BOYSONILAD AND HYTLAR LHESKLODNO RIJVHENYE BYSONILAD AND HYTLAR TO AND HYT	LAVOLTULANI YESUNDUNANI YESUNDUNANI YESUNDUNANI YESUNDUNANI YESUNDUNANI DEGISECOATI DEGISECOATI DEGISECOATI DEGISECOATI DEGISECOATI SUNDUNANI SUND	VENENGIATY ASSOLITATION ASSOLIT	NYTSTLESTT REGULANCIAN REGULANCIAN REGULANCIAN REGULANCIAN REGULANCIAN REGULANCIAN SITURNIA, SIGNA REGULANCIAN REG	120 180 240 360 420 180 120 180 240 360 660 660 660 660 1020 1140 1200 1140 1210 1210 1210 121
50 55 60 65 70 75	NYPEDVVPARE DIRLYASPORE BIRLYASPORE BIRLYA	International Control	LINESPUBLICA LIESENOBLE LIESENOBL	LAVCIGITYM YESPLAIESY YESPLAIESY PERSON DESIBECTAT PSINDY ISLA AQVILIDAT 1504.2 1504	VNETNOIGNTY ASSOLITATION ASSOLI	NYTSTLSFTT REGULANCIA REGULA REGULANCIA REGULA REGULANCIA REGULA REGULANCIA REGULA REGULANCIA REGULA REGULANCIA REGULA REGULA REGULA REGULA REGULA REGULA REGULA REGU	120 180 240 360 420 180 120 180 240 360 660 660 660 660 1020 1140 1200 1140 1210 1210 1210 121

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,	CCATTTTTTA AAAAAAAAAA	TTAAATAAAA AA	TGCTTATTTT	AGGCTCCGTC	CCCANANAN	AAAAAAAAA	1920
10	Protein Acc	253 Proteir ession #: N	P_003495.1				
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15	AFLEHKEQFH QDDDLEVFAY RRDILFDYEQ DVGVLORHVS	YEVVQSQRVL YFILINGAN EDIPRDEED YEYHGTSSAM RHNHRNEDEE	VDLLDILOPD EEHSGNDSDG VMFELAWMLS NTLSVDCTRI	EDTIPPVCDT SEPSEKRTRL KDLNDMLWWA SPEYDLRLVL	EEELVEQTMR IVGLTDQWVQ YQHWSLHDSL	NDTQIKLLIK RRQRREWEAR DKITQMKYVT CNTSYTAARF	60 120 180 240 300
20	PSIHPGPKHK KQLRATQQTI TKNRRCKLLP	Loefladngl Flasdvvfat Asclotnlvi Lvmaaplsme Aedrskflda	MSLMESPEKD SQGPFLYCSL HGTVTVVGIP	GSGTDHFIQA MEGTPDVMLF	LDSLSRSNLD	KLYHGLELAK KHLLKSFVCS	360 420 480 540
25	Nucleic Ac:	254 DNA sec ld Accession lence: 48	1 #: NM_0223	37			
30			21	31	41	51	
	ACAAGGAGCA	11 CCCTGGTCAG CCTGTACAAG	GCACGGCACG TTGCTGGTGA	TCTGGCCGGC TTGGCGACCT	CGCCAGGATG GGGCGTGGGG	CAGGCCCCGC AAGACCAGTA	60 120
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33	ATATOTOGG	TCAAGAAAGA	TTTGGAAACA	TGACGAGGGT	CTATTACCGA	GAAGCTATGG	300
	GTGCATTTAT	TGTCTTCGAT	GTCACCAGGC	CAGCCACATT	TGAAGCAGTG	GCAAAGTGGA	360 420
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40	ACTITICITICAL	GGAGCACGGT	TTCGTAGGAT	GGTTTGAAAC	ATCAGCAAAG	GAAAATATAA	540 600
	ACATTGATGA	AGCCTCCAGA TGAGCCGGAC	TGCCTGGTGA	CCCATCTCAC	ATCAACCAAG	TGTGACCTAA	660
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45	THEOTOCOLCA	AATTCTCCCT	CTATTTTAC	CATTTTCCCT	AAACGTCAGG	ATAGATATAC AATAGCAAAT	780 840
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60							
00	1	11	21	31	41 .	51	
	<u> </u>	1		I CONTROCTOR A	TTOMPAT.KU	LHWDPETVVR	60
65	LOLWDIAGOR	RECEIMTRUYY	REAMGAPIVE	DVTRPATFEA	VAKWKNDLDS	KLSLPNGKPV RCLVKHILAN	120 180
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	1	11	21 	1	ĺ.	1	
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75	CONTRACTO	COCTACORC	TYTERACTOR	CCCCCACTGG	TGGTCAGAGA	TTCTCTTCGG GGACGCACAA	180
	GAACTTGAGG	GACATGGAGA	ACGAATTCTA	CTATCGCTAC	CCAAGCTTCC	AGGACGTGCA	240
	CONCAROGEC	THEORYCECOM	TOGGCTTCCT	CATGACTTTC	CTGCAGCGCT	ACGGCTTCAG TGCTCATGCA	300 360
80	COCCTCCTTC	CACTACATAC	AAGACCGCT	CATCGTCGTG	GGCGTGGAGA	ACCTCATCAA	420
	OCCOMOR COMPC	- management	CHARACTANACA	COCCTTTCCC	GCACTTCTGC	GTAAAGTCAG	480 540
	COCCATTCAG	CIGCICATC	AGGTGAAGG	TGCAGGAGG	TOCATGACCE	TGAATGAGTT	600
~~							660
85	CAAGGAGAGA	CAGAATTCIC	TGTACCAGTO	GGACCTCTTT	GCCATGATTC	GCACCCTCTT ACAGCCAGCA	720 780
	CCGAGCCGCC	ATCAACACC	ACTICTOCT	GGCAGCCTGC	GTGCTTACCT	CGGTGGCAAT	840

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15	A TOTA A GOOG	ATCCCAGGGG GGTTCTGGCT	GCAGAAGTTC	TGCCTCTGCC	TGGGGTCTTG	GCCACATTGG	1740					
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	ACAACTTAGC	TGCCAGTCAC ATGCTCCCTG	CACCTATGAG	GCTCTTCTAC	CCCGTGCCTG	CACCTOGGCC	1860 1920					
	CAGGAATAAA	CATTCTTGTT	GTCCTTTGTA	AAAAAAAA	AAAAAAA	1000100010						
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25	· .	11	21	31	41	51. i						
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	PSFQDVHVMV	FVGFGFLMTF	LQRYGPSAVG	PNFLLAAFGI	QWALLMQGWF	HFLQDRYIVV	120 180					
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30							300					
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40	1	11	21	31	41	51						
	1	 GTTGGAGCCG	<u>L</u>	1		CTCCTTTTCT	60					
	THE PROPERTY OF THE PARTY OF TH	OCCUPATION OF THE PROPERTY OF	CTGCAGCTCT	CCCGGGGGGGCA	GGGAATCACC	CTGCGCGGGA	120					
40	CCCCCGAAAT	CCTCCCCCGAG	TTCTTCTCAT	TCGGCATCAA	CAGCATTTTA	TATCAGCGTG	180 240					
45	GCATATATCC	ATCTGAAACC TGAGCTCATA	TTTACTCGAG	TGCAGAAATA	GGAACAACTG	AAAGATTGGT	300					
	TATACAAGTG	TTCAGTTCAG	AAACTGGTTG	TAGTTATCTC	AAATATTGAA	AGIGGIGAGG	360					
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50	CAGCTACGGT	GACATTTCTG	CCACTGITGG	AAGTTTCTTG	TICATITGAT	CTCCTGATTT	540					
••	BTRCBCBCBB	A CATTTOOTT	GTACCTGAAA	AATGGGAAGA	CTCGGGACCA	CAGTTTATTA	600					
	CCAATTCTGA	GGAAGTCCGC CAAAATTCCT	CTTCGTTCAT	CAGGATGACA	THEGGARAST	AATGTAATTG	720					
	THE REPORT OF B	ATCICCITTE	CCTCAAATCA	COTCATCTAT	AGTTGATATG	TTTTTTTTCA	780					
55	TTCCTTA ATT	TTTACATGGA TTTGGTACCT	GAAAACCAAA	ATGATACTTA	CTGAACTGTG	TGTAATTGTT	840 900					
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	CATACTARCE	CTACATCCAA	AAACTTGTGC	TATAAAGCTA	GATGCTTTCC	TAAATCAGAT	1020					
60		AGTAGTTTGA TAAATATTCA					1140					
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65	алалалала											
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,,	1	11	21	31	41	51 .						
	1	 ITLRGSABIV	I	I VODGI VDS	Prerenovy	LATITATEDIA	60					
	T TUVI MARAD	OT WINDLY VECO	DOKT VVVT CN	TESGEVLERW	OFDIECDKTA	KDDSAPREKS	120					
75	OKAIQDEIRS	VIRQITATVT	PLPLLEVSCS	FDLLIYTDKD	LVVPEKWEES	GPQFITNSEB	180					
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85	ON NO OCCUPATION	CTCTGAGTGA	AGCCATGTCC	CTGGAGGGAG	ATGAATGGGA	ACTGAGTAAA	120					
						AGCACTGGCA ATATGAAATT	180 240					
	CAAGAATCTG	CCTGTAACAA	INCICITCAG	CHUCHONNIC								

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	CGATTTTACA	CTGGAAATGA	CCCTCTGGAT	GTTTGGGATA	GGTATATCAG	CTGGACAGAG	300
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	CTACCTCAAC	TABACACCAA	DAGGAAAAAG	ACAGCAAGAG	CTCCAATCAT	CCGTGTAGGA	780
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15	ACTOCACAAC	ACCCACTTAT	CACACCATGT	ARARTTGAAC	CTAGTATAAA	CCACATCCTA	1140
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20	GAAGAGATGG	AGAAGAAGCT AGACGATGCC	AAAAGAAATC	CAAACTACTC	AGCAAGAAAG	AACAGGTGAT	1440
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	CGCAGACAGC	TACTGAAGTC	CCTACCAGAG	TTAAGTGCCT	CTGCAGAGTT	GTGTATAGAA	2280
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55	TAAAATAGTA	TCTGTTAAAA	AAAAAAAAA	AAAAAAAA	AAA		
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60	Protein Ac	cession #:	W5_001505		•		
••	1	11	21	31	41	51	
	1	1	1	1		- COOKE	60
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75	mideompoi	T. POT DOT CAC	ADTATEDOD	OKLETEKET!	F LGNEDYCIKE	BYLICEDYKL	780
15							840
							900
	NKNNQALKI	V DFSYSVDLRV	QLDVFTLSGI	KINGILEGO	I LNANDEATUS	VDLFGIADLA VLGELAAEMN	960
80	GVPDTTPOS	H LNKALWKVGI	LTSPGALLE) LUMBINE PVR	- MUNICIPALITY		
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	Seq ID NO	: 262 DNA B	quence				
	Nucleic A	cid Accessio quence: 365	on #: NM_003	784			
85	Couring se	quemour 303					

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	RGTGCTCAAC	TGGTAAGGAG	AACGTAGAAG	TAGCCCTAGG	GATCCTTTTT	GAAACTCTAC	1860 1920
	AGTTATCGCA	GATATTCTAG	CTTCATTGTA	AGCAATCTAG	GAAATAAGCC	CTGCTGCTTT	1920
25	CTAGAAATAA	GTGTGAAGGA	TAAATTTTCT	TTGTTGACCT	ATGAAGATTT	TAGAGTTTAC	2040
35	CTTCATATGT	TTGATTTTAA	ATCAGTGTAT	AATCTAGATG	GTAAAAAATG	TGAAATTGGG	2100
	ATTAGGGACC	TACCARARTA	TTTCATTAAT	GCTTTCAATT	GACAAATTTT	GGCCTTTCTT	2160
	TGATAAGACA	ATATGTACAT	GTTTTTCAA	ATATTAAAGA	ICITITAACT	GIIGGCAGII	2220
	GTTATCTACA	GAATCATATT	TCATATGCTG	TGTAGTTTAT	AAGTTTTCC	TCIATTIATC	2220
40	AGAATAAAGA	AATACAACAT	ACCIGIANA				
40		aca Breked					

Seq ID NO: 263 Protein sequence: Protein Accession #: NP_003775

45	1	11	21	31	41	51	
	1	1		COT CT. PAAT A	1.VPI GAODDS	LSQIDKLLHV	60
	NTARGYGNES	NSOSGLOSOL	KRVFSDINAS	HKDYDLSIVN	GLFAEKVYGF	HKDYTECABK	120
50	LYDAKVERVD	FTNHLEDTRR	NINKWVENET	HGKIKNVIGE	GGISSSAVMV	LVNAVYFKGK	180
50	WQSAFTKSET	INCHPKSPKC	SGKAVAMMHQ	YVKVFFPOFK	DESMKIDSON	YNGGINMYVL	300
	DESKADLSGI	ASGGRLYISR	MMHKSYIEVT	EBGTEATAAT	GSNIVEKOLP	OSTLFRADHP	360
	FLFVIRKDDI	ILFSGKVSCP					

55 Seq ID NO: 264 DNA sequence Nucleic Acid Accession #: AB052906 Coding sequence: 74-814

60	1	11	21	31	41	51 	
00	AAAACCTTCA	GGTGATTCAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	' 60
	MONCCITON	TTAATGGCAG	CNGCCGCCGC	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
	COTOCOCCE	TCCGGCTGGT	CCCGGGCTGG	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	180
	CATCACCCTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
65	CALCACCALC	ACTITICITO	ACTATGACTG	TOGCAACAAG	ACAGTCACAC	CTGTCAGTCC	300
00	CCTCCCCAAG	AAACTAAATG	TCACAACGC	CTGGAAAGCA	CAGAACCCAG	TACTGAGAGA	360
	CCTGGGGGGG	ATACTTACAG	AGCAACTIGGG	TGACATTCAG	CTGGAGAATT	ACACACCCAA	420
	CCFFCCCCCC	ACCCTGCAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
	OCCUPATION OF	CAGTTCAGTT	TOGATGGGCA	GATCTTCCTC	CTCTTTGACT	CAGAGAAGAG	540
70	TOGNICIIGO	ACCOTTCATC	CTCCAGCCAG	ABAGATGAAA	GAAAAGTGGG	AGAATGACAA	600
70	ARTGIGGACA	ATGTCCTTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
	GGIIGIGGCC	GGCATGGACA	CCACCTGGA	CCCAACTICCA	GGAGCACCAC	TOGOCATOTO	720
	CITCITUALO	ACCCAACTCA	GCGCCACAGC	CACCACCCTC	ATCCTTTGCT	GCCTCCTCAT	780
	CICKGGCACA	TGCTTCATCC	TOCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
75	PACCECTOCCC	CAAAAGGCTC	CTCTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
13	ARGUTGATAC	ACGACCTACG	CIGIONGCAC	ACTIGOTIC	AGCAGATCAT	GATGACATCA	960
	CCAGCIGCCC	AGCTCATTCA	CHCCCTTCAT	TOTTTTTCCC	AACAATTTTA	CCAGCAGTTA	1020
	TOGACCCAAT	ATTATGCAAT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TOCTACTGA	TGGAATTCCT	GCACTTAAAG	1080
	TACCIAACAI	CTAAACAAGA	TITCICITOO	TOCTIOCIAN.	CATALACTA	GGAAAATCAA	1140
80	TTCTGGCTGA	GAATGATGAT	CHARACTER	CARATCATAT	TGTCAGTAAA	ATAATCACCT	1200
٥U	GTACTTCTTT	ACCTCTGGGG	CTCTTTCTTG	CAMMIGNIAL	CACAATTTT	BARTTATTA	1260
	TAGACTTCAG	ATTTATATTA	ATTCTTTCCG	TGTCCTGAAA	ORGANITITE C	TOTA CTCATA	1320
	ATAAGAAAAA	ATTTATATTA	ATGATTGTTT	CCTTTAGTAA	TITALIGITO	IGIACIGNIA	1320
	TTTAAATAAA	GAGTTCTATT	TCCCAAAAAA	AAAAAAAAA	~		

Seq ID NO: 265 Protein sequence: Protein Accession #: BAB61048.1

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	MAAAAATKIL PLHYDCGNKT	11 CLPLLLLS VTPVSPLGKK ABGHSSGSWQ IGWLEDFLMG	LNVTTAWKAQ PSPDGOIFLL	HSLCYDITVI NPVLREVVDI PDSEKRMWTT	PKPRPGPRWC LTEQLRDIQL VHPGARKMKE	KWENDKVVAM	60 120 180 240
10	Nucleic Aci	266 DNA seq d Accession ence: 127-4	#: XM_084	853.1			
	1	11	21	31	41	51	
15	GACAAGATCA AACACCATGA AAAAAGGCCA	TATTTAACGA ACTTACCAGA GTGGCATCCA TTCGAAGAGA AGATGTTGGA	TTTCCTAAAA CAAGAGCTTT GGACTTCCTG TTGCTTTGCT	GTGTACCTTA GAGGTGCTCG AGACTGCTCG TCACTGTTTG	ACCACAAGCC GTTATACCAA TTACTAAAGG GCCTGAATCC	CTCCAAAGGG TGAGCATATG CGAGGGATGG	60 120 180 240 300
20	CCAGACGAAA GATTCCGGCC GTGTGTGTGC	CTGCAACCTG TCACTGCAGA AGGATGGTCA ATGCACATGT ATCTTTAGAA	AATATTCGCG GTGAAGTTAC GTGTGTTTTC	ACTGARATTC CAGGARTGTT CATGAGGCAC	TTGGCTTGA TTGGCTTAAC TAAAGCACAA TGCTTTTTAT	CATTTCAGAA AGGACTTTGG GCATTTCCCT	360 420 480 540
25							
	Seq ID NO: Protein Acc	267 Protein cession #: 7	sequence: (P_084853.1				7
30	1	11	21	31	41	51 	
	EPATCSVKGS	EICTEEFT D	EITAEIPATE	LVTKGEHMTE	EEMLDCFASL GQDGQ	PGLNPEGWKS	60
35	Nucleic Ac	268 DNA sec id Accession uence: 57-4	n #: NM_001 32				
40	1	11	21	31	41	51 	
,,,	GCCCCAGGA	GGAGGATAGG	ATAATCCCGG	GTGGCATCTA	TAACGCAGAC	CTCAATGATG ACCAAAGATG	60 120 180 240
45	ACTACTACAG	CGACGTAGAG	GTGGGCCGCA	CCATATGTAC	CAAGTCCCAG	CCCAACTTGG	300 360 420 480 540
50	CCACCCCTGG	GAAGGCTGCA GCTTCTAATA	CCCACCCTGC	GTTGCTCAGC	AGGGCGCTCT	TGCGCCAAGA GCCCTCCCTC TCCTGCAATT	600 660 720
55	Seq ID NO: Protein Ac	269 Protei cession #:N	n sequence: P_001889.1				
	1	11	21	31	41	51 1	
60	DDYYRRPLRV	LLATLAVALA LRARQQTVGG RSLVKSRCQB	ANALLDARAC	PGGIYNADLN RTICTKSQPN	DEWVORALHE	AISEYNKATK ELQKKQLCSP	120 60
65	Mucleic Ac	270 DNA se id Accessio puence: 13-1	n. # : XM_093 854				
70						51 GGTCCGCACC C GATGGACCAG C GCGGGACGTA C GCCCACGTAC	60 120 180 240
75	GCCTTCAAA GGCGGCGGGA ACGAGTAAC GGAACGCCCC	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TGAACTGAA TGAACTCAAG GGGACCGCTG CAGCAGCGGG	TACCOGACA TOGAGGTCCC	CGCCTCCAC CCAAGCCAAC CCAATGGCCA	TTCTACCACC GACGCAAGGA CGGAACTCAG	300 360 420 480 540
80	GCCGAGGACC CTGCCCAAGC ATGGCCGCCC CTGTCCAGC	CAGCTAGGCC CCCGAGCCC CCAGGCTCCC	GTCACCCGG AGGCTCCCTG GAGCCATGGG	GCGGAGGCCI	COGCTGGTCC	ACCAGGCAAA CGCCCAGATC GGCGTCCTGG	600 660 720
85	Protein A	: 271 Protei cession #:	XP_093210			51	
	1	11	21	31	41	21	

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5	SRAEDPARPS	RARKKWDFLP PLSRSPKPRT PRLLPREGAP RPGAGQQRRA PKAPSPGSLA	GKLPKAPSPG	SLAEASAGLL	AHVRLQNADA	QRVSISQALP RTOLEPSPRL	60 120 180 240
10	Nucleic Aci	272 DNA seq d Accession lence: 173	t #: Eos se	quence			
15	1 GGATACTGTG	11 TCACTCAAAG TTTTTTCCCA	21 TAATGGGAGG	31 GAGAGAGAAC	41 AGGGAGGGTA	51 GGGATGCTTT	60 120
13		GAAGCCTCTG CTTGTTTCTG TTATTTATCT					180 240 300
20	TARATTATTT TTAGTATCAC AARATTGCAG TTAAGCC	TTATTTATCT AATTTATGGG AAGTCATAGG	TTCATATAGT AGAGGGTTTT ACTGTCATGT	TCTTACAATT TTGTATTTTT ATTGCAGCTC	TCTAAAAAT AAGCATATGT TGAGAACCAA	TAACACTCAT GGCTTATATA TGCCTGAAAC	360 420 480
25	Seq ID NO: Protein Acc	273 Proteir ession #: E	Sos sequence				
30	1 MGGRENREGR	11 Dapekapppt	21 PNLL	1	41 	51 	
	Nucleic Ac:	274 DNA sec id Accession lence: 299-5	#: NM_003	1976.2			
35	1	11	21	31	41	51	
	<u></u>	CTCTGAGCCT	1	1	1	CONTENCCE	60
40	CATGGAGTTG CTACTTCTGC GGGTGGCAGG CAGGAGGGTG GGAACTTGGA	TGAAGAATA TGGGTTGAGT CCGGTCCCC GGGGAACAGC CTTGGAGGCC CCCACCCTGG	GCTGCAAAGC CTAGCTGTGT ACAAAAGATA TCAACAATGG TCTCCACGCT	ACCTAACACA AGGCCCCTTG ACTCATCTCT CTGATGGGCG GTCCCACTGC	TAGTAAGGTT TTCCTCACCT TAATTTGCAA CTCCTGGTGT CCCTGGCCTA	CCCAGTGCAG GGAGAAACTG GCTGCCTCAA TGATAGAGAT GGCGGCAGCC	120 180 240 300 360 420
45	GGGCTCCGCG CGCCGGCCAC	CCCGCAGCC CTGCCGGGGG CCTTCTCGGC GCGCGCGGGG CTGCGCTCGC	GACGCACGGC	CGAAGGCCCC	AGTGGAAGAG CCCCCATCTG	CCCGGCGGCC	480 540 600 660
50	CGACGAGCTG	CTGCGCTCGC GTGCGTTTCC CTGGCCAGCC CAGCCCTGCT TGGAGAACCG CCAGGGCTTT AGTCCCACTA	TACTGGGGGG	CGGGGCCCTG	CGACCGCCCC	CGGGCTCCCG	720 780 840 900 960 1020
55	AGGCCCCTAC CAGCCCCAGA	GCCTCACCC GGACCCACTT	TGGGTATCCC TGCGGATCCC	AGCCTAAAAG CTGGCACTGG	ACACCAGAGA CCAGGCCTCG	CCTCAGCTAT AACCTGGGAC	1080 1140 1200 1260
60	ACAGCATTTG	ATGAACACTA AAGGACACAT CTCATGGGAG	CAGTGGCTGA ATTGCAGTTG	GGCATCAGCC	CCCGCCCAGG	CCCTGTAGGG	1320 1380
65	Seq ID NO: Protein Acc	275 Protein cession #: 1	NP_003967.1				
	ì	11	21 	31 	41	51 	
70 .	PAGHLPGGRT	LSHCPWPRRQ ARWCSGRARR PVRALGLGHR TRYEAVSFMD	PPPQPSRPAP SDELVRFRFC	PPPAPPSALP	LGSAPRSPAP RGGRAARAGG HDLSLASLLG	REGPPPVLAS PGSRARAAGA AGALRPPPGS	60 120 180
75	Nucleic Ac	276 DNA sec id Accession Lence: 783-:	n #: NM_0570 1445				
	1	11	21 	31 1	1	51 	
80	TOGCTCCCCAA CGCGTGTCTA	GAGAGAAGAA ATCTGCACGT CCCTCACTCA CAAACTCAAC	ACCAGCAGTC CTTTCTCCCG TCCCGGTTTC	CCTCGGCCCA CCTCGGCCCC	GGCAGGGACC GGCCTCCCAG CACCGCTCGA	GGCTTACCCC CTCTCTACTT GTTCTCTACT	120 180 240
85	CACCEGACGG	GAGGGGCCCC GGGACTGGAT GCGCTCCCAG	CCCACCCCG CCCACCCCG	GAGCAGCCAG GGATCTGGTG	GTGAGCCCGG ACGCTGGGGC ATGGAGTTGG	AAAGGTGGGG TGGAATTTGA	300 360 420 480 540

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	CCCGGGCCTG	GAGCCCCACA	CCCGAGGGTG	CAGACTGGCT	GCCAAGGCCA	CACTTTTGGC	600 660
	TARARGAGGC .	ACTGCCAGGT	DACCOCCU	GOGCATGCGC	CTGCAGGACC	COCTOCTOC	720
	TCAACAGGAG	GGTCCCCGGA	CAGCTCAACA	ATGGCTGATG	GGCGCTCCTG	GTGTTGATAG	780
5	AGATGGAACT	TGGACTTGGA	GGCCTCTCCA	CGCTGTCCCA	CTGCCCCTGG	CCTAGGCGGC	840
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	CCCTGGGCTC	CGCGCCCCGC	AGCCCTGCCC	CCCGCGAAGG	CTCCCCCCCCCT	AGAGCCCGGC	1020
	GGCCGCCCCC	GCAGCCTTCT	CGGCCCGCGC	cccccccccc	TGCACCCCCA	TCTGCTCTTC	1080
10	cccacaaaaa	congagagag	CGGCCTGGGG	GCCCGGGCAG	CCGCCCTCGG	GCAGCGGGGG	1140
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	GGACCCTCCC TGAGAGGCCC	GCAGAGTCCC	ACTAGCCAGC	GGCCTCAGCC	AGGGACGAAG	GCCTCAMAGC	1620
	CTAGCAGCCC	CAGAGCCCTC	ACCCTGCGGA	TCCCAGCCTA	AAAGACACCA	GAGACCTCAG	1680
20	CTATGGAGCC	CTTCGGACCC	ACTTCTCACA	GACTCTGGCA	CTGGCCAGGC	CTCGAACCTG	1740
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25	Seg ID NO:	277 Protein	sequence:				
	Protein Acc	ession #: N	IP_003967.1				
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30	DACULDCOOPT	ADMCCCDADD	DDDCDCDDAD	PPPAPPSALP	RGGRAARAGG	PGSRARAAGA	120
	RGCRLRSOLV	PURALGLIGHR	SDELVRFRFC	SGSCRRARSP	HDLSLASLLG	AGALRPPPGS	180
	RPVSQPCCRP	TRYEAVSFMD	VNSTWRTVDR	LSATACGCLG			
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35	Nucleic Act	d Accession	1 8: NM_057	160.1			
	Coding sequ	ence: 1-714					
			21	31	41	51	
	1	11	11	11	1	ĭ [*]	
40	ATGCCCGGCC	TGATCTCAGC	CCGAGGACAG	CCCCTCCTTG	AGGTCCTTCC	TCCCCAAGCC	60
	CACCTGGGTG	CCCTCTTTCT	CCCTGAGGCT	CCACTTGGTC	TCTCCGCGCA	GCCTGCCCTG	120 180
	TGGCCCACCC	TGGCCGCTCT	GGCTCTGCTG	AGCAGCGTCG	CAGAGGCCTC	CCTGGGGCTCC	240
	CACCTGCCGG	GGGGAGGCAC	GGCCCGCTGG	TGCAGTGGAA	GAGCCOGGCG	GCCGCCGCCG	300
45	CAGCCTTCTC	GGCCCGCGCCC	CCCGCCGCCT	GCACCCCCAT	CTGCTCTTCC	CCGCGGGGGC	360
	controport.	acceptage and	CYCCOCCACC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CAGCGGGGGGC	GCGGGGCTGC	420
	CCCCTCCCCT	CGCAGCTGGT	GCCGGTGCGC CAGCGGCTCC	GCGCTCGGCC	TGGGCCACCG	CTCCGACGAG	480 540
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50							660
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	CCTCCAGGGC	TTTGCAGACT	GGACCCTTAC	CGGTGGCTCT	TCCTGCCTGG	GACCCTCCCG	780 840
	CAGAGTCCCA	CTAGCCAGCG	GCCTCAGCCA CATCCCCGAA	CACCTCAACC	GACAACTGAC	TAGCAGCCCC	900
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	TTCGGACCCA	CTTCTCACAG	ACTCTGGCAC	TGGCCAGGCC	TCGAACCTGG	GACCCCTCCT	1020
	CTGATGAACA	CTACAGTGGC	TGAGGCATCA	GCCCCCGCCC	AGGCCCTGTA	GGGACAGCAT	1080
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60	TCACTCATGG	GMGCIGGCCC					
	Seq ID NO:	279 Protein	n sequence:				
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		11	21	31	41	51	
65	î	1	1 .	. I	i"	Ī	
	MPGLISARGQ	PLLEVLPPOA	HLGALFLPEA	PLGLSAQPAL	WPTLAALALL	SSVAEASLGS	60
	APRSPAPREG	PPPVLASPAG	HLPGGRTARW	CSGRARRPPP	QPSRPAPPPP	APPSALPRGG	120 180
	RAARAGGPGS	RARAAGARGC	RLRSQLVPVR	RAUSPMDVNS	TWRTVDRLSA	TACGCLG	100
70	SUNSDINGNOR	Diversion:	ogi ceni ini				
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	CTGATGGGCG	CTCCTGGTGT	TGATAGAGAT	GGAACTTGGA	CTTGGAGGCC	AGCCTGCCCT	60 120
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	CCGCGCGGCG	CGGGCTGGGG	GCCCGGGCAG	CGCGCTCGC	CTGGGCCAC	GCTCCGACGA	420 480
85	CCTGGTGCGT	TTOTACT	GCAGCGGCTC	CTGCCGCCGC	GCGCGCTCTC	CACACGACCT	540
00	anacemence.	ACCOMPAGE OF	acceccance	CCTGCGACCG	CCCCCCGGGCT	CCCGGCCCGT	600
	CAGCCAGCCC	TGCTGCCGAC	CCACGCGCTA	CGAAGCGGTC	TCCTTCATGO	ACGTCAACAG	660

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5	CAGAGCCCTC	GTGATGGATA ACCCTGCGGA	TCCCAGCCTA	ACAGGTGAAG	GAGACCTCAG	CTATGGAGCC	960
•	CTTCGGACCC	ACTTCTCACA	GACTCTGGCA	CTGGCCAGGC	CTCGAACCTG	GGACCCCTCC	1020
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10	CICACICATO	oanacrace					
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	Protein Acc	ession #: N	P_476431.1				
	1	11	21	31	41	51	
15	L	!	1	1	!		60
	CODDUTAGO	LSHCPWPRRQ GHLPGGRTAR	WCSCRARRED	POPSEDAPOP	PAPPRALPRG	GRAARAGGPG	120
	SRARAAGARG	CRLRSOLVPV	RALGLGHRSD	ELVRFRFCSG	SCRRARSPHD	LSLASLIGAG	180
20	ALRPPPGSRP	VSQPCCRPTR	YEAVSFMDVN	STWRTVDRLS	ATACGCLG		
20	Sea ID NO:	282 DNA sec	nence				
	Nucleic Aci	d Accession	#: Eos seq	ruence			
	1	11	21	31	41	51	
25	ì	11	1	i*	i.	i	
	CTACTGCACC	TGCCCTCTGT	TTCCTTTGGA	AATCTCTTAC	CTTTCATTAG	GCTTTCTTTC	60
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	GCTAAAAATG	AACTTGAAAC CCTGGCTGTA	ACGGAAGTAG	TGGTTGGTCC	AGTTTGAAAG	ATCTTACTAG	360 420
	CACTCTTAAG	GATTTTATGT	GTATTATTCA	AATTGCTATT	ACTOTTCTTT	TTATAGTTGA	480
35	GAATCTCAGG	ATACCTACAT	TTATCACTTT	TTCAATATAT	ATGTATTTCT	TATT	
33	Coc ID NO.	283 DNA sec	mence				
	Nucleic Act	d Accession	ı#: Eos se	quence			
	Coding sequ	ence: 564-1	1481				
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45	* COMMCCO MCC	BOTTO CONTO	CONTOURCE	ABBTATATO	ACTIVITY TYSCTYS	ABACABATCA	240
	CGACOGATGC	TCACAATTCT TTCAGTGGCA	GACCTCGTAA	TTATATAGGG	AAATGAACTG	CAACACCACG	300 360
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	CCCCCCCCCCCC	CCCAGCGCCC	GCTGGGBAAG	CGCGTCCCCG	CCGCGGCTCC	GCCAGTTTGA	660
	ACTTGGCGGG	CCAGATGTGG TGCTGACTGC	AGACCCRGGC	CTCGGCGGGCC	CTCGGACTCC	TOTTCCTACG	720 780
55	CTATGACGGG	CGCACGTGGG	CAGGGGCTGG	AGGTGGTGCG	CTCGCCGTCG	CCGCCGCTGC	840
	OGCTGAGCTG	CAGCAATTCC	ACCAGGTCGC	TGTTGTCTCC	CCTTGGCCAC	CAGAGCTTCC	900 960
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	AGGGGTGCGC	CAGCACTCAG	GTTGAATCAG	AAAATAACCA	AGAAGAACAG	AAACAGGTGC	1080
60	GCTTACCAGA	AAGCCGCCTG	ACACCATGGG	AGGTGTGGTT	TATTGGCAAA	GAAAAAGAAG	1140 1200
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65	AGGAAAAAGC	AGCAAAGGAA	CTGGAGAAAG	AATACTTGCA	GAGGAAGAAG	ADAAAADAAA	1380 1440
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70	GAAGAGTAAA	AGACCTGTGA	TAAGTCAGCC	ACACAAGTCA	TCATCTCTGG	TAATTCATAA	1740
	AGCCAGGAGC	AATCTTTGCC	TTGGAACTCT	GTGCAGAATA	CAAAGATAGC	GTATGTGGAA	1800 1860
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							1980
75	GTTGATCTTG	GCATGTTGTT	TTGCAGAATA	AGTGGCTGAA	TATGTAAGAA	TTGTGTTTGT	2040
	ATTIAGCITG	TATTAAAAGT	ACACIGIAAT	ACCANTARAR	CIMMONITT		
	Seq ID NO:	284 Protei	n sequence:				
80	Protein Ac	cession #:	Bos sequenc	0			
00	1	11	21	31	41	51	
	1	1	L	L	1	1	
	MATRGLEWPG	LAGLARAGPA	GKARPRRGSA	PLDLSCSNOT	RSLLSPICEO	SYAGFSADCR SFOFDEDDGD	60 120
85	CEUEEDADDE	PRUDEDARDS	PAKVASLECM	RLOGCASTOV	ESENNOREOK	OVRLPESRLT	180
	PWEVWFIGKE	KEERDRLQLK	ALEELNOOLE	KRKEMEEREK	RKIIAEEKHK	EMVQKKNEQK	240 300
	RKEREQKINK	EMEEKAAKEL	EKEYLQEKAK	BKYQEWLKKX	NABECERKK	EKKNINSKLKY	300

Seq ID NO: 285 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1-1746

,	Cournd sed	ience: 1-174	.0				
	1	11	21	31	41	51	
	1	1	1	1	!	1	
10	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	120
10	GCCTACCATG	GCTGCCCTAG	CCCACTCCCCT	CTCCCCCCCC	ACGCCATGAG	CCTGCAGATC	180
	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCCGTTCC	TCAATATCTC	TGCAGGGTTG GGAGTGCACC CCTGCAGATC AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTCG	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
	GCTCGCTGC	ACATCACTGA TTGAGAAGAA GCTATCTCAG TGGACAGCCT ACTTCTCCCA TCCCTGACGG	CCTCGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCTC	360
15	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAGCT	GTTGCAGATC	420 480
	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	CACTCACCAA	CCTCAATCTG	540
	CIGGAATACA	TCCCTGACGG	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCCTCCGGC	GCCTGACGG GCCTCACCCA TGTATGAGAA AGGAACTGGC ACCACAACCT TCTTCATGCA	CAGGCTCACG	GATATCCCCA	TGGGCACTTT	TGATGGGCTT	660
20	GTTAACCTGC	AGGAACTGGC	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACAT	CTCCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840 900
	CIGNAGGAGC	1CICICIOGG	more cooce	AATCTCTTCA	CCAACCTCCC	CCACTTGCAG	960
25	TATUACOUCC	TTAGCCGCAA GGGAGCTGTC TGGCCAACCT	TCAGATCAGC	TTCATCTCCC	CGGGTGCCTT	CAACGGGCTA	1020
23	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCATGT	TGGCCAACCT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCAG	1200 1260
30	CTGGAGAACT	TCTTCGCCAA TGCCCCTCGG CCTGGAGGTG GGTTAGGGAC TCATTATCAT	CATCTTCGAT	CACCTGGGGA	TOTAL	GCTGCGGCTG	1320
30	TATGACAATC	CCTGGAGGTG	CONCRCTOTA	CCTCTCTCTCT	TCAGCCCAGC	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTTGCTGTTC	CAAGCGTCCA	TGTCCCTGAG	1440
	GTGCCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
~~	TCCGTCTCTT	CTACCACTGA	GCTAACCAGC	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560 1620
35	ATTCAGGTCA	ACCCAGAAAC CTACCACTGA CTGATGACCG TTGTAATTGG	CAGCGTTTGG	GGCATGACCC	AGGCCCAGAG	CTGCGTCGCC	
	ATTGCCGCCA	TTGTAATTGG	CATTOTOGCC	CTCCTCATCC	ACATGAAGGC	ACCCAATGAG	1740
	TOTTGCTGCT	GCAGGCTGGA	GCAGGGCTGG	GGAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
40	CTAGATAAAG	GTGTGCCTAC	CTCTTCCTGA	CTTGCCTGAT	TCTCCCGTAG	AGAAGCAGGT	1920
	CGTGCCGGAC	CTTCCTACAA	TCAGGAAGAT	AGATCCAACT	GGCCATGGCA	AAAGCCCTGG	1980 2040
	GGATTTCCGA	CARACTACCCC	CTTCCCTCCC	CCCAGGCCCC	CTCCGGGCCT	CTGTAGACTC	2100
	ACCIGICCIO	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	CRIGGTCGGC ACCAATGAG ACCCAATGAG ACCGGGAATT CTITCTGGCC AGAAGCAGGT AAAGCCCTGG AATCCTCGC CTGTAGACTC GCCCTCTCG CTATAGGCTTG GAAGGCAGGG AGCCGTCAAT	2160
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	TGAGTTCTCT	CCTCAAAGAA	GACTTCAAAC	CATTTAACTG	GTTTCTTAAG	AGCCGTCAAT CAGTTCCTGG GGAAGAAACA	2400
	CAGCCTGGTT	TIGGGGATGC	CTCTCTCACT	TOTGATTTT	ATCTGGAAAA	GGAAGAAACA	2460
50							
-	TGAAAAGTTT	AGCCCTTTAA	GGAATGAAAT	CATGTAGAAT	TTTGGACTTC	TAAAAACATT	2580
							2640
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	TCCCCCCAC	GTCAGCCTGT	GCAAAGGCCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
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60	AGAGACCCTC	AGACCTGGGG	CACCATGGCT	GGCCAGGTC	GAAGCATCCI	CCCACCACACAC	3120
00	GTCCGTGCAG	CCACACCCTC	CACCATGATA	CCTCTATCT	CTTTTTAATT	TTCATTCTTC	3180
	ACTTAGGGG	AGTGAAATCG	CTCAGAGATO	AGATOCTTTA	ATTGAAAACG	TTCATTCTTC AAGTGTAACG AGCTGGCAGC GTCACACTGG	3240
	GAATCTAGT	TCTTTCTAAT	GTGGTAAAAT	TCTCCATCA	CATCACAGTO	AGCTGGCAGC	3300
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65	GTCTGGGGG	TCCCTGGAGC	TCCTCCTGCC	TGTGGTCTGG	TTAGGAGTIC	AGTTGTTTGC TCTGGCTTTC GTGTGTCTTT ACGTCTGCCC CCCGATCGGC CCAATCCGA TACCACCAAT	3420
	TCCAGGGTT	Trefeerees	TOTAL	CARCACGAA	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGGACA	CTGGCCCAGT	TTACAGTGA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCCC	3 600
	AGGAAAGAA	TTCAGCTGAG	TCCACGGGG	TCTGGAAAT	CACGACCAAT	CCCGATCGGC	3660
70	TCTTATTAGG	Tecconered	ACANGACAC	TGTGCTTTGC	AAATCCACC	CCAATCCCGA CTACCACCACT TCCAGGGCCA TCCAGGGGCCA TCCAGGGGCCA GGAATTTCCAC GGAACTGAGC GGTGCCAACA AGACCTGTCG GCCAGGGCTG AGACCCTTA	3720
	TOGGCTCTT	A TTAGCTCCCC	GCTCCACAAC	ACACCTGTG	TCTGGAAAT	TACCACCAAT	3780
	CCCGATCGG	CTCTTATTAGC	TCCCCGCTC	CACAAGACAC	TGIGACATC	TCCAGGGCGC	3900
	CAGGAGCAC	CACTACTCC	CTTTCTAGC	TTTCACCCT	TOTCCCAGG	AATCTAGGAG	3960
75	AGATGAGGC	COTCAGAGTO	AAGAGATGT	ATCCCCCCA	GGTCTCCAAC	GCATTTCCAC	4020
	ACTATTGGT	GCACCTGGAC	GACATGCAC	AAGGCTTGC	C AGAGCCAAC	GGAAGTGAGC	4080
	CCAGAGCAT	GCACATGAGG	ATCACCCGC	GATGGTGGC	TGCTGTGCC	GGTGCCAACA	4140
	GGGGCATCC	C GGCCCGTACC	CCTCCAGAC	GGAAGCATG	3 GTTTGCCCA	AGACCIGICG	4200
80	GGTGCTCCT	TGAGTGGCC	CCAGATGTC	COCCOCCCC	A ATCTTARCC	AGAACCCTTA	4320
30	GAUGGAGGT	GGAGGETACCC	TGACATTGG	GCACCTTCC	CTCCAGCCAG	AGGCTGACCT GTGAGGGCCC GGAGCCATTG	4380
	GAGGGCCAC	T GTCCTCAGAT	GACACCACO	AGGAGCACO	CTAGGTGAGG	GTGAGGGCCC	4440
	CCTTATGTG	A ACCTCTTGC	TCTTCCTTT	TCCCATCAG.	A GTGGTTGGA	GGAGCCATTG	4500
0.5							
85							
	GGGCTGGAA	T GAGCCGGCTY	P TOACAGTCC	ACCCCCATC	T GGAGTGGGA	GTTCAGTTTT CTGGGAGTTA	4740
	CCTCTCTGT	T INCAUCICU	I IGACAGICO				

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	GTGTTGGAGA TGCACAGATA GGTAGGAGTG GGTGTTCAAT	CTCTTCAAGC CCGCCTCTAC AGGCTGGGAG	ACTGGACGTG CCACTTGTGA TTTTATTTAT	TGGGGTACAG CTCTTCAAAC	AGGCACTTGC TTTGTACAAG	TCTTCTGCAT AGCTCATGGC	4800 4860 4920 4980
5	TTGTCTTGGG TTAGTCTTGG GGAAAAAATA TGGGCTGTAT	TCATCAGAAC AACTCTTCCA GTATATTGTT	CTCACTTGGT TCCCTTAAAG CTTCCTCCTT	ACCATATAGA AATAGAATAG AGAATTTAGA	TCAAAAGCTT TTTGTCCCTC GATACAAGAG	TGTAACCACA TCATGGGAAT TTCTACTTAG	5040 5100 5160 5220
10	AACTTTTCAT GAACTTCCAA ACTTGCTCGA	GGACACAATT ACTCAGGAAG CAGATGTTAG	TCCACAACCT TTTGCAGAGA ATGTATCCTA GAACTGAATC	TTCAGATGCT GCAGACAGCT GCTTTTAGCC TGCGTTGTTG	GATGTAGAGC AGAGATAACT ATAAACCACT GGAAGCCAGC	TATTGGGAAA CGGGACCCAG CAAAGATTCA AGTGGCCTTG	5280 5340 5400 5460 5520
15	GCCCCAGTGC AGCCCTGGTG		ATTTACAGAT GGGGGTCTGT	TTGCCTTGCT TTCTAGGCCC CTTCTGCTGG			5580 5640 5700 5760
20	Protein Acc	286 Protein ession #: N	sequence: IP_570843.1	31	41	51	
25	TAPPUTTET ME	11 VGCQAWGAGL SPFLNISALI LLSSNQLLQI RVPQHLGNLQ	AYHGCPSECT ALPTEKNELS	CSRASQVECT RITPGAPENL	 GARIVAVPTP GSLRYLSLAN	 LPWNAMSLQI NKLOVLPIGL	60 120 180
30	PHNNHNLORL YDNHISSLPD	RVFQHLGNLQ YLSNNHISQL NVFSNLRQLQ SLQNNRLRQL ILPLRNWLLL PDTPSYPDTT LACSLAACVG	VLILSRNQIS DOWNERS	PISPGAPNGL	TELRELSLAT	NALQDLDGNV NALQDLDGNV	240 300 360 420 480 540
35	Seq ID NO: Nucleic Ac	LACSLAACVG 287 DNA sec ld Accession sence: 19	uence 1 ∦: NM_0023		С		
40	1	11 .	21	31	41	51	
45	GAGGCCCTGG TCCTCCTCCT GGTCCTCCCC TGGAGGCAAC	AGCAGAAGAG GCCTGGTGGG CTCCTCTGGT AGAGTCCTCA CCAATGAGGG CCTTGTTCCG	TGCACAGGCT CCCTGGCACC GGGAGCCTCT TTCCAGCAGC AGAAGCACTC	CTACTACTG CTGGAGGAAG GCCTTACCCA CAAGAAGAGG AGTAACAAGG	TGCCTGCTGC CTACCATCAG AGGGGCCAAG TGGATGAGTT	TGAGTCAGCA CTTCACTTGC CACCTCGCCT GGCTCATTTT	60 120 180 240 300 360
50	ATCAAAAATT ATGATCTTTG ACCTGCCTGG GGCCTTCTGA	AGTATCGAGC ACAAGCGCTG GCATTGACGT GCCTTTCCTA TAATCGTCCT AGGAGCTGGG	CAAGGAGCTG CTTTCCTGTG GAAGGAAGTG TGATGGCCTG GGGCACAATT TGTGATGGGG	GTCACAAAGG ATCTTCGGCA GACCCCGCCA CTGGGTAATA GCAATGGAGG GTGTATGATG	CAGAAATGCT AAGCCTCCGA GCAACACCTA ATCAGATCTT GCGACAGCGC GGAGGGGAGCA	GGAGAGAGTC GTCCCTGAAG CACCCTTGTC TCCCAAGACA CTCTGAGGAG CACTGTCTAT	420 480 540 600 660 720 780
55	GGGGAGCCCA CAGGTACCCG GAAACCAGCT GCCTACCCAT	GGAAACTGCT GCAGTAATCC ATGTGAAAGT CCCTGCGTGA	CACCCAAGAT TGCGCGCTAT CCTGGAGCAT AGCAGCTTTG	GAGTTCCTGT GTGGTCAGGG TTAGAGGAGG	GGGGTCCAAG TCAATGCAAG AAGAGGGAGT	GGAGTACCGG GGCTCTGGCT AGTTCGCATT CTGA	840 900
60	Seq ID NO: Protein Acc	288 Protein	n sequence: NP_002353.1				
65	LLRKYRAKEL TCLGLGYDGL	11 KPEEGVEAQE ALPTTISFTC VTKAEMLERV LGENQIFPKT	CHAILTUIGH	IFGKASESLK	BIWEBLGVMG	VYDGREHTVY	60 120 180 240
70	GEPRKLLTQD AYPSLREAAL	WVQENYLEYR LEEEGV	QVPGSNPARY	EFLWGPRALA	ETSYVKVLEH	VVRVNARVRI	300
75	Nucleic Ac	289 DNA seid Accession	n #: NM_0023 1344			_	
80	GGCGACCTGA CATCAGCGCG CTCAACAGAC	11 GCCCTGGTTG AGCAGGCGCT GCAGCAGCAC ATAATATTGT ATGTGCAGTC	TCCCTGTGTG TGCAAAGAAA GTTTGGTGAT TGTGTCTATT	GCCGAGTCGC GAAGACATAA TACACATGGA ATTGACACAG	CAACGGTCCA ACCTGAGTGT CTGAGTTTGA AATTAAAGGT	TAGAAAGCTA TGAACCTTTT TAAAGACTCA	60 120 180 240 300
85			ATGCACTGTT GGAGGAAGAG CCATGGGCTT	ACAGAAAACA TGGGACAGCT		AAATCACTGG TGTGGAAGTC	360 420 480 540

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	ACCUACCECA .	TCACCTGGAA	CCGGGTGGTG	CTGCTCCACG	GTCCTCCTGG	CACTGGAAAA	600
	ACATCCCTGT (GTAAAGCGTT	AGCCCAGAAA '	TTGACAATTA	GACTTTCAAG	CAGGTACCGA	660 720
	COCKNOCTEG :	TARCCARGAT	AAACAGCCAC .	ATTCAGGATT	TGATTGATGA	TAAAGACGCC	780
5	CARCING ALL CAR	TGCTGATTGA	TGAGGTGGAG	AGTCTCACAG	CCGCCCGAAA	TGCCTGCAGG	840 900
	GCGGGCACCG CAGATTAAAA	AGCCATCAGA	TGCCATCCGC	GTGGTCAATG	CTAACATCAC	CCAAATTGAT	900 960
	GACGTGGCCT	TOTTGGACAG	GGCTGACATC	AAGCAGTACA	TTGGGCCACC	CTCTGCAGCA	1020
••	COCKTOTTCA	TODATOTAGA	CTCTTGTTTG	GAAGAACTGA	TGAAGTGTCA	GATCATATAC	1080
10	CCTCGCCAGC	AGCTGCTGAC	CCTCCGAGAG TTTGAATGAC	CTAGAGATGA	TTGGCTTCAT	TGAAAACAAC	1200
	COCCTCCTGA	GAAAACTCCC	CTTTCTGGCT	CATGCGCTGT	ATGTCCAGGC	CCCCACCGTC	1260
	ACCEPTACEGO	COTTOTOTA	CCCCCTGTCT	CTGGCAGTGG	ACAAGCAGTT	TGAAGAGAGA	1320 1380
15	AAGAAGCTTG AACACACAAC	CAGCTTACAT	CTGATCCTGG	CACACCCCAT	TOTAGGAA	TOCCATGGAG	1440
13	BBB 000 BB 000	TTACTTACAC	TOCABOCTAG	BARGCCACCA	AGGCCAGGCT	TTGTTAAAAG	1500
	A SOTOTATTC	TEXTATUTE AT	GTTTTTAAAAT	GCATACTGAG	AGACAAACAT	CTTGTCATTT	1560 1620
	TCACTGTTTG	TAAAAGATAA	TTCAGATTGT	CATCCATAAT	GCCAGCAAGT	TTTGTTTAAC	1680
20	ACCES BARRE	TAKTTANKEN	GCAGGTGTTA	TAGAAGCCAG	AAGAGAAACT	GTGTCACCCT	1740
	BARGBROCKT	DATASTCATAC	CATTAAAAAT	GCACACATTA	CTCCAGGTGG	AAGGTGGCAA	1800 1860
	TIGCTITCIG	ATATCAGCTC	GTTTGATTTA TACATTATAC	CARCICAGAA	GTTTTCAAGA	GGTAAAGTGT	1920
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30		290 Protei:					
30	Protein Acc	ession #: 1	IP_004228				
	1	11	21	31	41	51	
25	Ī.	1	VHVEVHQRGS			TUDODATE	60
35	MDEAVGDLKQ PDEPFLTRNV	QSVSIIDTEL	KYKDSQPIDL	SACTVALHIF	OLNEDGPSSE	NLEERTENII	120
	A SMILIWITT, DA A	REHCLWDSLV	YDVEVKSHLL	DYVMTTLLFS	DENVISNLIT	WNRVVLLHGP	180
	PGTGKTSLCK	ALAQKLTIRL	SSRYRYGQLI RNACRAGTEP	EINSHSLESK	WESESGKLVT	CHUNTITEN	240 300
40	TTEKTOVARV	DRADIKOYIG	PPSAAAIPKI	YLSCLEELMK	CQIIYPRQQL	LTLRELEMIG	360
	FIENNVSKLS	LLLNDISRKS	EGLSGRVLRK	PERFERENCE	QAPTVTIEGP	LQALSLAVDK	420
	QFEERKKLAA	YI					
45	Nucleic Ac:	291 DNA se Ld Accessic	n. #: NM_002	658.1			
45	Nucleic Act	ld Accessio Lence: 77-1	n #: NM_002		41	E1	
	Nucleic Ac:	ld Accessic sence: 77-1	n #: NM_002	31	41 	51 	
45 50	Nucleic Ac Coding sequ	id Accessionence: 77-1	n #: NM_002	31 GCAGGCCACC	GAGGCCGCCG	CCGTCTAGCG	60
	Nucleic According sequences of the control of the c	Id Accession Lence: 77-1 11 CGCCGTCGCG GCCACCATGA	21 CCCTCCTGCC	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA	60 120 180
	Nucleic Act	Ld Accession Lence: 77-1 11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA	120 180 240
50	Nucleic Act	Ld Accessionience: 77-1 11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA	21 CCCTCCTGCC GAGCCCTGCT ATGACTTCA ACAAGTACTT GTGAATAGA	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA CTCCAACATT	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG	120 180 240 300
	Nucleic Ac: Coding sequence GTCCCCGCAG CCCCGACCTC GAGCGACTCC TGGAGGAACA GAATTCGGA	Ld Accession Lence: 77-1 11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCAGCAC TGGAGAAAGG	1 #: NM_002: 372 21	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCAA CTCCAACATT TAAGTCAAAA CACCATGGGC	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCCTGGAA	120 180 240 300 360 420
50	Nucleic Ac Coding seq I GTCCCCGCAG CCCCGACCTC GAGCGACTCC TGGAGGAACA GAATTCGGA TCACTTTAC CTCTGCCACT CCTGGCGAAA	Ld Accessio Lence: 77-1 11 	21	31 GCAGGCCACC GGCGGCGCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGC TGCCCACAGA AGACAACCGG	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG CACTGGTGTG ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGAATGG TGCCTGGAA TTCAGCTGGG GGTGCTATGT	120 180 240 300 360 420 480
50	Nucleic Ac: Coding seq I GTCCCCGCAG CCC GAGCACTC GAGCAGACTC TGGAGGAACA GAATTCGGA TCACTITTAC CTCTGCCAAT CCTTGCGAAA GCAGGTGGGC	Ld Accessic Lence: 77-1 11 	n #: NM_002: 372 21	31 GCAGGCCACC GGCGCGCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGGC TGCCACAGA AGACAACCGG GTGCATGGTG	GAGGCCGCCG CTTCTCTGG TCGAACTGTG CACTGGTGCA ACCTGCTATG CGGCCTGCC TCTGATGCT CAGGCGACCCT CATGACCTCC	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA	120 180 240 300 360 420 480 540
50 55	Nucleic Act Coding sequence I GEOCCEGACE GAGCACTCC GAGCACTCC TOGAGGAACA GAAATCGGA TCACTTTAC CTCTGCCACT CCTGGGGAAA GCAGGTGGGC	Ld Accessic Lence: 77-1 11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT GTCCTCCACC CATAATTACT CTAAAGCCGC	n #: NM_002: 372 21] CCTTCTTGCC GAGCCCTGCT ATGAACTTCA ACAGTACTTA AAACGTACTA GCAGGAACCC TTGTCCAAGA AAGAATTAAA	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGGC TGCCCACAGA AGACAACCGG GTGCATGGTG ATTTCAGTGT	GAGGCCGCCG CTTCTCTGCG TCGAACTGTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT CATGACTGCC GGCCAAAAGA AACCAGCCCT	CCGTCTAGCG CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC	120 180 240 300 360 420 480 540 600 660
50	Nucleic Act Coding sequence of the coding seq	Ld Accessic Lence: 77-1 11 GSCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT GAGGAAAGG GTCCTTCAGC CATAATTAGT TCTCCTCCAG ATTATTGGG AGGCACCGGG	n #: NM_002: 372 21 j ccctcctgcc gagccctgct ATGAACTTCA ACAGTACTT GTGAAATAGA CCAGGACTGA AAACGTACCA GCAGGACCC TTGTCCAAGA AAGAATTACA GAGAATTCAC GGAGGTCCCAGGA GAGAATTCAC	31 GCAGGCCACC GGCGGCCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGGC TGCCCACGA AGACACCGG GTGCATGGTG ATTTCAGTGT CACCATCGAG	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCT CATGACTGCG GGCCAAAAGA AACCAGCCT TGTGGAGGCA	CCGTCTAGCG CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA ACTGCCCAGAA TTCAGCTGGG TGCCCTGGAA TTCAGCTGGG CGGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC	120 180 240 300 360 420 480 540 600 660 720
50 55	Nucleic Actoring sequence of the control of the con	Id Accessic Lence: 77-1 11 GCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGCCA GGCAGCACT CGAGGAAAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC TCTCCCAG ATTATTGGGG AAGCACCGGG GTGATCAGCG	n #: NM_002: 372 21	31 GCAGGCCACC GGCGGCCTG TCAAGTTCCA CTCCAACATT TAMGTCAAAA CACCATGGGC TGCCCACGA AGACAACCGG GTGCATGGTG ATTTCAGTGT CACCATGGAG CACCTACGTG CACCATGGAG CACCTACGTG	GAGGCCGCCC CTTCTCTGGG TCGAACTGTG CACTGGTATG GGGCCTGCC TCTGATGCT AGGGGACCCT CATGACTGCG GGCCAAAAGA AACCAGCCCT TGTGAGGCCA TACCCAAAGA TACCCAAAAGA	CCGTCTAGCG TCCTGGTCGT ACTGCCCAAA ACTGCCCAAA ACGGCAATGG TGCCCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GGTTTGCGGC GCTCTATGG AGGAGGACTA	120 180 240 300 360 420 480 540 600 660
50 55 60	Nucleic Actoring semi coding coding semi coding semi coding semi coding semi coding semi coding semi coding semi coding semi	Ld Accessic Lence: 77-1 11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGCAGCACT CGAGGAAAGG GTCCTTCAGG AATAATTACT CTAAAGCCGC TCTCCTCCAG AGGCACCGG GTGATCAGCG CTGGGTCGCT CTCACTCAGC	n #: NM_002: 372 21	31 GCAGGCCACC GGCGGCCTG TCAAGTTCCA CTCCAACATT TAMGTCAAAA CACCATGGG TGCCACGAG AGACAACCG GTGCATGGTG CACCATGAG CACCTACGTG CTTCATTGAT CTCCAACAG CAGCGTGAC	GAGGCCGCCG CTTCTCTGCG CTTCTCTGCG CTCGAACTGTG AACTGCTATG CGCCCTACC AGGCGAACCT AGGCGAACCT CATGAATGCTC GGCCAAACGA AACCAGCCT TCTGATGCGC CATGAGGCAACGA AACAGGCGACA TACCCAAAGG	CCGTCTAGCG TCCTGGTCOT ACTGTCTANA ACTGCCCANA AGGGRATGG TGCCCTGGNA TTCAGCTGGNA TTCAGCTGGN GCTGCTATGT CAGATGGNAC GCTTTTGCGGC GCTCATCAG AGGAGGACTA TGAAGTTTGA AGGAGGACTA TGAAGTTTGA ACGACAAGGA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
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50 55 60 65 70 75	Nucleic Actoring Coling segment of the Colin	In control of the con	18: NM -002 21 21 21 21 22 21 22 23 24 25 26 26 26 26 26 26 26 26 26	31 GRAGGICACC GGGGGGCTG TOAGITTCA TAGGTCTA TAG	GAGGCGCCC GTCTCTGGG GAGGCGCCC GTCTCTGGG GAGGCGCCC GTCTCTGGG GCCANAGG AACCAGCC TTGGAACTTG GAGGAGCCT TTGAACTGCC GATGACTGCC ATGACTGCC ATGACTGCC GATGACTGCC GATGACTGCC GATGACTGCC GATGACTGCC GAGGCAAAAGA AACCAGCCC TTGGAAGGCC GAGGCAATTCCC GAGGCAATTCCC GAGGCAATTCCC GAGGCAATTCCC GAGGCAATTCCCC GAGGCAATTCCCC GAGGCAATTCCCCC GAGGCAATTCCCCC GAGGCAATTCCCCC GAGGCAATTCCCCC GAGGCAATT	COTICTAGOS TOCHOSTOST ACTOCICAS TOCHOSTOST ACTOCICAS ACGUSTATOS TOCHOSTOST TOCHOST TOCHOSTOST TOCHOSTOST TOCHOST TO	120 180 240 360 420 480 540 660 780 900 1080 1140 1260 1260 1320 1440 1500 1500 1620 1620 1740 1860
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50 55 60 65 70 75	Nucleic According segment of the control of the con	In the control of the	18: NM 002 21 21 21 21 22 21 22 23 24 25 26 26 26 26 26 26 26 26 26	31 GORGGICACC GOCGOGCTG TOAGTTCSA TAGGICACA TAGGICACA TAGGICACA AGACAACCG CACCATOGGIC CA	GAGGICACCA GAGGICACCA	CONTENSOS TOCHAGOS TO	120 180 240 360 540 540 560 660 720 840 960 1020 1140 1260 1320 1440 1560 1620
50 55 60 65 70 75 80	Nucleic According to the control of	LI ACCESSA DE LE CONTROLLA DE LA CONTROLLA DE	18: NM .002 21 21 21 22 21 22 23 24 25 26 26 26 26 26 26 27 26 27 26 27 27 27 27 27 27 27 27 27 27 27 27 27	31 GOAGGICACC GOCHOCACC	GOGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	COSTETAGOS TOCTOSTOSTOS TOCTOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTOST	120 180 240 360 480 660 720 960 1020 1030 1140 1250 1380 1440 1500 1540 1620 1640 1740 1860 1920 1860 1920 1980 2040 2100 2100 2100 2100 2220

ATCAATAAAA TGTGATTTTT CTGA

5	Seq ID NO: Protein Acc	292 Protein ession #:NI	n sequence: P_002649.1				
,	1	11	21	31	41	51	
	ī	ī	1	1	1	i	
	MDATTABLET.	CVLVVSDSKG	SNETHOVESN	CDCLNGGTCV	SNKYFSNIHW	CNCPKKFGGQ	60
	HCELDKSKEC	YEGNGHFYRG	KASTOTMORP	CLPWNSATVL	QOTYHAHRSD	ALQLGLGKHN	120
10	ACBIDIONIC	PHCYVQVGLK	DIVOECHAND	CANGEKERSSP	PEELKFOCGO	KTLRPRPKII	180
10	COPPTTEMO	PWFAAIYRRH	PEGGVTYVCG	GSLISPCWVI	SATHCFIDYP	KKEDYIVYLG	240
	DODE LITTORY	EMKPEVENLI	LHKDASTOLT	AHHNDTALLK	TRSKEGRCAO	PSRTIOTICL	300
	DEMONDOFO	TSCBITGPGK	ENSTRYLYPE	OLKMTVVKLI	SHRECOOPHY	YGSEVTTKML	3,60
	CAADDOWITTO	SCOGDSGGPL	VCSLOGRMTL	TGIVSWGRGC	ALKDKPGVYT	RVSHFLPWIR	420
15	SHTKEENGLA		· someonaria				

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Seq ID NO: 293 DNA sequence Nucleic Acid Accession #: NM_001498

20	Coding sequ	ience: 932	1006				
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25	AGGAGGAGGA	GGAGGAGGAG	GAGGGGGCGG	CCATGGGGCT	GCTGTCCCAG	GGCTCGCCGC	120
	managaga a	DEADORAGED	CCCCATCCCG	ACCACGTGCG	GCGGCACGGG	ATCCTCCAGT	180
	TOTTCACAT	CTACCACGCC	GTCAAGGACC	GGCACAAGGA	CGTTCTCAAG	TGGGGGCGATG	240
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30	CTACCCTTTG	GAGACCAGAG	TATGGGAGTT	ACATGATTGA	AGGGACACCA	GGACAGCCCT	420
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	CCAAGTCCCT	CTTCTTTCCA	GATGAAGCAA	TAAACAAGCA	CCCTCGCTTC	AGTACCTTAA	660
35	CAAGAAATAT	CCGACATAGG	AGAGGAGAAA	AGGTTGTCAT	CAATGTACCA	ATATTTAAGG	720
	ACAAGAATAC	ACCATCTCCA	TTTATAGAAA	CATTTACTGA	GGATGATGAA	GCTTCAAGGG	780
	CTTCTAAGCC	GGATCATATT	TACATGGATG	CCATGGGATT	TGGAATGGGC	AATTGCTGTC	840
	TCCAGGTGAC	ATTCCAAGCC	TGCAGTATAT	CTGAGGCCAG	ATACCTTTAT	GATCAGTTGG	900
	CTACTATCTG	TCCAATTGTT	ATGGCTTTGA	GTGCTGCATC	TCCCTTTTAC	CGAGGCTATG	960
40	TGTCAGACAT	TGATTGTCGC	TGGGGAGTGA	TTTCTGCATC	TGTAGATGAT	AGAACTCGGG	1020
	AGGAGGGAGG	ACTGGAGCCA	TTGAAGAACA	ATAACTATAG	GATCAGTAAA	TCCCGATATG	1080
	ACTCAATAGA	CAGCTATTTA	TCTAAGTGTG	GTGAGAAATA	TAATGACATC	GACTTGACGA	1140
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45	ATGATGCTAA	TGAGTCTGAC	CATTTTGAGA	ATATTCAGTC	CACAAATTGG	CAGACAATGA	1320
	GATTTAAGCC	CCCTCCTCCA	AACTCAGACA	TTGGATGGAG	AGTAGAATTT	CGACCCATGG	1380
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	GAGTGATCCT	TTCCTACAAA	TTGGATTTTC	TCATTCCACT	GTCAAAGGTT	GATGAGAACA	1500
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50	TTTGCAAAGG	TGGCAATGCA	GTGGTGGATG	GTTGTGGCAA	GGCCCAGAAC	AGCACGGAGC	1620
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	TGTTTCCTGG	ACTGATCCCA	ATTCTGAACT	CTTACCTTGA	AAACATGGAA	GTGGATGTGG	1740
	ACACCAGATG	TAGTATTCTG	AACTACCTAA	AGCTAATTAA	GAAGAGAGCA	TCTGGAGAAC	1800
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	ACTGGCTACA	GTACCATGCC	TCTCAGCCCG	TGTGTATAAT	ATGAAGACCA	AATGATAGAA	2100
	CTGTACTGTT	TTCTGGGCCA	GTGAGCCAGA	AATTGATTAA	GGCTTTCTTT	GGTAGGTAAA	2160
60	TCTAGAGTTT	ATACAGTGTA	CATGTACATA	GTAAAGTATT	TTTGATTAAC	AATGTATTTT	2220
	AATAACATAT	CTAAAGTCAT	CATGAACTGG	CITGTACATT	TTTAAATTCT	TACTCTGGAG	
	CAACCTACTG	TCTAAGCAGT	TTTGTAAATG	TACTGGTAAT	TGTACAATAC	TTGCATTCCA	2340
	GAGTTAAAAT	GTTTACTGTA	AATTTTTGTT	CTTTTAAAGA	CTACCTGGGA	CCTGATTTAT	2400
	TGAAATTTTT	CTCTTTAAAA	ACATTTTCTC	TOGTTAATTT	TCCTTTGTCA	TITCCTTTGT	2460
65	TGTCTACATT	AAATCACTTG	AATCCATTGA	AAGTGCTTCA	AGGGTAATCT	TGGGTTTCTA	2520
	GCACCTTATC	TATGATGTTT	CTTTTGCAAT	TGGAATAATC	ACTTGGTCAC	CTTGCCCCAA	2580
	GCTTTCCCCT	CTGAATAAAT	ACCCATTGAA	CTCTGAAAAA	AAAAAAAAA	AAAA	

70 Seq ID NO: 294 Protein sequence: Protein Accession #: NP_001489

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	STATEMANTS	GEKYLETLOR.	KGERTNPNHP	TLWRPEYGSY	MLEGTPGQPY	GGTMSEFNTV	120
	DAMMDADDKE	ATSILEENQA	LCTITSPPRL	GCPGFTLPEV	KPNPVEGGAS	KSLFPPDEAI	180
	MYUDDDOCTIA	RNIRHRRGEK	VVINVPTPKD	KNTPSPPIET	FTEDDEASRA	SKPDHIYMDA	240
80	MCDCMCNICCI.	QVTFQACSIS	PARVIVIOLA	TICPTYMALS	AASPFYRGYV	SDIDCRWGVI	300
80	MGPGMGNCCI	ERGLEPLKIN	MANUTO CHEDYD	ernevi eros	PRYNDIDIAL	DKETYROLLO	360
	SASVDDRTRE	VAHLFIRDPL	MIKIBASKID	DAMEGDUREM	TOOTHINOTHE	PKPPPPNSDI	420
	EGIDHLLAQH	VAHLFIRDPL	LPARRYTHED	DAMESONAL DEL	TOT COMPANY	KVAQKRDAVL	480
	GWRVEPRPME	VQLTDFENSA	AAABAAPPIK	ATPRIVIDED	TEDSKADEWA	PROCE TRATEMO	540
	QGMFYFRKDI	CKGGNAVVDG	CCKAQNSTEL	AVERALIWAI	DTIINGKEGV	FPGDIPIDAS	
85	YLENMEVDVD	TRUSILNYLK	LIKKRASGEL	MTVARWMREP	IANHPDYKQD	SVITDEMNYS	600
	LILKCHOLAN	ELCECPELLG	SAFRKVKYSG	SKTDSSN			

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Nucleic	O: 295 DNA seque Acid Accession : equence: 247-816	: Eos	sequence

	Courng sequ	lence: 24/-8	10				
5	1	11	21	31	41	51	
	1	1	1	1	!	1	60
	AGTGTTCGGC	TGGGGCAGGC GATCGGTGCT	ACGCTGTGGC	TGGCTACTTC	CCTTCCTCCC	ATCCCCCTTG	120
	GGCCAAACGG	ACATTTCCCA	CARCOCCAC	ACCCCACCT	TOTACABACT	CCCACCACTG	180
10	CCTAGGGGGC	ACAACTTCAC	WCCCATTTY.	TGACGTCCCC	CONTORON	TCCAGCAAGG	240
10	GARACARTGA	CCGATAAAAC	AGAGAAGGTG	GCTGTAGATC	CTGAAACTGT	GTTTAAACGT	300
	CCCAGGGAAT	GTGACAGTCC	TTCGTATCAG	AAAAGGCAGA	GGATGGCCCT	GTTGGCAAGG	360
	AAACAAGGAG	CAGGAGACAG	CCTTATTGCA	GGCTCTGCCA	TGTCCAAAGA	AAAGAAGCTT	420
	ATGACAGGAC	ATGCTATTCC	ACCCAGCCAA	TTGGATTCTC	AGATTGATGA	CTTCACTGGT	480
15	TTCAGCAAAG	ATAGGATGAT	GCAGAAACCT	GGTAGCAATG	CACCTGTGGG	AGGAAACGTT	540
	ACCAGCAGTT	TCTCTGGAGA	TGACCTAGAA	TGCAGAGAAA	CAGCCTCCTC	TCCCAAAAGC	600
	CAACGAGAAA	TTAATGCTGA	TATAAAACGT	AAATTAGTGA	AGGAACTCCG	ATGCGTTGGA	660 720
	CAAAAATATG	AAAAAATCTT TTGAATCCAT	CGAAATGCTT	GAAGGAGTGC	AAGGACCTAC	TGCAGTCAGG	780
20	AAGCGATTTT	AGAAGAAACT	CATCOMGGAA	ATTRICACIONI	PULLGURACO	CCACCATTAT	840
20	CACACCCTA	ATGCATAATC	TYTTATTA	TTGAGGAGAG	AAAAGGATCA	GATTGCTGTT	900
	TTCTACAATG	GAGCAGGATA	TTGCTGAAGT	CTCCTGGCAT	ATGTTACCGA	ATCAAATAGC	960
	CTTCCAGAGG	CTAAGAAATT	TCTGTTAGTA	AAAGATGTTC	TTTTTCCCAA	AGCATTTTAT	1020
	TTGAAAGGAT	AACTTGTGTT	TTGGTTATTT	TGTATTCCCA	CCTGTGCTGG	TAGATATTAT	1080
25	TAACCCATTA	GGTAAATACT	ATTACAGTOG	TOGTTTCTGC	A		
		296 Protein					
	Protein Ac	cession #: 1	Sos sequence				
30	1	11	21	31 .	41	51	
50	î	1	ī	ī	i	Ī .	
	MTDKTEKVAV	DPETVFKRPR	ECDSPSYOKR	ORMALLARKO	GAGDSLIAGS	AMSKEKKLMT	60
	GHAIPPSOLD	SOIDDFTGFS	KDRMMOKPGS	NAPVGGNVTS	SFSGDDLECR	ETASSPKSQR	120
0.5	EINADIKRKL	VKELRCVGQK	YEKIFEMLEG	VQGPTAVRKR	FFESIIKEAA	RCMRRDFVKH	180
35	LKKKLKRMI						
		297 DNA sec id Accession		mionao			
	Coding sea	ence - 247-1	815	•			
40	Coding seq	uence: 247-	315	•			
40	Coding seq	uence: 247-	815				
40	Coding sequents	11	21	31	41	51	
40	1	11	21 1	31 }	i	}	
-	1 AGTGTTCGGC	11 TGGGGCAGGC	21 ACGCTGTGGC	31 TGGCTACTTC	CCTTCCTCCC	ATCCCCCTTG	60
40 45	1 AGTGTTCGGC	11 TGGGGCAGGC	21 } ACGCTGTGGC	31 TGGCTACTTC	CCTTCCTCCC	ATCCCCCTTG TCCCAGGTGC	120
-	1 AGTGTTCGGC GGCCAAACGG CCTAGGGGGC	11 TGGGGCAGGC GATCGGTGCT ACATTTCCCA	21 ACGCTGTGGC TCTGGTGAGA CAACTCCCAG	31 TGGCTACTTC GGGCTCCCCA AGGGCAGGTT	CCTTCCTCCC TGCACATCAC TCTAGAAAGT	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG	
-	1 - AGTGTTCGGC GGCAAACGG CCTAGGGGGC GGGAGGCGCC	11 TGGGGCAGGC GATCGGTGCT ACATTTCCCA	21 ACGCTGTGGC TCTGGTGAGA CAACTCCCAG TGCCATTTTG	31 TGGCTACTTC CGCCTCCCCA AGGGCAGGTT TGAGGTGCCG	CCTTCCTCCC TGCACATCAC TCTAGAAAGT CCGTCTCTCC	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGCAAGG	120 180
45	1 AGTGTTCGGC GGCCAAACGG CCTAGGGGGC GGAACGACGC GAACAATGA CCCAGGGAAT	11 TGGGGCAGGC GATCGGTGCT ACAACTTCACA ACAACTTCAAC CCGGATAAAAC GTGACAGTCC	21 ACGCTGTGGC TCTGGTGAGA CAACTCCCAG TGCCATTTTG AGAGGAAGGTG TTCGTATCAG	31 TGGCTACTTC GGCCTCCCA AGGGCAGGTT TGAGGTGCCG TGAGGTGCCG	CCTTCCTCCC TGCACATCAC TCTAGAAAGT CCGTCTCTCC CTGAAACTGT GGATGGCCCT	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGCAAGG GTTTAAACGT GTTGGCAAGG	120 180 240 300 360
-	1 AGTGTTC3GC GGCCAAACGG CCTAGGGGGC GGAAGGACATGA CCCAGGGAAT ABACAAGAG	11 TGGGGCAGGC GATCGGTGCT ACAATTCAC ACAACTTCAC CCGATAAAAC GTGACAGTCC CAGGAGACAG	21 ACGCTGTGGC TCTGGTGAGA CAACTCCCAG TGCCATTTTG AGAGAAGGTG TTCGTATCGCA	31 TGGCTACTTC CGCCTCCCCA AGGGCAGGTT TGAGGTGCCG GCTSTAGATC AAAAGGCAGG	CCTTCCTCCC TGCACATCAC TCTAGAAAGT CCGTCTCTCC CTGAAACTGT GGATGGCCCT TGTCCAAAGA	ATCCCCTTG TCCCAGGIGC GCCACCAGTG TCCAGCAAGG GTTTAAACGT GTTGGCAAGG AAAGAAGCTT	120 180 240 300 360 420
45	1 AGTGTTCGGC GGCCAAACGG CCTAGGGGGC GGAAGGCGCC GAACAATGA CCCAGGGAAT AAACAAGGAG	11 TGGGGCAGGC GATCGGTGCT ACATCTCCA ACAACTTCAC CCGATAAAAC GTGACAGTCC CAGGAGACAG	21 ACGCTGTGGC TCTGGTGAGA CAACTCCCAG TGCCATTTTG AGAGAAGGTG TTCGTATCAG ACCCAGCCAA	31 TGGCTACTTC CGCCTCCCA AGGGCAGGTT TGAGGTGCG GCTTAGATC AAAAGGCAGA GGCTCTGCA	CCTTCCTCCC TGCACATCAC TCTAGAAAGT CCGTCTCTCC CTGAAACTGT GGATGGCCCT TGTCCAAAGA AGATTGATGA	ATCCCCCTTG TCCCAGTIGC GCCACCAGTG TCCAGCAAGG GTTTAAACGT GTTGGCAAGG AAAGAAGCTT CTTCACTGGT	120 180 240 300 360 420 480
45	1 AGTGTTCGGC GGCCAAACGG CCTAGGGGGC GGAACACGC GAAACAAGGAC ACCAGGGAT AAACAAGGAC	11 TGGGGCAGGC GATCGGTGCT ACATTTCCCA ACAACTTCAC CCGATAAAAC CTGATAAGTCC CAGGAGACAG ATGCTATTCC	21 ACGCTGTGGC TCTGGTGAGA CAACTCCCAG TGCCATTTTG AGAGAAGGTG TTCGTATTCAG CCTTATTGCA ACCCAGACAA	31 TGGCTACTTC CGCCTCCCCA AGGGCAGGTT TGAGGTGCCG GCTATAGATC AAAAGGCAGA GGCTCTGCCA TTGGATTCTC GGTAGCAATG	CCTTCCTCCC TGCACATCAC TCTAGAAAGT CCGTCTCTCC CTGAAACTGT GGATGGCCCT TCTCCAAAGA AGATTGATGA CACCTGTGGG	ATCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGCAAGG GTTTAAACGT GTTGGCAAGG AAAGAAGGTT CTTCACTGGT AGGAAACGTT	120 180 240 300 360 420 480 540
45	1 AGTGTTCGGC GGCCAAACGG CCTAGGGGGC GGAACAATGA CCCAGGGAAT AACAAGGAG ATGACAGAC TTCAGCAAAG	11 TGGGGCAGGC GATCGGTGCT ACATTTCCCA ACAACTTCAC CCGATAAAAC GTGACAGTCC CAGGAGACAG ATGCTATTCC ATAGGATGAT TCTCTGGAGA	21 ACGCTGTGGG CAACTCCCAG TGCCATTTG AGRAAGGTG TTCGTATCAG CCTTATTGCA ACCCAGCCAA GCAGAAACT TGACCTAGAA	31. TGGCTACTTC GGCTCCCA AGGGCAGGTT TGAGGTGCCG GCTGTAGATC AAAGGCAGAA TGGATTCTC GGTAGCAATG TGCAGAGAAA	CCTTCCTCCC TGCACATCAC TGTAGAAGT CCGTCTCTCC CTGAAACTGT TGTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGGTAGG GTTTAAACGT GTTGGCAAGG AAAGAAGCTT CTTCACTGGT TCGCAAAAGCTT TCCCAAAAGC	120 180 240 300 360 420 480 540
45	1 	11 TGGGGCAGGC GATCGGTGCT ACACTTCAC CCGATAAAAC GTGACAGTCC CAGGAGACAG ATGCTATTCC ATAGGATGAT TCTCTGGAGA TTAATGCTGA	21 ACGCTGTGGC ACGCTGTGGA CAACTCCCAG TGCCATTTIG AGGGAAGGTG TCGTATCAG ACCCAGCCAA GCAGAAACCT TGACCTAGAA TATAAAAACT	31.	CCTTCCTCCC TGCACATCAC TGTAGAAGT CCGTCTCTCC CTGAAACTGT TGTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AGGAACTCCG	ATCCCCCTTG ATCCCCCTTG ACCAGGTGC GCCACCAGTG TCCAGCAAGG GTTTAAACGT GTTGGCAAGG AAAGAAGCTT CTTCACTGGT AGGAAACGTT ACCAAAAGC ATGCGTTGGA	120 180 240 300 360 420 480 540 600
45	1 AGTGTTCGGC GGCCAAACGG CCTAGGGGGC GGAAGCACTG GGAAGCAGGAA ATGACAGGA TTCAGCAGAA ATGACAGGAA ACCAGCAGT CAACAAGAAA	11 TGGGGCAGGC GATCGGTGCT ACATTTCCCA ACAACTTCCA CGGTGACAGTCC CAGGAGACAG ATGCTATTCC ATAGGATGCT TCTCTGGAGA TTATTCTGAGA	21) ACGCTGTGGC TCTGGTGAGA CAACTCCCAG TGCCATTTTG AGAGAAGGTG TCCTTATTGGC ACCCAGCCAA ACCCAGCCAA ACCCAGCAA TGACCTAGAA TATAAAACGT TGAAATGCTT	31.	CCTTCCTCCC TGCACATCAC TCTAGAAAGT CCGTCTCTCC CTGAAACTGT GGATGGCCCT TGTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AGGAACTCCC AAGGAACTCCC	ATCCCCCTTG TCCCAGGTGG GCCACCAGTG TCCAGGTAGG GTTTAAACGT GTTGGCAAGG AAAGAAGGTT CTTCACTGGT AGGAAACGTT TCCCAAAAGC ATGCGTTGGG ATGCGTTGGG	120 180 240 300 360 420 480 540 600 660 720
45	1 AGTGTTCGGC GGCAAACGG CCTAGGGGGC GGAGGCGCC GAAACAAGGAA ATGACAGGAC TTCAGCAAAG ACCAGCAGTT TAACAAGAAA CAAAAAGAAA	11 TGGGGCAGGC GATCGGTGCT ACAACTTCAC ACAACTTCAC CCGATAAAAC CTGAGAGTCC CAGAGACAG ATGCTATTCC ATAGGATGAT TCTCTGGAGA AAAAAATCTT TTGAATCCTA	21 ACGCTGTGGC TCTGGTGAGA CAACTCCCAG TGCCATTTG AGRAAGCT TTCGTATCAG CCTATATTGG ACCCAGCCAA GCAGAACCT TGACCTAGAA TATAAAACGT CATCAAGGTA	31.	COTTCCTCC TGCACATCAC TCTAGAAAGT CGGTCTCTCC TGTCAAACTGT GGATGGCCT TGTCCAAAGA AGATTGATGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AGGAACTCCG AAAGAACTCAC GTATGAGACG	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGCAAGG GTTTAAACGT GTTGGCAAGG AAAGAAGGTT CTTCACTGGT AGGAAACGTT TCCCCAAAAGC ATGCGTTGGA TGCAGTCAGG AGACTTTGTT	120 180 240 300 360 420 480 540 600
45	1 AGTGTTCGGC GGCCAAACGG GGAAGGGGC GGAAGCATGA CCCAGGGAT TAACAAGGA ATGACAGGAC TICAGCAGTA TACAAGAAA ACAAGAATATO AAAAAATATO AAACAATATA AAACAATATA AAACAATATA	11 TGGGGCAGGC GATCGGTGCT ACAATTCCCA ACAACTTCAC CCGATAAAAC GTGACAGTCCA ATGCTATTCC ATAGGATGAT TCTCTGGAGA TTAATGCTGA AAAAAATCTT TTGAATCCTT TTGAATCCTT TTGAATCCTA	21 AGGCTGTGGG TCTGGTGAGA CAACTCCCAG TGCCATTTTG AGAGAAGGTG CCTTATTGGA AGCCTACTAC GCAGAAACCT TGACCTAGAA TATAAAACCT CGAAATGCTT CATCAAGGAA	31 TGGCTACTTC GGCTCCCA AGGCAGTT TGAGGTGCCA CCTGTAGATC AAAGGCAGA TGGATTCTC GGTAGCAATG TGCAGGAAA AAATTAGTCA AAATTAGTCA AAATTAGTCA AATTAGGAAT ATTTAGGAAT	COTTCCTCCC TGGACATCAC TCTAGAAAGT TCTAGAAAGT TCTAGAAACT TGTCCAAAGA AGATTGATAA CACCTGTGGG CAGCCTCCTC AAGGACTCAC GTATGAGACA ACTTGTCCCT	ATCCCCTTG ATCCCAGGGG GCCACCAGGG GCCACCAGGG GTTTAAACGT GTTGGCAAGG AAGAAGCTT CTTCACTGGT AGGAAACGT TCCCAAAAGC ATGCGTTGGA TGCAGTCAGG AGACTTGTGG AGGATTAGT	120 180 240 300 360 420 480 540 600 660 720
45 50 55	1 AGTGTTCGGC GGCCAAACGG GGAACAATGA CCAGGGAAT AAACAAGGA ATGACAGGA TTCAGCAAAG ACAGCAGT CAACAAGAAA ACAGCAGTT CAACAAGAAA TAAACAATATG AAACAATATG AAACACTTA CACCCCCAA	11 TGGGGCAGGC GATCGGTGCT ACAATTCCCA ACAATTCCCA ACAACTTCAC CGGATAANAC GTGACAGTCC CAGGAGACAG ATGCTATTCC ATAGCAGTAC TCTCTGGAGA TTAATGCTGA AAAAAATCTT TTGAATCCAT AGAACAAAACT AGAACAAAACT AGAACAAAACT AGAACAAAACT	21 ACGCTGTGGC TCTGGTGGA TCCACTTCCAG TGCCATTTG AGGGAAGGTG TCTTATCAG ACCCAGCCAA ACCCAGCCAA TATAAAACGT TGACTAGAA TATAAAACGT CAAAAGGTATO CAAAAGGTATO TCATTAATGA TCATTAATGA TTGCTGAAGT TTGCTGAAGT TTGCTGAAGT	31. TOGGTACTTC GSCTTCCCA AGGGCAGGTT TGAGGTGCCA GCTGTAGATC AGAGGCAGA TTGAGTTCTC GGTAGCAATG TGCAGAGAA AAATTAGTGA GAAGGAGAA ATTTAGGAAAT TTGAGGAGAA TTGAGGAGAA TTGAGGAGAC TTGAGGAGGCAGGT TTGAGGAGGCAGGT TTGAGGAGGAC TTGAGGAGG	CCTTCCTCCC TGCACATCAC TGTAGAAGTT CGGTCTCTCC TGAAACTT TGTCCAAAGA AGATTGATGA GAGCTCCCC AAGGACTACC AGGACTCCC AAGGACTAC GTATGAGACG TATGAGACG TATGAGACG TATGAGACG AAGAGATTACCGA AAGATTACCGA AAGATTACCGA ATGTTACCGA	ATCCCCTTG TCCCAGGTGC GCCACCAGTG GCCACCAGTG TCCAGCAAGG GTTTAAACGT CTTCACTGGT AGGAAAGGTT TCCCAAAAGG TAGGATGGA TGCAGTCAGG AGAGTCAGG AGACTTGGT GGAGGATTAT GATTGCTGTT GATGGTATGCATTTGTAGTAGTAGATCAGGTAGAGAGTTAGAGAGATTAGAGAGAG	120 180 240 300 360 420 540 600 720 780 840 900 960
45	1 I AGTOTTOGIC GGCCAAACGG CCTAGGGGGC CGAACGAATGA CCCAGGGAAT TAACCAAGGA ATGACAGGAAT TCAGCAAAG AAAAATATO AAACAATTT AAGCACTTA AAGCACTTA AACACCCCAA TICTACAATG TTTCACAATG TTTCACAAGGA	11 CONTINUE CONTINU	21) AGGENGTIGGE CATCATGAGA CAACTCCAG GECANTTI AGAGAAGOTS CCTTATTIGCA ACCCAGCCAA ACCCAGCCAA ACCCAGCAA ACCCAGCAA ACCCAGCAA ACCAGAACCT TATAAAAACTATO CATCAAGGAA GAAACGTATO TCATTAATAA TTGCTGAAGTA TTGCTGAAGTA	31. TGGCTACTTC GGCTCCCA AGGGCAGGTT TGAGGTGCCG GCTGTAGATC AAAGGCAGA GGCTCTGCCA TGGATTCTC GGTACAATG GAGGAGAA AAATTAGTGA GAGGAGGAGA TTTTTTGAGAAT TTTTTTTT	CCTTCCTCCC TGCACATCAC TGTAGAAAGT CGGTCTCTCC CTGAAACTGT GGATTGGCCT TOTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AGGAACTCAC GTATGAGACG ATGTTACCGA ATGTTACCGA ATGTTACCGA ATGTTACCCAC	ATCCCCTTG TCCCAGGTGC TCCCAGGTGC TCCAGCAGG GTTTAAACGT GTTTGCAAGG AAAGAGCTT TCCCAAAAGC ATCCGTGGA AGGATAGT GGAGGATTAGT GGAGGATTAGT ATCAACTGGT AGCGTTTTAT	120 180 240 300 360 420 600 660 720 780 840 900 960 1020
45 50 55	1	11. TGGGGCAGGC GATCGGTGGT ACRACTTCAC ACRACTTCAC CCGATARANA GTGRCAGTCC CAGGAGRACAG ATGCTATTCC ATGGATTCAT TCTCTGGAGA TTATATGCTAT TTATATCAT AGRAGRACAT AGRAGRACAT AGGAGGAT AGGAGGAT AGGAGGAT ATGATGGTTT AGGAGGAT ACTTGTGTT	21) AGGENGTGGC TCTGGTGAGA CAACTCCCAG TGCCATTTIG AGGGAAGGTG TCTTATCAG CCCAGCCAA ACCCAGCCAA TATAAAGCT CATCAAGGAA TCATCAAGGAA TCATCAAGGAT TCATCAAGGAT TCATCAAGGAT TCGTGAAGT TCGTGAAGT TCGTGAAGT TCGTGAAGT TCGTGAAGT TCGTGAAGT	31. TSGCTACTTC GSCTTCCCA ASGCCAGGTT TGAGGTGCCA AAAGGCAGA GGCTCTGCCA TTGGATTCTC GGTAGCAATG TTGCAGAGAA AAATTAGTGA GAAGGAGAA AATTAGTGA TTTGAGGAGAA TTTGAGGAGAA CTCCTGGCAT AAAGTGTTC TGTATTCCCA	CCTTCCTCCC TGCACATCAC TGCACATCAC TCTAGAAAGTT CGGTCTCTCC TGAAACTT GGATGGCCT TOTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC TTTTTCCCA AAGGATCA AAAGGATCA AAAGGATCA AAAGGATCA CTGTTCCCT AAAAGGATCA CTGTTCCCT CACACGCTCCCC CCCCCCCCCC	ATCCCCTTG TCCCAGGTGC TCCCAGGTGC TCCAGCAGG GTTTAAACGT GTTTGCAAGG AAAGAGCTT TCCCAAAAGC ATCCGTGGA AGGATAGT GGAGGATTAGT GGAGGATTAGT ATCAACTGGT AGCGTTTTAT	120 180 240 300 360 420 540 600 720 780 840 900 960
45 50 55	1	11 CONTINUE CONTINU	21) AGGENGTGGC TCTGGTGAGA CAACTCCCAG TGCCATTTIG AGGGAAGGTG TCTTATCAG CCCAGCCAA ACCCAGCCAA TATAAAGCT CATCAAGGAA TCATCAAGGAA TCATCAAGGAT TCATCAAGGAT TCATCAAGGAT TCGTGAAGT TCGTGAAGT TCGTGAAGT TCGTGAAGT TCGTGAAGT TCGTGAAGT	31. TSGCTACTTC GSCTTCCCA ASGCCAGGTT TGAGGTGCCA AAAGGCAGA GGCTCTGCCA TTGGATTCTC GGTAGCAATG TTGCAGAGAA AAATTAGTGA GAAGGAGAA AATTAGTGA TTTGAGGAGAA TTTGAGGAGAA CTCCTGGCAT AAAGTGTTC TGTATTCCCA	CCTTCCTCCC TGCACATCAC TGCACATCAC TCTAGAAAGTT CGGTCTCTCC TGAAACTT GGATGGCCT TOTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC TTTTTCCCA AAGGATCA AAAGGATCA AAAGGATCA AAAGGATCA CTGTTCCCT AAAAGGATCA CTGTTCCCT CACACGCTCCCC CCCCCCCCCC	ATCCCCTTG TCCCAGGTGC TCCCAGGTGC TCCAGCAGG GTTTAAACGT GTTTGCAAGG AAAGAGCTT TCCCAAAAGC ATCCGTGGA AGGATAGT GGAGGATTAGT GGAGGATTAGT ATCAACTGGT AGCGTTTTAT	120 180 240 300 360 420 600 660 720 780 840 900 960 1020
45 50 55	1	11. TGGGGCAGGC GATCOGTGCT ACATITCCCA ACAACTTCCCA CGGATANAAC GGGAGACAG GTGACAGTCC CAGGAGACAG ATGCTATTCC ATAGGATGAT TCTCTGGGAT ATAGCTGAT ATAGAACAACT ATGCATAATC AGAACAAACT ATGCATAATC AGAACAAACT ATGCATAATC AGACAGAACT ATGCATAATC AGACAGAACT AGACAAACT AGACAAACT AGACAAACT GGGAGAGGT GGGAGAGGT GGGAGAGT GGGAGAGT GGGAGAGT GGGAGAGT GGGAGAGT GGGAGAGT GGTAAATACT	21 } ACGETGTGGC TCTGGTGAGA CACTTCCAG TGCCATTTTG AGAGAAGCT TCTTATTCAG ACCCAGCCAA ACCCAGCCAA ACCCAGCCAA GCAGAACCT CATCAAGGAA TATAAAACCT CAGAATCT CATCAAGGAA GAAAGCT CATCAAGGAA TCATCAAGAA TCAT	31 TOGGTACTTC COGCTCCCCCA ANAGACCAGT TOGACTTCCCCA ANAGGCAGT TOGACTCCCCCAGACAAAAAAAAAAAAAAAAAAAAAAAAA	CCTTCCTCCC TGCACATCAC TGCACATCAC TCTAGAAAGTT CGGTCTCTCC TGAAACTT GGATGGCCT TOTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC TTTTTCCCA AAGGATCA AAAGGATCA AAAGGATCA AAAGGATCA CTGTTCCCT AAAAGGATCA CTGTTCCCT CACACGCTCCCC CCCCCCCCCC	ATCCCCTTG TCCCAGGTGC TCCCAGGTGC TCCAGCAGG GTTTAAACGT GTTTGCAAGG AAAGAGCTT TCCCAAAAGC ATCCGTGGA AGGATAGT GGAGGATTAGT GGAGGATTAGT ATCAACTGGT AGCGTTTTAT	120 180 240 300 360 420 600 660 720 780 840 900 960 1020
45 50 55 60	1 AGTGTTCGGC GGCCAAACGG CCTAGGGGGC CCTAGGGGGC CCAGGGAT AAACAACGGA ATGACAGGAA AAACAAGGAA CAAAAATATGAAACACACCCAA TICTACAAAG TTACACAGGAG TTACACAGGAG TTACACAGGAG TTACACAGGAG TTACACACGCCAA TICTACAATG TTACACAGGAG TTACACACTC	11. I TGGGGCAGGC GATCGGTATTCCA ACAATTCCCA GTGAAAAAC CCAAGAATTCCA CAGAAATAC ATGCGATATAA ATAAAAATCTT TGGAATCAT AGAAGAAACT AGAAGAAACT AGAAGAAACT AGAAGAAACT ATGCATTCAGGCAGATA TAACTTGTATTCAGGCAGGATAT AACTTGTATTAACTTGTATTCAGGAGATAT AACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTGTTTG	21. ACGCTGTTGGC ACGCTGTGGAA CAACTCCCAG GCAGTTTTG AGAGAAGGTTG CATTATTCAG AGCCAGAAACCT TGACCTAGGAA TATAAAACCT GAAATGCTT TATCAGGAA GAAATGCTT TCATCAGGAA TGCTGAGAAT TTGCTGAATGT TCATCAAGGT TTGCTGAATGT TTGGTTATTTA TTAGTTAGTTA	31 TGGCTACTTC CGCCTCCCCA AGGGCAGGT TGAGGTCGCG AAAAGGCAGA GCTCTCACA AAAAGCAATTCTC GGTTACAGAA AAAATTCTCC GAAACACTTTAGAGAAA ATTTAGGAAAT ATTTAGAGAAT TTTAGAGAAT TTTAGAGAAT TTTAGAGAT TTTAGAGAT TTTAGAGTTCCCC TGGTTTCTCCC	CCTTCCTCCC TGCACATCAC TGCACATCAC TCTAGAAAGTT CGGTCTCTCC TGAAACTT GGATGGCCT TOTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC TTTTTCCCA AAGGATCA AAAGGATCA AAAGGATCA AAAGGATCA CTGTTCCCT AAAAGGATCA CTGTTCCCT CACACGCTCCCC CCCCCCCCCC	ATCCCCTTG TCCCAGGTGC TCCCAGGTGC TCCAGCAGG GTTTAAACGT GTTTGCAAGG AAAGAGCTT TCCCAAAAGC ATCCGTGGA AGGATAGT GGAGGATTAGT GGAGGATTAGT ATCAACTGGT AGCGTTTTAT	120 180 240 300 360 420 600 660 720 780 840 900 960 1020
45 50 55	1 AGTGTTCGGC GGCCAAACGG CCTAGGGGGC CCTAGGGGGC CCTAGGGGAT ACACAGGAA ACACAGGAA ACACAGGAA ACACAGGAA CAAAATATAT AAGCACCCAA TICTACAATG CTTCCAGAGG TTGAAAGGAT TAACCACTA ACACACCCAA TICTACAATG TTGAAAGGAT TAACCACTA ACACACCCAA TICTACAATG TTGAAAGGAT TAACCACTA ACACACCCAA TICTACAATG TTGAAAGGAT TAACCACTA ACACACCCAA TICTACAATG TTAACCAGTA ACACACCCAA TICTACAATG TTGAAAGGAT TAACCACTA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACATA ACACACAC	11. TGGGGCAGGC GATCOGTGCT ACATITCCCA ACAACTTCCCA CGGATANAAC GGGAGACAG GTGACAGTCC CAGGAGACAG ATGCTATTCC ATAGGATGAT TCTCTGGGAT ATAGCTGAT ATAGAACAACT ATGCATAATC AGAACAAACT ATGCATAATC AGAACAAACT ATGCATAATC AGACAGAACT ATGCATAATC AGACAGAACT AGACAAACT AGACAAACT AGACAAACT GGGAGAGGT GGGAGAGGT GGGAGAGT GGGAGAGT GGGAGAGT GGGAGAGT GGGAGAGT GGGAGAGT GGTAAATACT	21. ACGCTGTTGGC ACGCTGTGGAA CAACTCCCAG GCAGTTTTG AGAGAAGGTTG CATTATTCAG AGCCAGAAACCT TGACCTAGGAA TATAAAACCT GAAATGCTT TATCAGGAA GAAATGCTT TCATCAGGAA TGCTGAGAAT TTGCTGAATGT TCATCAAGGT TTGCTGAATGT TTGGTTATTTA TTAGTTAGTTA	31 TGGCTACTTC CGCCTCCCCA AGGGCAGGT TGAGGTCGCG AAAAGGCAGA GCTCTCACA AAAAGCAATTCTC GGTTACAGAA AAAATTCTCC GAAACACTTTAGAGAAA ATTTAGGAAAT ATTTAGAGAAT TTTAGAGAAT TTTAGAGAAT TTTAGAGAT TTTAGAGAT TTTAGAGTTCCCC TGGTTTCTCCC	CCTTCCTCCC TGCACATCAC TGCACATCAC TCTAGAAAGTT CGGTCTCTCC TGAAACTT GGATGGCCT TOTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC TTTTTCCCA AAGGATCA AAAGGATCA AAAGGATCA AAAGGATCA CTGTTCCCT AAAAGGATCA CTGTTCCCT CACACGCTCCCC CCCCCCCCCC	ATCCCCTTG TCCCAGGTGC TCCCAGGTGC TCCAGCAGG GTTTAAACGT GTTTGCAAGG AAAGAGCTT TCCCAAAAGC ATCCGTGGA AGGATAGT GGAGGATTAGT GGAGGATTAGT ATCAACTGGT AGCGTTTTAT	120 180 240 300 360 420 600 660 720 780 840 900 960 1020
45 50 55 60	1 AGTGTTCGGC GGCCAAACGG CCTAGGGGGC CCTAGGGGGC CCTAGGGGAT ACACAGGAA ACACAGGAA ACACAGGAA ACACAGGAA CAAAATATAT AAGCACCCAA TICTACAATG CTTCCAGAGG TTGAAAGGAT TAACCACTA ACACACCCAA TICTACAATG TTGAAAGGAT TAACCACTA ACACACCCAA TICTACAATG TTGAAAGGAT TAACCACTA ACACACCCAA TICTACAATG TTGAAAGGAT TAACCACTA ACACACCCAA TICTACAATG TTAACCAGTA ACACACCCAA TICTACAATG TTGAAAGGAT TAACCACTA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACCATA ACACACATA ACACACAC	11. I TGGGGCAGGC GATCGGTATTCCA ACAATTCCCA GTGAAAAAC CCAAGAATTCCA CAGAAATAC ATGCGATATAA ATAAAAATCTT TGGAATCAT AGAAGAAACT AGAAGAAACT AGAAGAAACT AGAAGAAACT ATGCATTCAGGCAGATA TAACTTGTATTCAGGCAGGATAT AACTTGTATTAACTTGTATTCAGGAGATAT AACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTAACTTGTATTTGTTTG	21. ACGCTGTTGGC ACGCTGTGGAA CAACTCCCAG GCAGTTTTG AGAGAAGGTT TCGTATTCAG AGCCTAGAAC TTGTATCAG AGCAGAACCT GAAATGCTT GAAATGCT GAAATGCTT TATCAAGGAA GAAAGGTAAT TCGTTAATTA TTGTTAATTA TTGGTTAATTA TTGAATTA TTGGTTAATTA	31 TGGCTACTTC CGCCTCCCCA AGGGCAGGT TGAGGTCGCG AAAAGGCAGA GCTCTCACA AAAAGCAATTCTC GGTTACAGAA AAAATTCTCC GAAACACTTTAGAGAAA ATTTAGGAAAT ATTTAGAGAAT TTTAGAGAAT TTTAGAGAAT TTTAGAGAT TTTAGAGAT TTTAGAGTTCCCC TGGTTTCTCCC	CCTTCCTCCC TGCACATCAC TGCACATCAC TCTAGAAAGTT CGGTCTCTCC TGAAACTT GGATGGCCT TOTCCAAAGA AGATTGATGA CACCTGTGGG CAGCCTCCTC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC AAGGACTCCC TTTTTCCCA AAGGATCA AAAGGATCA AAAGGATCA AAAGGATCA CTGTTCCCT AAAAGGATCA CTGTTCCCT CACACGCTCCCC CCCCCCCCCC	ATCCCCTTG TCCCAGGTGC TCCCAGGTGC TCCAGCAGG GTTTAAACGT GTTTGCAAGG AAAGAGCTT TCCCAAAAGC ATCCGTGGA AGGATAGT GGAGGATTAGT GGAGGATTAGT ATCAACTGGT AGCGTTTTAT	120 180 240 300 360 420 600 660 720 780 840 900 960 1020
45 50 55 60	1 ARTOSTICUES GOCCANACOS GOCCANACOS GOCCANACOS GOCCANACOS GOCANACOS GOCANA	11 TORRECTANGE TANTESPRETE TANTESPRETE TANTESPRETE TANTESPRETE COLORIANA CALITICAL COLORIANA CALITICAL COLORIANA TORRECT TANTECTA TANTESTA TANTESTA TANTESTA TANTESTA TANTESTA TANTESTA TANTESTA TANTESTA TORRECT TANTESTA TORRECT TANTESTA TORRECT TANTESTA TORRECT TANTESTA TORRECT TANTESTA TORRECT TANTESTA TORRECT TANTESTA TORRECT TANTESTA TORRECT TANTESTA TORRECT T	21 CONTROPOSE CONTROL CON	31 GOSTACTTC COSCITCACCO GOSTACTTC COSCITCACCO GOSTACTC COSCITCACCO GOSTACCO COTTOCTOCC TOCOCATIONS TOCOCATIONS TOCOCATIONS TOCOCATIONS CONTINUES CONTINUES CONTINUES CONTINUES CONTINUES CONTINUES CONTINUES CONCITOTOC ACCORDINATION CONCITOTOC ANGINACTOC ANGINACTOC ANGINACTOC ANGINACTOC ANGINACTOC ANTITUTOCOCA ATTITUTOCOCA ATTITUTOCOCA ATTITUTOCOCA COTTOTOC ANDITUTOCOCA COTTOTOCOC ANDITUTOCOCA COTTOTOCOCOC ANDITUTOCOCA COTTOTOCOCOC ANDITUTOCOCA COTTOCOCOC C ANDITUTOCOCA COTTOCOCOCOCOC ANDITUTOCOCA COTTOCOCOCOCOCOCOCO ANDITUTOCOCA COTTOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	ATCCCCATTG TCCCAGGTGC GCCACCAGTGC GCCACCAGTGC TCCAGCAGGC GTTTGAAACGT GTTGGCAAGGA GTTGGCAAGGA TAGCAAGCTTGGA TCCCACAAGGT TCCCACAAGGT TCCCACAAGGT TGCAGTCAGG AGACTTTGTT GGAGGTTAGT GATGCATTTAT TAGCATTTAT TAGATATTAT	120 180 240 300 480 540 660 720 780 840 900 900 1020	
45 50 55 60 65	1 AUTONITORICO GOCCANACIO COTTAGOGOGO GOGAGOCOC GOGAGOCOC GOGAGOCOC AND ANCACAGOGO ANTONIO GOCCANACIO CONTO	11 TOGOGICAGGE GATCUGTUCT ACACTTICAC GATCUGTUCT ACACTTCAC CCORTANAL GTUACATTCAC CCURTANAL TACTCTCAC ACACTTCAC CCURTANAL TACTCTCACAC ATACATCAC TACATCATAC TACTCTCACAC ATACATCATAC TACATCATAC	21 ACCIONTIGAC ACCIONTICA ACCIONTIGAC ACCIONTIGAC ACCIONTIGAC ACCIONTIGAC ACCIONTICA ACCIO	31 GGSTACTIC COCCIONATION OF THE PROPERTY OF	CCTTCCTCCC TGCACATCAC TTGCACATCAC TTGCACATCAC CCTTACACTCAC CCTTACACTCAC GGATGGCCT TTGCCACATCAC CACCTGTGCAC AGGACCTAC AGGACCTAC AGGACCTAC ATGTTACCAC ATGTTACAC AT	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGGTAGC GTTGACAGG ATTGACAGG AAAGAAGGT TCCCCAAAGC ATGCGTCAGG AGGAAAGGT TCCCCAAAGC ATGCGTCAGG AGGAATTAT TCCCAAAGC ATGCGTTGAG AGGATTATT ATGCATTGGG AGGATTATT ATGCATTGGG AGGATTATT ATGCATTGGG	120 180 240 360 420 480 540 660 720 780 900 900 1020 1080
45 50 55 60	1 ARTONICOSEG GOCCANACOS GOCCANACOS GOGGO GOCCANACOS GOGGO GOCANGOS GOCAN	11 TORRESCIAGO CONTROL OF THE PROPERTY OF TH	21 ACCUMUNACION	TOGGETACTIC GOCTICCOL AGGICAGUT TOGAGTICCOL AGGICAGUT TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGATICCOL TOGA	CCTTCCTCCC TGCACATCAC TATACAC TA	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGGTAGC GTTGACAGG ATTGACAGG ATTGACAGG ATGCTTGACAGG ATGCTTGACAGG AGACTTGGT GATGGATGAGG AGACTTGTTGATAGATTGAG ATCAGTTGAT GATTGATTGAT GATTGATTTAGATTAGA	120 180 240 300 300 420 480 540 660 720 780 840 900 1020 1080
45 50 55 60 65	1 AUTOTICISCE GOCCAAAOCO COTTAGOGOGO GAGAGCATCA COCCAGGAAT AACAACAGA AACAACAGA AACAACAGA AACAACAGA AACAACATCA AACAACATCA CAAAAATATCA CACACCCAATTCAACAAGAAA AACAACATTCAACAAGAAA TTCTAACAAGATTTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAAGAATTCAACAGAATTCAACAGAATTCAACAGAATTCAACAGAATTCAACAACAACAACAACAACAACAACAACAACAACAA	11 TORRESCIAGO CONTROL OF THE PROPERTY OF TH	21 ACCUMUNACION	TOGGETACTIC GOCTICCOL AGGICAGUT TOGAGTICCOL AGGICAGUT TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGATICCOL TOGA	CCTTCCTCCC TGCACATCAC TATACAC TA	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGGTAGC GTTGACAGG ATTGACAGG AAAGAAGGT TCCCCAAAGC ATGCGTCAGG AGGAAAGGT TCCCCAAAGC ATGCGTCAGG AGGAATTAT TCCCAAAGC ATGCGTTGAG AGGATTATT ATGCATTGGG AGGATTATT ATGCATTGGG AGGATTATT ATGCATTGGG	120 180 240 300 300 420 480 540 660 720 780 840 900 1020 1080
45 50 55 60 65	1 ARTONICOSEG GOCCANACOS GOCCANACOS GOGGO GOCCANACOS GOGGO GOCANGOS GOCAN	11 TORRESCIAGO CONTROL OF THE PROPERTY OF TH	21 ACCUMUNACION	TOGGETACTIC GOCTICCOL AGGICAGUT TOGAGTICCOL AGGICAGUT TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGATICCOL TOGA	CCTTCCTCCC TGCACATCAC TATACAC TA	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGGTAGC GTTGACAGG ATTGACAGG ATTGACAGG ATGCTTGACAGG ATGCTTGACAGG AGACTTGGT GATGGATGAGG AGACTTGTTGATAGATTGAG ATCAGTTGAT GATTGATTGAT GATTGATTTAGATTAGA	120 180 240 300 300 420 480 540 660 720 780 840 900 1020 1080
45 50 55 60 65	1 AUTOTICISCO GOCCANACOS COTTAGOGOGO GODAGOGOC GOGAGOGOC GOGAGOGOC GOGAGOGOC GOGAGOGOC GOGAGOGOC GOGAGOGOC GOGAGOGOC GOGAGOC GOGAC G	11 TORRESCIAGO CONTROL OF THE PROPERTY OF TH	21 ACCITOTOGIC TOTOGITAGA TOTOGITAGA TOCANTITIO TOCANTITIO ACCIAGOA GORGANACT TOTOGIACAGA GORGANACT TOTOGIACAGA CONTOGIAGA TOCATORAGA TOCATOR	TOGGETACTIC GOCTICCOL AGGICAGUT TOGAGTICCOL AGGICAGUT TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGAGTICCOL TOGATICCOL TOGA	CCTTCCTCCC TGCACATCAC TATACAC TA	ATCCCCCTTG TCCCAGGTGC GCCACCAGTG TCCAGGTAGC GTTGACAGG ATTGACAGG ATTGACAGG ATGCTTGACAGG ATGCTTGACAGG AGACTTGGT GATGGATGAGG AGACTTGTTGATAGATTGAG ATCAGTTGAT GATTGATTGAT GATTGATTTAGATTAGA	120 180 240 300 300 420 480 540 660 720 780 840 900 1020 1080

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80	AGTGTTCGGC	TGGGGCAGGC	ACCCTGTGGC	TGGCTACTTC	CCTTCCTCCC	ATCCCCCTTG	60
	GGCCAAACGG	GATCGGTGCT	TCTGGTGAGA	CGCCTCCCCA	TGCACATCAC	TCCCAGGTGC	120
	CCTAGGGGGC	ACATTTCCCA	CAACTCCCAG	AGGGCAGGTT	TCTAGAAAGT	GCCACCAGTG	180
	GGGAGGCGCC	ACAACTTCAC	TGCCATTTTG	TGAGGTGCCG	COGTCTCTCC	TCCAGCAAGG	240
	GAAACAATGA	CCGATAAAAC	AGAGAAGGTG	GCTGTAGATC	CTGAAACTGT	GTTTAAACGT	300
85	CCCAGGGAAT	GTGACAGTCC	TTCGTATCAG	AAAAGGCAGA	GGATGGCCCT	GTTGGCAAGG	360
	AAACAAGGAG	CAGGAGACAG	CCTTATTGCA	GGCTCTGCCA	TGTCCAAAGC	AAAGAGCTTA	420
	TGACAGGACA	TGCTATTCCA	CCCAGCCAAT	TGGATTCTCA	GATTGATGAC	TTCACTGGTT	480

5	CCAGCAGTTT AACAAGAAAT AAAAATATGA AACGATTTTT	TAGGATGATG CTCTGGAGAT TAATGCTGAT AAAAATCTTC TGAATCCATC	GACCTAGAAT ATAAAACGTA GAAATGCTTG ATCAAGGAAG	GCAGAGAAC AATTAGTGAA AAGGAGTGCA CAGCAAGATG	AGCCTCCTCT GGAACTCCGA AGGACCTACT TATGAGACGA	TGCGTTGGAC GCAGTCAGGA GACTTTGTTA	540 600 660 720 780
	AGCACCTTAA ACACCCCAAA TCTACAATGG TTCCAGAGGC	GAAGAAACTG TGCATAATCT AGCAGGATAT TAAGAAATTT	AAACGTATGA CATTAATGAT TGCTGAAGTC CTGTTAGTAA	TTTGAGAATA TGAGGAGAGA TCCTGGCATA AAGATGTTCT	CTTGTCCCTG AAAGGATCAG TGTTACCGAA TTTTCCCAAA	GAGGATTATC ATTGCTGTTT TCAACTGGCC GCGTTTTATT	900 960 1020
10	AACCCATTAG	ACTTGTGTTT GTAAATACTA 300 Proteir	TTACAGTOGT	GTATTCCCAC GGTTTCTGCA	CTGTGCTGGT	AGATATTATT	1080
15	Protein Acc	ession #: 1	sos sequence				
20	CUATERSOLD.	11 DPETVFKRPR SQIDDFTGFS VKELRCVGQK	KDRMMOKPGS	NAPUCCNUTS	SFSGDDLECR	ETASSPKSOO	60 120 180
25	Nucleic Act	301 DNA sec id Accession uence: 247-8	i #: Eos se	quence			
	1 AGTGTTCGGC	11 TGGGGCAGGC	21 ACGCTGTGGC	31 TGGCTACTTC	1 CCTTCCTCCC	51 ATCCCCCTTG	60
30	GGCCAAACGG CCTAGGGGGC GGGAGGCGCC GAAACAATGA	GATCGGTGCT ACATTTCCCA ACAACTTCAC CCGATAAAAC	TCTGGTGAGA CAACTCCCAG TGCCATTTTG AGAGAAGGTG	AGGGCAGGTT TGAGGTGCCG GCTGTAGATC	TGCACATCAC TCTAGAAAGT CCGTCTCTCC CTGAAACTGT GGATGGCCCT	TCCCAGGTGC GCCACCAGTG TCCAGCAAGG GTTTAAACGT GTTGGCAAGG	120 180 240 300 .
35	AAACAAGGAG TGACAGGACA TCAGCAAAGA CCAGCAATTT AACAAGAAAT	CAGGAGACAG TGCTATTCCA TGGGATGATG CTCTGGAGAT TAATGCTGAT	CCTTATTGCA CCCAGCCAAT CAGAAACCTG GACCTAGAAT ATAAAATGTC	GGCTCTGCCA TGGATTCTCA GTAGCAATGC GCAGAGGAAT AAGTAGTGAA	TGTCCARAGA GATTGATGAC ACCTGTGGGA AGCCTCCTCT GGRAATCCGA	AAAGAGCTTA TTCACTGGTT GGAAATGTTA CCCAAAAGCC TGCCTTGGAC	420 480 540 600 660
40	AATATGAAA GATTTTTGA ACCTTAAGAA	ATCCATCATC GAAACTGAAA	ANGGAAGCAG CGTATGATTT	CAAGATGTAT GAGAATACTT	GAGACGAGAC GTCCCTGGAG GGATCAGATT	TTTGTTAAGC GATTATCACA GCTGTTTTCT	720 780 840 900 960
45	AAGGATAACT CCATTAGGTA	AGGATATTGC GAAATTTCTG TGTGTTTTGG AATACTATTA	CAGTCGTGGT	TTCCCACCTG	TCCCAAAGCG TGCTGGTAGA	TTTTATTTGA TATTATTAAC	1020 1080
50	Seq ID NO: Protein Ac	302 Protein cession #: 1	n sequence: Eos sequence	31	41	51	
	MTDKTEKVAV	DPETVFKRPR	1	ì	GAGDSLIAGS	AMSKEKKI.MT	60
55	CHAIPPSQLD EINADIKCQV KKKLKRMI	SQIDDFTGFS VKEIRCLGQY	KDGMAQKPGS EKIPEMLEGV	NAPVOCNUTS	NESCODLECE	GIASSPKSOO	120 180
60	Nucleic Ac	303 DNA seid Accession uence: 247-	n #: Bos se 815				
65	GGCCAAACAG CCTAGGGGGC GGGAGGCGCC	TOGGACAGGC GATCGGTGCT ACATTTCCCA ACAACTTCAC	TCTGGTGAGA CAACTCCCAG TGCCATTTTG	AGGGCAGGTT TGAGGTGCOG	TGCACATCAC TCTAGAAAGT CCGTCTCTCC	GCCACCAGTG TCCAGCAAGG	60 120 180 240
70	CCCAGGGAAT AAACAAGGAG TGACAGGACA TCAGCAAAGA	CCGATAAAC GTGACAGTCC CAGGAGACAG TGCTATTCCA TAGGATGATG	TTCGTATCAG CCTTATTGCA CCCAGCCAAT CAGAAACCTG	AAAAGGCAGA GGCTCTGCCA TGGATTCTCA GTAGCAATGC	GGATGGCCCT TGTCCAAAGC GATTGATGAC ACCTGTGGGA	GTTGGCAAGG AAAGAGCTTA TTCACTGGTT GGAAACGTTA	360 420 480 540
75	CCAGCAGTTT AACAAGAAAT AAAAATATGA	CTCTGGAGAT TAATGCTGAT AAAAATCTTC TGAATCCATC GAAGAAACTG TGCATAATCT	GACCTAGAAT ATAAAACGTA GAAATGCTTG	GCAGAGAAAC AATTAGTGAA AAGGAGTGCA	AGCCTCCTCT GGAACTCCGA AGGACCTACT	TGCGTTGGAC GCAGTCAGGA	600 660 720 780 840
80	TCTACAATGG TTCCAGAGGC TGAAAGGATA	TGCATAATCT AGCAGGATAT TAAGAAATTT ACTTGTGTTT GTAAATACTA	CTGTTAGTAA	AAGATGTTCT	TTTTCCCAAA	GCGTTTTATT	900 960 1020 1080
85	Seq ID NO:	304 Protei	n sequence:				

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5	ETWADINDEN.	VKELRCVGQK	VEKTPEMLEG	VOGPTAVRKE	PPESIIKEAA	RCMRRDFVKH	180
	LKKKLKRMI	TTUDBITOT OUT					
	DIRECTION						
	Com YD MO.	305 DNA sec	mence				
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10	Nucleic Ac	ience: 87-68	1 B: EOS Sed	luence			
10	coarna sed	Terree: 01-00	,,				
				31	41	51	
	1	11	21	31	41	71	
	1	GCTAGCGCGA			- Commonwood	CONTROL	60
15	CGTGGAGGCA	GCTAGCGCGA	GGCTGGGGAG	CGCTGAGCCG	CGCGTCGTGC	CCTGCGCTGC	120
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	AATCCACAAA	CCCCGGCATC	TCTATTGGAG	ACGTGGCAAA	AAAGCTGGGT	GAGATGTGGA	480
	ATRATTTABA	TGACAGTGAA	A A G C A G C C TT	ACATCACTAA	GGCGGCAAAG	CTGAAGGAGA	540
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	CTCCTABACT	TOCCCGGAAA	BAGGTGGAAG	AGGAAGATGA	AGAAGAGGAG	GAGGAAGAAG	660
25	ACCACCACCA	GGAGGAGGAG	CATCRATARA	GAAACTGTTT	ATCTGTCTCC	TTGTGAATAC	720
		GG & GGGGGGGGG	A DESCRIPTION CACA	THE PARTY AND PA	CAGBACTOTO	TOTTGCCCTC	780
	ITAGAGIAGG	ATTACA A A A A	TOTATCACCA	TCATATTCTA	CTCTCTCAAA	GTGCTCTAGA	840
	ATTAGGITTA	ATTACAAAAT GGTTTACATG	P D C C C C C C C C C C C C C C C C C C	COCCUCATION	ACCACCCTGA	AACTGTATCA	900
	AATIGICAGI	GGITIACAIG	AMUTUUCCAT	3001010100	* CONCOCCTOR	TOTOTOTO	960
30	AAGTTGTACA	TATTTCCAAA	CATTTITAGA	ATGARAGGC	ACTUTOR	MANUSCO CONCT	1020
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40	AGTCAATTTC	TGACTCACAG	CAGTGAACAA	ACCCCCACTC	CATTGTATTT	GGAGACTGGC	1620
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	ATGAAGTCTG	GAGGAGTTAG	GAGAACGACA	TAGGCAAGGT	TCAGCAGCCT	TCCAAGGTAT	1800
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45	CCTATTTTGT	GGGGCCAAAT	GCATTGCTAA	ACAGCAATTT	CAGAGTGTAT	GGTGTGTCAA	1920
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	ACATTATTTC	TEGTECCCAA	CATTTGGGGGT	CTTGAGCCTG	CTGCTGGTCT	CCTGGATGCC	2040
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	TTOCABACAC	CAAACACCCC	AAGGAAGATG	ATAGGCTCCA	TCTTGGGCCA	CCTGAGCTAT	2160
50	ACCCCACCCC	AATGGAATCA	ACCATTTCTC	ACCACTAAAT	GTATCATGAA	AAGTTGAATG	2220
50	ACCORDING TO	AAGTTTAGCT	CAMPCACTCC	ABATCTACAT	TOATOTTCAA	TGTTAAACTG	2280
	GCCTGCTCAT	GGTTTGTGTG	TOTAL CONCERNA	TATTACTOCC	TACTOTABOA	TTTTATCCAG	2340
	GAAGGAGCTT	GGGGAGATGG	CAGIGGIIA	PACTROTOGG	ACTION APPROC	ATTTTGAAGG	2400
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70	CTACTCCCTC	TAACCACCTC	ACCCCATTCT	TGAATGACAT	TTTATCCTTC	GGAAAGAACA	3420
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	GTATTTGGGG	ACGTTGGATG	CATTCATTTT	CTGTAATAAA	G		
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	1	. 1	1	· ·	I BOYNGOD	I PHONE PROPERTY	60
80	MAKGDPRKPB	GKMSAYAPFV	Q'ICREBHKKK	MERVEVNEAR	FARRCSERNK	TMSGKEKSKP	120
ου	DEMAKADKVE	YDREMKDYGP	AKGGKKKKDP	MAPRICEPSOR	FULCOURE	IKSTNPGISI GPAKVARKKV	180
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	TTCACGATG C	CTCCCAGGA C	TTGGTTTAT C	AGACAGTTG C	AAAGGATGT C	GTTTCTCAG	240 300
	CCCTCGATG G	CTATAATGG C	ACCATCATG	GTTATGGGC F	GACGGGAGC 1	rggcaagaca	360
10	AGCAGGTTT T	TAGGATGAT (CARGARITAC A	CCACACAGG C	CATCACTGT C	CGTGTTTCC	420
10	ACTTGGAAA T	CTATAATGA C	AGCCTGTTT (ATCTCCTGT C	CACTCTGCC (TATGTTGGA	480
	COTOACTOA C	ACCANTGAC (ATCCTCCAA	ACCCTCAAG C	AGTCTTCAT 1	DTTDDDDAA	540
	CAGTTCACC T	CACAAGTCA C	GAGGAGGAT (CATTCAGCC T	CCTTTTTGA C	GGTGAGACC	600 660
15	ACAGGATTA T	AGCCTCCCA C	CACTATGAAC A	MANACTOTT (CAGATCACA (TIGCATITIC	720
13	TTAACTTGG T	AGAGGCCCA 1	CCCTCACAC !	COCTOCOL I	CTCTCCCTC	GAGGGCCAA	780
	TOTTGAAGG A	AGCCACCTA (CATCAACAAA 1	CCCTCTCAT 7	CCTGGAGCA (JGCCATCATT	840
	CCCTTGGGG A	CCAGAAGCG C	GACCACATC (CCTTTCGGC A	GTGCAAGCT (CACCCACGCT	900
20	TORROGACT C	YOTTMOOGGG Z	AAACTGCAAT J	TGGTCCTCG 1	GACAAACAT (TATGGAGAA	960 1020
20	CCACTGAGC C	AGAAGAAAC C	CTATCTTCA (TGAGATTTG C	CAGCAGGAT C	BAAGCTAGTC	1020 1080
	AGGAACTAG C	TGCCATCAA T	CAGAAAGTAT C	CTATCCATC I	CAGCCTGAC	CAACCGCACC	1140
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25	TGTTCAACC A	GTTCCGGGT (GTTCTGAGC	CAACAGGAAC A	AGGAAGTGGA (TCCACTTTG	1320
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	ARCRECCAC T	CACCCCCCA C	TACHCOCACCC '	CASTORAGES	CCCCTTTGA (CAGTTTAAG	1560
30	ATGAGCAAG G	TAGTGAGAT (CAACCGAATT '	TCANAGAAA A	CAAATCCAT (CTTGAATGAA	1620
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	TGACCAAGG A	GGCCCTGAA 1	TTTCCAGAAG 'CGATGAGGAA	CACTACGG I	CARCCARGO	CTCABAGAC	1800
	TORRORDO S	CTACCCCAG (TRACTACCAG (INCOMPANIE	ACCTCAGGGC '	rgagatecag	1860
35	ATTGCCAGC A	CCTAGTGGA 1	CCTGAGGAC	ACCECCTEC 1	CATGGAATT '	TGACATCTGG	1920
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	AATTCAGCC A	AGCTGCAGCA C	GAGGGTGCTT GCAGAAGCAT	ATTACTOR	AACCATGAT	GGCCTCCAG	2160
40	AGGCACATA C		JCAGAAGGAT A	uta anos a un a			
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45	1	11	21	31	41	51	
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45	LHDASODLVY	11 VRVKPTDDFA ETVAKDVVSO	21 HEMIRYGDDK ALDGYNGTIM	RSIDIHLKKD CYGQTGAGKT	I IRRGVVNNQQ YTMMGATENY	TDWSFKLDGV KHRGILPRAL	
	LHDASQDLVY	11 VRVKPTDDFA ETVAKDVVSQ	21 HEMIRYGDDK ALDGYNGTIM YUNESLE	RSIDIHLKKD CYGQTGAGKT	IRRGVVNNQQ YTMMGATENY DSVTPMTIVE	TDWSFKLDGV KHRGILPRAL NPOGVFIKGL	120 180
45 50	LHDASQDLVY QQVPRMIEER SVHLTSOEED	11 VRVKPTDDFA ETVAKDVVSQ PTHAITVRVS APSLLFEGET	21 BEMIRYGDDK ALDGYNGTIM YLEIYNESLP NRIIASHTMN	RSIDIHLKKD CYGQTGAGKT DLLSTLPYVG KNSSRSHCIF	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT	TOWSFKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK	120 180 240
	LEDASQDLVY QQVFRMIEER SVHLTSQEED INLVDLAGSE	11 VRVKPTDDFA ETVAKDVVSQ PTHAITVRVS AFSLLFEGET RIGKSGSBGQ	21 EEMIRYGDDK ALDGYNGTIM YLEIYNESLP NRIIASHTMN VLKEATYINK AAOLEVILSE	RSIDIHLKKD CYGQTGAGKT DLLSTLPYVG KNSSRSHCIF SLSFLEQAII LRPASRMKLV	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY	TDWSFKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE	120 180 240
	LHDASQDLVY QQVFRMIEER SVHLTSQEED INLVDLAGSB LKDSLGGNCN XRLALLKOEL	11 VRVKPTDDFA ETVAKDVVSQ PTHAITVRVS AFSLLFEGET RIGKSGSBGQ MVLVTNIYGE ATHDSLTNRT	21 	RSIDIHLKKD CYGQTGAGKT DLLSTLPYVG KNSSRSHCIF SLSFLEQAII LRFASRMKLV QIAZINSOVR	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI	TDWSFKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE	120 180 240 300 360 420
50	LHDASQDLVY QQVPRMIEER SVHLTSQEED INLVDLAGSE LKDSLGGNCN KELALLKQEL VPNOPRVVLS	11 VRVKPTDDFA ETVAKDVVSQ PTHAITVRVS AFSLLFEGET RLGKSGSBGQ MVLVTNIYGE AIHDSLINET OODOEVESTL	21	RSIDIHLKKD CYGQTGAGKT DLLSTLPYVG KNSSRSHCIF SLSFLEQAII LRFASRMKLV QIABINSQV DFAAISAIOK	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI AGLVDVDGHL	TDWSFKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE VGEPBQQNFG	120 180 240 300 360 420 480
	LHDASQDLVY QQVFRMIEER SVHLTSQEED INLVDLAGSB LKDSLGGNCN XELALLKQEL VPNQFRVVLS	11 VRVKPTODPA ETVAKDVVSQ PTHAITVRVS APSLLFEGE RIJGKSGSEGQ MVLVTNIYGE AIHDSLTNRT QQEQEVESTL	21	RSIDIHLKKD CYGQTGAGKT DLUSTLPYYO KNSSRSHCIF SLSFLEQAII LRFASRMKLV QIAEINSQVR DPAAISAIQA SKPVAPRRPK	IRRGVVNNQQ YTMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI AGLVDVDGHL NEGGSEINRI	TDWSFKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE VGEPEGQNFG FKENKSILNE	120 180 240 300 360 420 480 540
50	LHDASQDLVY QQVPRMIEER SVHLTSQEED INLVDLAGSE LKDSLGGNCN KELALLXQEL VPNQFRVVLS LGVAPFSTKP REKRASETTO	11 VRVKPTDDFA ETVAKDVVSQ ETHAITVRVS APSLLFEGET RIGKSGSBGQ MVLVTNIYGE AIHDSLINRT QQEQEVESTL GKKAKSKKTF HINAIKREID	21 HEMIRYGDDK ALDGYNGTIM YLEIYNESLF NRILASHTMN VLKEATYINK AAQLESTLSS FYTYDPMDEI RRKYTLIDRN KBPLRPDTPP YTKEALNFOK	RSIDIHLKKD CYGGTGAGKT DILGTLPYVG KNSSRSHCIF SLSFLEQAII LRPASRMKLV QTABINSQVR DPAAISAIQK SKPVAFEEFK SLREKGGKYE	IRRGVVNNQQ YTMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI AGLVDVDGHL NEQGSEINRI NKGLMIDEE	TDWSFKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE VGEPBOQNFG FKENKSILNE BFILILKLKO	120 180 240 300 360 420 480 540
50	LHDASQDLVY QQVPRMIEER SVELTSQEED INLVDLAGSE LKDSLGGNCN KELALLKQEL VPNQFRVVLS LGVAPFSTKP RRKRASETYQ	11 VRVKPTODFA ETVAKOVVSQ PTHAITVRVS APSLLFEGET RLGKSGSEGQ MVLVTNIYGE AIHDSLINRT QQEQEVESTL GKKAKSKKTF HINAIKREID	21	RSIDIHLKKD CYGQTGAGKT DILBTLPYVG KNSSRSHCIF SLSFLEQAII LRFASRMKLY QIABINSQVR DPAAISAIQK SKPVAPEEFK SLREKQGKYE HBLIMEFDIW	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI AGLVDVDGHL NEQGSEINRI NKGLMILDEI WESSFVIPED	TOWSPKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE VGEPEOQNFG FKENKSILNE EPLLILKLE MOMALKPGGS	120 180 240 300 360 420 480 540 660
50	LHDASQDLVY QQVPRMIEER SVELTSQEED INLVDLAGSE LKDSLGGNCN KELALLKQEL VPNQFRVVLS LGVAPFSTKP RRKRASETYQ	11 VRVKPTODFA ETVAKOVVSQ PTHAITVRVS APSLLFEGET RLGKSGSEGQ MVLVTNIYGE AIHDSLINRT QQEQEVESTL GKKAKSKKTF HINAIKREID	21	RSIDIHLKKD CYGQTGAGKT DILBTLPYVG KNSSRSHCIF SLSFLEQAII LRFASRMKLY QIABINSQVR DPAAISAIQK SKPVAPEEFK SLREKQGKYE HBLIMEFDIW	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI AGLVDVDGHL NEQGSEINRI NKGLMILDEI WESSFVIPED	TDWSFKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE VGEPBOQNFG FKENKSILNE BFILILKLKO	120 180 240 300 360 420 480 540 660
50	LHDASQDLVY QQVPRMIEER SVBLTSQEED INLVDLAGSB LKDSLGGNCN KELALLKQEL VPNQFRVVLS LGVAPFSTKP RRKRASETTQ LKKQYRSEYQ IRPGMVPVNR QAHRK	11 VRVKPTDDFA ETVAKOVVSQ PTHAITVRVS APSLIPEGET RLGKSGSEGQ MVLVTNIYGE AIHDSLINET QQEQEVESTL GKKAKSKITH HINAIKPBID DLRDLRABIQ IVSLGEDDQD	21 HEMIRYGDDK ALDGYNGTIM YLEIYNESIP MRIIASHTMN VLKEATYINK AAQLEETLISS RRKYTLIDRM KEPLRPDTPP VTKEALNFQK YCQHLVQCR KFSQLQQRVL	RSIDIHLKKD CYGQTGAGKT DILBTLPYVG KNSSRSHCIF SLSFLEQAII LRFASRMKLY QIABINSQVR DPAAISAIQK SKPVAPEEFK SLREKQGKYE HBLIMEFDIW	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI AGLVDVDGHL NEQGSEINRI NKGLMILDEI WESSFVIPED	TOWSPKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE VGEPEOQNFG FKENKSILNE EPLLILKLE MOMALKPGGS	120 180 240 300 360 420 480 540 660
50	LHDASQDLVY QQVPRMIEER SVHLTSQEED INIVDLAGSE LKDSLGGNCN KELALLXQEL VPNQFRVVLS LGVAPFSTKP RRRRASETTQ LKKQYRSEYQ LRPGMVPVNR QAHRK Seg_ID_NO:	11 VRVKPTODFA ETVAKDVVSQ PTHAITVRVS APSLIFEGET RIGKSGSEGQ MVLVTNIVGE AIHDSLIMRT QQEQEVESTL GKKAKSKKTF HINNIRREID DLRDLRABIQ IVSLGEDDQD	21	RSIDIHLKKD CYGGTGAGKT DILGTTLPYUG KNSSKSHCIF SLSFLEQAII LRFASKMKLV GIABINSOVR DFAAISATQK SKPVAFEEFK SLREKQGKYE HRLLMEFDIW PEGPDSISFY	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI AGLVDVDGHL NEQGSEINRI NKGLMILDEI WESSFVIPED	TOWSPKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE VGEPEOQNFG FKENKSILNE EPLLILKLE MOMALKPGGS	120 180 240 300 360 420 480 540 660
50	LHDASQDLVY QQVPRMIEER SVHLTSQEED INIVDLAGSE LKDSLGGNCN KELALLXQEL VPNQFRVVLS LGVAPFSTKP RRRRASETTQ LKKQYRSEYQ LRPGMVPVNR QAHRK Seg_ID_NO:	11 VRVKPTODFA ETVAKDVVSQ PTHAITVRVS APSLIFEGET RIGKSGSEGQ MVLVTNIVGE AIHDSLIMRT QQEQEVESTL GKKAKSKKTF HINNIRREID DLRDLRABIQ IVSLGEDDQD	21 HEMIRYGDDK ALDGYNGTIM YLEIYNESIP MRIIASHTMN VLKEATYINK AAQLEETLISS RRKYTLIDRM KEPLRPDTPP VTKEALNFQK YCQHLVQCR KFSQLQQRVL	RSIDIHLKKD CYGGTGAGKT DILGTTLPYUG KNSSKSHCIF SLSFLEQAII LRFASKMKLV GIABINSOVR DFAAISATQK SKPVAFEEFK SLREKQGKYE HRLLMEFDIW PEGPDSISFY	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI AGLVDVDGHL NEQGSEINRI NKGLMILDEI WESSFVIPED	TOWSPKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE VGEPEOQNFG FKENKSILNE EPLLILKLE MOMALKPGGS	120 180 240 300 360 420 480 540 660
50 55 60	LHDASQDLVY QQVPRMIEER SVHLTSQEED INIVDLAGSE LKDSLGGNCN KELALLXQEL VPNQFRVVLS LGVAPFSTKP RRRRASETTQ LKKQYRSEYQ LRPGMVPVNR QAHRK Seg_ID_NO:	11 VRVKPTODFA ETVAKDVVSQ PTHAITVRVS APSLIFEGET RIGKSGSEGQ MVLVTNIVGE AIHDSLIMRT QQEQEVESTL GKKAKSKKTF HINNIRREID DLRDLRABIQ IVSLGEDDQD	21	RSIDIHLKKD CYGCTGAGKT DILGTIPYUG KNSGRSHCIF SLSFLEQAII LRFASRKILV GIABINSOVR DFAAISATOK SKPVAPEEFK SLREKOGKYE HRLLMEFDIW PEGPDSISFY	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE TIYLEAHSRT ALGDQKRDHI TTEPAINEKY RYLEGTLDEI AGLVDVDGHL NEQGSEINRI NKGLMILDEI WESSFVIPED	TOWSPKLDGV KHRGILPRAL NPQGVFIKGL LSEEKYITSK PFRQCKLTHA DAERMVKNLE DIISLRQIKE VGEPEOQNFG FKENKSILNE EPLLILKLE MOMALKPGGS	120 180 240 300 360 420 480 540 660
50	LHDASQDLVY QOVPENLES SVHLTSQEED INLVDLAGSB LKDSLIGGNCN KELALLKQEL LWOSEL LGVADFSTKP RRKRASETY LKKQYRSEYQ IR PGMVPVNR QAHRK Seq ID NO: Nucleic Aci	11 VRVKPTDDPA ETVAKOVVSQ PTHAITVRVS APSILPEGET RLGKSGSSGQ WVLVTNIYGE AIHDSLITHRT GMCAKASKKTP HINAIKREID DLRDLRABIQ IVSLGEDDQD 309 DNA see id Accession	21 EMMIRYGODK ALDGYNGTIM YLBIYNBELF NRILASHTON VLKERTYINK AAQLEETLSS FVTTOPMOBI RRKYTLING KEPLAPDTPP VTKEALNPY YCGHLVDQCR KFSQLQQRVL Quence a #: CAT clu	ESIDIHLKKD CYGQYGAGKT DILGSTLPYVG KNSGRSHCIF SLSFLEQAII LRPASRMKLV QIABINSQVR DFAAISAIQK SKPVAFEEFK HRLLMEFDIW PEGFDSISFY 11	IRRGUVNNOO YTHOGATENY PSVITMITUE TIYLEAHBRT ALGDOKENHI TTEPAINEKY RYLEGTLDEI NEGGSEINRI NEGGSEINRI NEGGSEINE YNESFVIPED NAKVKIEGKH	TOWSFKLDGV KHRGILPRAL MPGGVFIKGI LSEEKYITSK PFRCCKLTHA DAERMYKHA DIISLRQIKP GKENFSILNE MGEPBOGNP KKENKSILNE MGMALKPGGS NYLKTHMGLQ	120 180 240 300 360 420 480 540 600 720
50 55 60	LHDASQOLVY QVPRMIEER SVHLTSQEED INLVDLAGSB LKOSLGGNCN KELALLKQEL VPNOPRVLS LGVAPFSTKP RRKRASETTQ LKKQYRSEYQ IRPGMVPVNR QAHRK Seq ID NO: Mucleic Aci	11 VARVENTODPA ETVAKOVVSQ PTHAITVEVS APSLLFEGET RLGKSGSEGO WILLTYIYGE AIHDSLINGT GKKAKSKETP GKKAKSKETP LINGLIKEEI DLRDLRABIQ IVSLGEDDQD 109 DNA see id Accession 11	21 EMMIRYGDDK ALDGYNGTIM ALDGYNGTIM YLEYINESLP NRITASHTMN VLKEATYINK AQQLESTLISS PVITOPMDEIL TYPE VCGHLVDQCR KEPLRPOTTPP VCGHLVDQCR KFSQLQQRVL Quence a #: CAT clv I I I IIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ESIDIHLKKD CYGOTGAGK CYGOTGAGC CYGOTGAGK CYGOT	IREGVVNNQQ YTMQATENY PSVTPMITVE TIYLEAHBRT ALGDQKENHI TTEPAINEKY RYLEGTLDBI AGLVDVDGI NKGCMIHEN NEQGSEINRI NKGCMIHEE YNESFVIPED NAKVKIEQKH	TOWSFKLDGV KHRGILPRAL HPQGVPIKGL LSERKYITSK PPROCKLING DISLARIKE DISLARIKE VGEPBOONPG FKENKSILNE MQMALKPGGS NYLKTMMGLQ 51 GAATTTCCAA	120 180 240 300 360 420 480 540 660 720
50 55 60	LHDASQOLVY QOVPENLES SVHLTSQEED INLVDLAGSE LKDSLGGNCN KELALLKQEL LKOSLGGNCN KELALLKQEL LGVAPPSTKP RRKRASETY LKKQYRSEYQ LKKQYRSEYQ RPGMVPVNR QAHRK Seq ID NO: Nucleic Ac:	11 VRVKKDTODPA ETVAKDVVSQ ETVAKDVVSQ PTHALTVKSQ APSLLFEGET RIGKSGSSG WILVENTNIGE AIHDSLINEN QQEGVESTL GKKAKSKKF HINAIRREID LVSLGEDDQD 309 DNA see id Accession 11 TTITITITAA	21 BEMIRYGDDK ALDGYNGTIM YLEIYMESIM YLEIYMESIM YRIIASHTMN WAGLESTIMS PYTTOPMOSI RRKYTLIDRN REPLRPDTPP YTKRALNYQK YCQHLVQCK KFSQLQQRVL Quence n #: CAT clu TICCTGCTGTTT TIGCCTGAAAAC	ESIDIHLKKD CYGQTGAGKI CYGQTGAGKI DLLGTLPYVG KNSSRSHCIF SLSFLEQAII LRFASRMKLV GIABINSOVR SKPVAFEBFK SLREKGGYE HRLLMEFDIW PEGPDSISFY 11 CATGGTCTGT TATATATGTT	IREGVENICO YTMOGATENY PSVTPMITVE TIYLEAHERT ALGDOKENHI TIEPAINEKY RYLEGTLDEI MEGGSINRI TERCCAGGGT TERCGGGAGGA	TOWSFKLDGV KHRGILPRAL MPQGVFIKGI LSERKYITSK PFRQCKLTHA DAERNYKHA DIISLRQIKE VGEPBOGNE VGEPBOGNE KYENSILNE MQMALKPGGS NYLKTMKLQ	120 180 240 300 360 420 480 540 600 660 720
50 55 60 65	LINDASQOLIVY QOVPRENIES SVHLITSQEED INLVDLAGSB LKDSIGGNUS LKDSIGGNUS LYNDGREVILS LYNDGREVILS LKRGYRESFYQ LREGMVPVNR QAHRK 1	11 VAVKPTDDFA ETVAKOVSQ ETVAKOVSQ PTHAITYWS APSLIPSGET RIGKSGSSGQ MULTWITYGE ATHGSILMNI QQBGBVESTL QQBGBVESTL QQBGBVESTL QQBGBVESTL QDROLLASES IVSLGEDDQD 309 DNA see id Accession 11 TTITITITAA ACCAANGGAA AATAGCAATT	21 BMIRYGDDK ALDOWNOTIM YLEIYNBSI NRILASHTWN VLEXHYSIE, NRILASHTWN VLEXHYSIE, RREYTLIDBN KREGLERDTP YTKEALHFCK KFSQLQQRVL Quence n #: CAT clu TIGCCTGCTGT TIGCCCABAAC AGAGTQAAGA GGCCAGAGGC GCCAGAGGC AGCCCAGAGGC AGGCCAGAGGC AGGCCAGAGGC AGGCCAGAGGC AGGCCAGAGGC AGGCCAGAGGC AGGCCAGAGGC AGGCCAGAGGC AGGCCAGAGC AGCCAGAGC AGGCCAGAGC A	ESIDIHLKKO CYGGYGAGKT CYGGYGAGKT CYGGYGAGKT LLGSTLPYYG KNSSRSHCIF SLSFLEGAL LRPASRMKLU L	IRRGVVNNQQ YTMMGATENY PSVTPMTIVE PSVTPMTIVE TIYLEAHBRT ALGDQKRDBII TTEPAINEN AGLUDVOGGII NEGASINRI NKGLMIIDEE VNESFVIPED NAKVKIEQKB 41 1 CTACCAGGGT CTACCAGGGT CTGGGGAGGA GGTCATTGTG	TOWSFKLDGV KHRGILPRAL HPQGVPIKGL LSERKYITSK PPRQCKLTISK PPRQCKLTSK USEPBOONFG FKENKSILE BFLLILKLKO MGMALKRGS NYLKTMKLQ 51 GAATTTCCAA TAGGCATAGG AATGGATTT	120 180 240 300 360 420 480 540 600 720
50 55 60	LHDASQOLVY QOVPENIER SVHLTSQEED INLVDLAGSB LKDSLGGNCN RELALLKQBL VPNQFRVVLS LGVAPFSTKP RKRAASETTQ LKKQYRSETQ IRPGMVPVNR QAHRK Seq ID NO: Nucleic Aci 1 TITTITITIT AAATITCTQC CACATTQAC CACATTGAC TATTGATTCTC	11 VAVKPTODFA ETVAKOVVŠQ ETVAKOVVŠQ PTHAITVRIV APSLIPPGET RIGKSSBSO MVLTPBITYCE ATHOSIANEI COMPONENTIYCE ACHOSINEI COMPONENTIYCE ACHOSICO 309 DNA see dd Accession 1 TITTETTITAA ATAGCAATTI ACCAAGGAA ACCAAAGGAA ACCAAACGAA ACCAAACCAA CCAA CCAA ACCAAACCAAACCAAACCAAACCAAA ACCAAACCAAACCAAACCAAA ACCAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAA	21 BMIRYGDDK ALLOYNOTIM YLEIYNSEL NILIASHTWI NILIASHT	ESIDIHLEKD CYGGYGAGKI CYGGYGAGKI CYGGYGAGKI CYGGYGAGKI CYGGYGAGKI KISPLOGII LEPASIMKLU LIPASIMKLU LIPASIMKLU LIPASIMKLU LIPASIMKLU EST SIREKOGKYE EST SIREKOGKYE EST SIREKOGKYE EST SIREKOGKYE CATGCTCTGT TATATATGTTT CCACCTCACA TATGGTGTCTGT CCATGCTCTGT TATATATGTTT CCACCTCACA TTGGTGTCTGT	LIBRGUVANOQ YTMOGATENY PSYTPMITUS PSYTPMITUS TIYLEANIST ALGONGDMIL TITERAINEX TITERAINEX TITERAINEX THERGITIDEI ANGUNYUNGHI NOQOSINNI NOGOSINNI NOGOSINNI NOGOMI DEC YMESFVIFED NAKVXIEQUH 41 CTACCAGGGT CTGGGGAGGG GGTCATTGGI CTAGGAGGGG	I TOMSFKLDGV KHRGILPRAL MPQGVPIKGL LSEEKYITSK PFRCCKLTSK PFRCCKLTSK UGEPBOONFG FKENKS LINE EPILLILKG MCMALKFG NYLKTMGLQ I GAATTCCAA TAGGCATAGG AATGGATGTT AATTGCCTCT CTCAACAAAG	120 180 240 300 420 480 540 600 720
50 55 60 65	LHDASQOLLYY QOVPRHIESE SVHLTSQEED INLVOLAGSE LKDSIGGNU VENDFEVILS LKDASPSTVLS LKDASPSTVLS LKRQYRSEV RRKRASETTO LKKQYRSEV REGMVPVNR QAHRK 1	11 VRVKPTDDFA ETVAKOVSQ FTHAITVRVS APSLIFEGET RIGKRSSEGO MULTWHITGE ARESLIFER GTKAKSKETP HIMAIREEL DERDERAELQ 1VSLEEDODD 11 TITTITITIAA ATAGCAATTI AACCAAGGAA AGCAAAGTA AGCAAAGTA AGCAAAGTA AGCAAGTT	21 EMIRYGDDK ALDGYNGTIM YLEIYNSEY NRILIASHTON WIREATTIME ANGLESTLOS REPETALDS YCENTLINES UPON UPON UPON UPON UPON UPON UPON UPON	BSIDIHLKKD CYGOTGAGKT DILGTLEYBYO KYGSRSHCLF LGTLGYBYO KYGSRSHCLF LGTLGYBYO KYGSRSHCLF LGTLGYBYO LGTLGYBY LG	LIRRGYWNNOO YTMGAATENY PSYTPHTIVE PSYTPHTIVE PSYTPHTIVE TTYLEARIST ALGOOXDBIT TTERAINEXY RYLEGTIDEI NRGLAHIEXY RYLEGTIDEI NRGLAHIEXY VERSFYLTED NAKVKIEÇKH 41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	I TOMSFKLDGV KHRGILPRAL HPQGVFIKGL LSEEKYITSK PFRCCKLTHA DAERHVKHLE UGBPBCOMPF STRICKLTHA DAERHVKHLE HPRCCHTHAL HRANG HRANGHE STLLILLKEN HQMALKPGGS NYLKTVØKGLQ 51 GAATTICCAA TAGGCATAGG AATGGATGTT AATTGCCTCA CTCAACAANT	120 180 240 300 420 480 540 660 720
50 55 60 65	LHDASQOLLYY QOVPRHIESE SVHLTSQEED INLVOLAGSE LKDSIGGNU VENDFEVILS LKDASPSTVLS LKDASPSTVLS LKRQYRSEV RRKRASETTO LKKQYRSEV REGMVPVNR QAHRK 1	11 VRVKPTDDFA ETVAKOVVSQ FTHAITVRVS APSLIFFGET RIGKRSSRSO MULTWHITGE ARESLIFER GTKAKSKETP HIMAIREEL LIVALEBOOD 10 JUNEARIO 11 TITTITITIAA ATAGCAATTI AACCAAGGAA AGCAAAGTA AGCAAAGTA AGCAAAGTA AGCAAGTT	21 EMIRYGDDK ALDGYNGTIM YLEIYNSEY NRILIASHTON WIREATTIME ANGLESTLOS REPETALDS YCENTLINES UPON UPON UPON UPON UPON UPON UPON UPON	BSIDIHLKKD CYGOTGAGKT DILGTLEYBYO KYGSRSHCLF LGTLGYBYO KYGSRSHCLF LGTLGYBYO KYGSRSHCLF LGTLGYBYO LGTLGYBY LG	LIRRGYWNNOO YTMGAATENY PSYTPHTIVE PSYTPHTIVE PSYTPHTIVE TTYLEARIST ALGOOXDBIT TTERAINEXY RYLEGTIDEI NRGLAHIEXY RYLEGTIDEI NRGLAHIEXY VERSFYLTED NAKVKIEÇKH 41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	I TOMSFKLDGV KHRGILPRAL HPQGVFIKGL LSEEKYITSK PFRCCKLTHA DAERHVKHLE UGBPBCOMPF STRICKLTHA DAERHVKHLE HPRCCHTHAL HRANG HRANGHE STLLILLKEN HQMALKPGGS NYLKTVØKGLQ 51 GAATTICCAA TAGGCATAGG AATGGATGTT AATTGCCTCA CTCAACAANT	120 180 240 300 420 480 540 660 720
50 55 60 65	LHDASQOLVY QQVFRNIERS SVHLTSQEES SVHLTSQEES SVHLTSQEES LKDSLIGGNGN KELALLAQEL VPNQFRVVLS LKDSLIGGNGN LKDQNPSTKP LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKCQVFSFYQ LKCQVFTQ	11 VEVETIDE A VEVETIDE A VEVETIDE A VEVETIDE A VEVETIDE A VEVETIDE A VETIL A	21	BSIDIHLKKD CYGOYGAGKT DILSTLEYUN KNISKSHCLF SISSTLEGALI LEPASHNKLV GIABINSOVE SISSTLEGALI LEPASHNKLV GIABINSOVE SISSTLEGALI SI	IRRGVVNNQQ YTMGARENY PSYTPMTIVE PSYTPMTIVE TYYLEARISH ALGOQUADIT TTERAHISET MOLOGUADIT TERAHISET MOLOGUADIT MOLOGUADIT TERAHISET VERSFVIPED NAKVKIEQKEI 1 CTACCAGGAT CTAGGAGGA CTAGGAGGA AGARACACA TCTTTAGGAGG CCCATTANAA	TOWSFKLDGV KHRGILDRAL NRGQVFJKGL LSEEKYITSK PFRQCKUTISK DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE SPLLILILIU NQNALKRGGS NYLKTHONGLQ 51 GANTTICCAA ANGGRAYOT ANGGRAYOT CTCMCALAGA CTCATHOL TCTGCTTCAA	120 180 240 300 420 480 540 660 720
50 55 60 65 70	LHDASQOLVY QQVFRNIERS SVHLTSQEES SVHLTSQEES SVHLTSQEES LKDSLIGGNGN KELALLAQEL VPNQFRVVLS LKDSLIGGNGN LKDQNPSTKP LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKKQVFSFYQ LKCQVFSFYQ LKCQVFTQ	11 VEVETIDE A VEVETIDE A VEVETIDE A VEVETIDE A VEVETIDE A VEVETIDE A VETIL A	21 EMIRYGDDK ALDGYNGTIM YLEIYNSEY NRILIASHTON WIREATTIME ANGLESTLOS REPETALDS YCENTLINES UPON UPON UPON UPON UPON UPON UPON UPON	BSIDIHLKKD CYGOYGAGKT DILSTLEYUN KNISKSHCLF SISSTLEGALI LEPASHNKLV GIABINSOVE SISSTLEGALI LEPASHNKLV GIABINSOVE SISSTLEGALI SI	IRRGVVNNQQ YTMGARENY PSYTPMTIVE PSYTPMTIVE TYYLEARISH ALGOQUADIT TTERAHISET MOLOGUADIT TERAHISET MOLOGUADIT MOLOGUADIT TERAHISET VERSFVIPED NAKVKIEQKEI 1 CTACCAGGAT CTAGGAGGA CTAGGAGGA AGARACACA TCTTTAGGAGG CCCATTANAA	TOWSFKLDGV KHRGILDRAL NRGQVFJKGL LSEEKYITSK PFRQCKUTISK DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE SPLLILILIU NQNALKRGGS NYLKTHONGLQ 51 GANTTICCAA ANGGRAYOT ANGGRAYOT CTCMCALAGA CTCATHOL TCTGCTTCAA	120 180 240 300 420 480 540 660 720
50 55 60 65	LIDASGOLYY QOYPENLERS SYELTSQEED INIVOLAGES LIDBILOGNET SYELTSQEED LIDBILOGNET SYELTSQEED LIDBILOGNET LIVELSGEE LIDBILOGNET LIVELSGEE L	11 YNYEPTODPA YNYEPTOD	21 IBHINYDDOR ALDONATUR ALDONATUR YERI YINSELP NIKILASHIVA YERI YINSELP NYITINGER YITINYDDOR ARGUSTISS YYTINYDDOR ARGUSTISS YYTINYDDOR ARGUSTISS YYTINYDDOR ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARGUSTISS ARTUSCETTAT TIGGARTITIT TIGGART TIGGART TIGGART TIGGART TIGGART TIGGART TIGGART TIGGART	BEIDIHLAND CYGGYGAGIC DILBTLBYDY SISSEBECLIF SISSEBECLIF SISSEBECLIF SISSEBECLIF GIABLE GIABLE GIABLE SISSEBECLIF SISSEBECLIF SISSEBECRIF	IRRGVVNNQQ YTMGARENY PSYTPMTIVE PSYTPMTIVE TYYLEARISH ALGOQUADIT TTERAHISET MOLOGUADIT TERAHISET MOLOGUADIT MOLOGUADIT TERAHISET VERSFVIPED NAKVKIEQKEI 1 CTACCAGGAT CTAGGAGGA CTAGGAGGA AGARACACA TCTTTAGGAGG CCCATTANAA	TOWSFKLDGV KHRGILDRAL NRGQVFJKGL LSEEKYITSK PFRQCKUTISK DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE SPLLILILIU NQNALKRGGS NYLKTHONGLQ 51 GANTTICCAA ANGGRAYOT ANGGRAYOT CTCMCALAGA CTCATHOL TCTGCTTCAA	120 180 240 300 420 480 540 660 720
50 55 60 65 70	LHDASGOLYY QOVPENLESS SYBLISGES INIAVDIAGS INIAVDIA	11 YRYKOTODPA FEVALOWSO PTHAITVRVS AFSLLFSGIT RUGKSSSGO WHITE RUGKSSSGO RUGKSSKIT RUGKSSSGO RUGKSSKIT RUGKSSGO RUGKSSGO RUGKSSGO RUGKSSGO RUGKSSGO RUGKSSGO RUGKSSGO RUGKSGO R	21 EBHIRYGIDER HENTENGENER HEN	BEIDIHLAND CYGGYGAGIC DILBTLBYDY SISSEBECLIF SISSEBECLIF SISSEBECLIF SISSEBECLIF GIABLE GIABLE GIABLE SISSEBECLIF SISSEBECLIF SISSEBECRIF	IRRGVVNNQQ YTMGARENY PSYTPMTIVE PSYTPMTIVE TYYLEARISH ALGOQUADIT TTERAHISET MOLOGUADIT TERAHISET MOLOGUADIT MOLOGUADIT TERAHISET VERSFVIPED NAKVKIEQKEI 1 CTACCAGGAT CTAGGAGGA CTAGGAGGA AGARACACA TCTTTAGGAGG CCCATTANAA	TOWSFKLDGV KHRGILDRAL NRGQVFJKGL LSEEKYITSK PFRQCKUTISK DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE SPLLILILIU NQNALKRGGS NYLKTHONGLQ 51 GANTTICCAA ANGGRAYOT ANGGRAYOT CTCMCALAGA CTCATHOL TCTGCTTCAA	120 180 240 300 420 480 540 660 720
50 55 60 65 70	LHDASGOLYY QOVPENLESS SYBLISGES INIAVDIAGS INIAVDIA	11 YNYEPTODPA YNYEPTOD	21 EBHIRYGIDER HENTENGENER HEN	BEIDIHLAND CYGGYGAGIC DILBTLBYDY SISSEBECLIF SISSEBECLIF SISSEBECLIF SISSEBECLIF GIABLE GIABLE GIABLE SISSEBECLIF SISSEBECLIF SISSEBECRIF	IRRGVVNNQQ YTMGARENY PSYTPMTIVE PSYTPMTIVE TYYLEARISH ALGOQUADIT TTERAHISET MOLOGUADIT TERAHISET MOLOGUADIT MOLOGUADIT TERAHISET VERSFVIPED NAKVKIEQKEI 1 CTACCAGGAT CTAGGAGGA CTAGGAGGA AGARACACA TCTTTAGGAGG CCCATTANAA	TOWSFKLDGV KHRGILDRAL NRGQVFJKGL LSEEKYITSK PFRQCKUTISK DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE DAESHVRNIE SPLLILILIU NQNALKRGGS NYLKTHONGLQ 51 GANTTICCAA ANGGRAYOT ANGGRAYOT CTCMCALAGA CTCATHOL TCTGCTTCAA	120 180 240 300 420 480 540 660 720
50 55 60 65 70 75	LHDASGOLYY QOVPENLESS SYBLISGES INIAVDIAGS INIAVDIA	11 YEVENTODPA SETVAROWSO PTHAITVEVS AVSILEPESIT RUGHSSSBOO WILVETTURE RUGHSSSBOO RUGHSTIT RUGHSSSBOO RUGHSTIT RUGHSSBOO RUGHSTIT RUGHSSBOO RUGHSSTIT RUGHSSBOO RUGHSSEN RUGHSSBOO RUGHSSEN RUGHSSBOO	Z1 IEMIRYGDDR ALDONNTIN YEMINSLE NIKINSTEM YEMINSLE NIKINSTEM YEMINSLE NIKINSTEM RERYTIME RER	BEIDIHLAND CYGOYGAGIC DILGTILAYU NISSERBICIF LISTORY NISSERBICIF NISSERBICIF NISSERBICIF DEPARIBACIO OTABLISOVA DEPARIBACIO SERPANBERIO SERPANBERIO SERPANBERIO SERPANBERIO SERPANBERIO SERPANBERIO SERPANBERIO SERPANBERIO SERPENBERIO SE	IRRGVVNNQQ YTHOGANESY PROTECTIVE TYPERISH TIYL	I TWEFFELDOW RESULTABLE IN THE STATE OF THE	120 180 240 300 420 480 540 660 720
50 55 60 65 70	LHDASGOLVY QOVPENLERS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS LGYAPESTEP REMONISTIC LGYAPESTEP REMONISTIC LGYAPESTEP SVELTSGESS LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPET LGYAPE	11 VRWRYTODPA FETVAROVVSO PTHALTVRVS APSILEPESET FETVAROVVSO PTHALTVRVS APSILEPESET REVIAROVVSO HOLIVITYORS AVELEPESET REVIAROVE REVIAROVE REVIAROVE AVELEPESET REVIAROVE 10 DIR DIA BER 11 11 11 11 11 11 11 11 11 11 11 11	21 EBHIRYGDOR ALDONOTIN FINELLY FINELL FINELLY FINELLY FINELLY FINELLY FINELLY FINELLY FINELLY FINELLY	BSIDIHLEND CYGOYGAGGT CHOCOTOGY CYGOYGAGGT CHOCOTOGY C	IRRGVVINOQUE TERGVVINOQUE TERGVVINOQUE TERGVINOQUE TER	I TOWNSPELLORY RIBGILLERAL RECOVERISE PROCESTING PROCES	120 180 240 300 360 480 660 660 720 60 120 180 300 360 420 480
50 55 60 65 70 75	LHDASGOLVY QOVPENLERS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS SVELTSGESS LGYAPESTEP REMONISTIC LGYAPESTEP REMONISTIC LGYAPESTEP SVELTSGESS LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPESTEP LGYAPET LGYAPE	11 VRWRYTODPA FETVAROVVSO PTHALTVRVS APSILEPESET FETVAROVVSO PTHALTVRVS APSILEPESET REVIAROVVSO HOLIVER MYLVEDTIVGR AVELEPESET REVIAROVE AVELEPESET REVIAROV 10 DIA DIA SE 11 11 11 11 11 11 11 11	21 EBHIRYGDOR ALDONOTIN FINELLY FINELL FINELLY FINELLY FINELLY FINELLY FINELLY FINELLY FINELLY FINELLY	BSIDIHLEND CYGOYGAGGT CHOCOTOGY CYGOYGAGGT CHOCOTOGY C	IRRGVVINOQUE TERGVVINOQUE TERGVVINOQUE TERGVINOQUE TER	I TOWNSPELLORY RIBGILLERAL RECOVERISE PROCESTING PROCES	120 180 240 300 360 480 660 660 720 60 120 180 300 360 420 480
50 55 60 65 70 75	LHDASGOLYY OVYPENLERS SYRLINGARE	11 YRIGHTODPA ETVARDIVOS PTHALTIVRUS APSILEPESIE RIGHESISTO RIGHES	21 EBHENYODER REMERYODER REMERYOD	BEIDIHLERO GYOGYOLOGI GYOTOCH GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOTOCI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOTOCH GYOGYOLOGI GYOGYOLOGI GYOTOCI GYOGYOLOGI GYOGYOLOGI GYOGYOLOGI GYOTOCI GYOGYOLOGI GYOTOCI GYOGYOLOGI GYOTOCI LERGYVENGO TERGON TO THE CONTROL TO	I TUMP FELDOW KIRKOLL PRALL LESERY LISE AND PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF T	120 180 240 300 420 480 540 660 720	
50 55 60 65 70 75 80	LHDASGOLYY QUYPENLESS SYRLTSGESS SYRLTSGESS SYRLTSGESS SYRLTSGESS SYRLTSGESS SYRLTSGESS LUSIAGENT LUSIAGE	11 VRWRYDDPA ETVAKOWSO PTHAITVRVS APSILEPEUE PTHAITVRVS APSILEPEUE ROUNTSIT	21 EBHIRYGDOR REMIRYGDOR REMIRYGD	STATEMENT	IRRGVVINCO YTHMOATENY PROVINCE YTHMOATENY PROVINCE YTHMOATENY PROVINCE YTHMOATENY YTHMOATEN ALGOROGE A	TOWN PELLOC TOWN PELLOC TOWN PELLOC TOWN PELLOC TOWN PELCOC TOWN PELCOC TOWN PERCOCATION PERCOCATION PERCOCATION PERCOCATION PERCOCATION PELCOCATION PERCOCATION PELCOCATION P	120 180 240 300 360 420 480 660 720 120 180 300 420 480
50 55 60 65 70 75	LHDASGOLYY QUYPENLESS SYRLTSGESS SYRLTSGESS SYRLTSGESS SYRLTSGESS SYRLTSGESS SYRLTSGESS LUSIAGENT LUSIAGE	11 VRWRYDDPA ETVAKOWSO PTHAITVRVS APSILEPEUE PTHAITVRVS APSILEPEUE ROUNTSIT	21 EBHIRYGDOR REMIRYGDOR REMIRYGD	STATEMENT	IRRGVVINCO YTHMOATENY PROVINCE YTHMOATENY PROVINCE YTHMOATENY PROVINCE YTHMOATENY YTHMOATEN ALGOROGE A	TOWN PELLOC TOWN PELLOC TOWN PELLOC TOWN PELLOC TOWN PELCOC TOWN PELCOC TOWN PERCOCATION PERCOCATION PERCOCATION PERCOCATION PERCOCATION PELCOCATION PERCOCATION PELCOCATION P	120 180 240 300 360 420 480 660 720 120 180 300 420 480
50 55 60 65 70 75 80	LHDASGOLYY OVYPERLEBEN SOVERHIEBEN NINVELLAGEN NINVEL	11 VRWRTDDFA ETVAKOWSO PTHAITURUS AFSILEFESIE FYNKOWSO PTHAITURUS AFSILEFESIE RESULEFESIE	21 EBHIRYGDOR ALDONOTIN THE INNSUF NEIL IN	BEIDIELERO CROGOTOCHO RESIDIELERO RESIDIEL	LERGYVENOG THE RESTRICT OF THE	I TUMP FELDOW KIRKOLL PRALL LESERY LISE AND PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF T	120 120 240 300 360 420 480 660 720 120 120 130 420 480

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		TGAAATCCAG	GGTCCAGAGT	TATTTTGATG	GTATAAAAGC	TGATTGGTTG	420
	GATAGCATAA	GACCACAAAA	AGAAGGAGAC	TTCAGAAAGG	AGATTAACAA	GTGGTGGAAT	480
		ATGGCCAGCG	GACTGTGACA	GGTATTATAG	CTGCAAATGT	CCTTGTATTC	540
5		GAGTACCITC	TCTGCAGCGG	ACAATGATCA	GATATTTCAC	ATCGAATCCA	600
,	GCCTCAAAGG	TCCTTTGTTC	TCCAATGTTG	CTGTCAACAT	CCAGCATAGT	CARCATTCTC	660 720
		AGTTCATGGC	AGTGTACCTA	TCTGCAGGTG	TTATTTCCAA	TTTTGTCAGT	780
		AAGTTGCCAC	AGGAAGATAT	GGACCATCAC	TTGGTGCATC		840
	ATGACAGTCC	TCGCAGCTGT	CTGCACTAAG	ATCCCAGAAG	GGAGGCTTGC	CATTATTTTC	900
10	CTTCCGATGT		AGCAGGGAAT	GCCCTGAAAG	CCATTATCGC	CATGGATACA	960
	GCAGGAATGA		GAAATTTTTT	GATCATGCGG GAACTGATTT	CACATCTTGG	GGGAGCTCTT	1020
	TTTGGAATAT	GGTATGTTAC GGCATGAAAT	TTACGGTCAT	GGCCCCAAAA	AAGGAGGTGG	CTCTBACTAR	1080
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	Seq ID NO:	311 Protein	sequence:				
	Protein Ac	cession #: N	IP_061092.2				
	1	11	21	31	41	51	
20	ī	ı	ī	Ĩ-	Ī	î .	
	MANRGWAQRG	WGCGQAWGAS	VGGRSCEELT	AVLTPPQLLG	RRFNFFIQQK	CGFRKAPRKV	60
		GEAYKRSALI	PPVEETVPYP	SPYPIRSLIK	PLFFTVGFTG	CAFGSAAIWQ	120
	YESLKSRVQS	YFDGIKADWL TMIRYPTSNP	ASKVLCSPML	PRKEINKWWN	NLSDGQRTVT HMAANMYVLW		180 240
25	CONKVPSIQR	SAGVISNEVS	VIGKUATGRY				300
	LPMPTPTAGN	ALKAIIAMDT	AGMILGWEFF	DHAAHLGGAL	PGIWYVTYGR	ELIWKNREPL	360
	VKIWHEIRTN	GPKKGGGSK					
30	Seq ID NO:	312 DNA 880	ruence				
30	Nucleic Ac	id Accession uence: 195	1 #: NM_0000	25			
	couring seq	dence: 195.	3030				
35	1	11	21 .	31	41	51	
33	CTCTCGGCCA	CCTTTGATGA	occurences	CAGTTCTAGA	CACTYCCCCAA	GTTCTCAAGG	60
	CACAGGTCTC	TTCCTGGTTT	GACTGTCCTT	ACCCCGGGGA	GGCAGTGCAG	CCAGCTGCAA	120
	GCCCCACAGT	GAAGAACATC	TGAGCTCAAA	TCCAGATAAG	TGACATAAGT	GACCTGCTTT	180
40		AGAGATGGCC			CAAGACCAAA	TTCCACCAGT	240
40	ATGCAATGAA		GGCATCAACA		GAAAGCCCCCC	TGTGCCACCT	300 360
	CCAGTCCAGT	GACACAGGAT CCTCGTGGAG	GACCTTCAGT ACGGGAAAGA	ATCACAACCT AGTCTCCAGA		CAGAATGAGT	420
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	CAGATGAGCT	TCTACCTCAA	GCTATCGAAT		ATATTACGGC	TCCCTCAAAG	660 720
	AGGCAAAAAT	AGAGGAACAT	CTGGCCAGGG	TGGAAGCGGT	AACAAAGGAG	CCCTCCCCCA	720
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50	GCTGTTCCAC	TGCCCGGGAA	ATGITTGAAC	ACATCTGCAG	ACACGTGCGT	TACTCCACCA	900
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	ACTTCCGGGT	GTGGAATGCT	CAGCTCATCC	GCTATGCTGG	GTGCATCGAC	CCAGATGGCA	1020
	ACCCCAACTA	CGGCCGCTTC	CATGTGGTCC	CCCTGGTCCT	GCAGGCCAAT	GGCCGTGACC	1140
55		CGAAATCCCA		TGCTTGAGGT	GGCCATGGAA	CATCCCAAAT	1200
	ACGAGTGGTT	TCGGGAACTG	GAGCTAAAGT	GGTACGCCCT	GCCTGCAGTG	GCCAACATGC	1260
	TGCTTGAGGT	GGGCGGCCTG	GAGTTCCCAG	GGTGCCCCTT	CAACATCCTG	TACATGGGCA GAGGAAGTGG	1320 1380
		AGTCCGGGAC GGGCCTGGAA			CTGGAAAGAC	CAGGCTGTCG	1440
60	TTGAGATCAA	CATTGCTGTG	CTCCATAGTT	TCCAGAAGCA		ATCATGGACC	1500
	ACCACTOGGC	TGCAGAATCC	TTCATGAAGT	ACATGCAGAA	TGAATACCGG	TCCCGTGGGG	1560
	GCTGCCCGGC	AGACTGGATT	TGGCTGGTCC	CTCCCATGTC	TGGGAGCATC	ACCCCCGTGT	1620
		GATGCTGAAC	TACGTCCTGT	CCCCTTTCTA	CTACTATCAG GAGAAGAGAG	GTAGAGGCCT	1680 1740
65		CAAAGCTGTG		GTATGCTGAT	GCGCAAGACA	ATGGCGTCCC	1800
	GAGTCAGAGT	CACCATCCTC	TTTGCGACAG	AGACAGGAAA	ATCAGAGGCG	CTGGCCTGGG	1860
	ACCTGGGGGC	CTTATTCAGC	TGTGCCTTCA	ACCCCAAGGT	TGTCTGCATG	GATAAGTACA	1920
	GGCTGAGCTG	CCTGGAGGAG			GACCAGTACG	TTTGGCAATG	1980 2040
70	GAGACTGCCC ACAACAAATT	TGGCAATGGA CAGGTACGCT	GAGAAACTGA		CATGTACCCT	CGGTTCTGCG	2100
,,,		TGACATTGAT			GGCCTCTCAG	CTCACCCCGA	2160
	TGGGAGAAGG	GGATGAGCTC	AGTGGGCAGG	AGGACGCCTT	CCGCAGCTGG	GCCGTGCAAA	2220
			ACGTTTGATG		ACAGCACATT	CAGATCCCCA	2280
75	AGCTCTACAC	CTCCAATGTG	ACCTGGGACC GCCCTCAGCA		CAGGCTCGTG	CAGGACTCAC	2340 2400
13		TOGGCAGAAT	CTACAAAGTC			ATCCTGGTGG	2460
	AACTCTCCTG	TGAGGATGGC	CAAGGCCTGA	ACTACCTGCC	GGGGGAGCAC	CTTGGGGTTT	2520
		CCAGCCGGCC		GCATCCTGGA	GCGAGTGGTG	GATGGCCCCA	2580
80		GGCAGTGCGC	CTGGAGGCCC	TGGATGAGAG	TGGCAGCTAC	TGGGTCAGTG GACATCACCA	2640 2700
δU		CCACCTCCTGC	TCACTCAGCC		GGCCACAGAA		2700 2760
		GGAGGCCCTG	TGCCAGCCCT	CAGAGTACAG	CAAGTGGAAG	TTCACCAACA	2820
	GCCCCACATT	CCTGGAGGTG	CTAGAGGAGT	TCCCGTCCCT	GCGGGTGTCT	GCTGGCTTCC	2880
0.5		GCTCCCCATT	CTGAAGCCCA		CATCAGCTCC	CCCCGGGATC	2940
85	ACACGCCCAC		CTGACTGTGG		CTACCACACC	CCCCAAGACC	3000 3060
	AGGGTCCCCT	GCACCACGGC CTTTGTGCGG	GTCTGCAGCA	GCTTCCACCT	CCCCGAGGAY	CCCTCCCATC	3120
				_ ,			

	GGCTCCATGA	CTCCCAGCAC	AAGGGAGTGC	GGGGAGGCCG	CATGACCTTG	GTGTTTGGGT	3240
	GCCGCCGCCC	AGATGAGGAC	CACATCTACC	AGGAGGAGAT	GCTGGAGATG	GCCCAGAAGG	3300
	GGGTGCTGCA	TGCGGTGCAC	ACAGCCTATT	CCCGCCTGCC	TGGCAAGCCC	AAGGTCTATG	3360
5	TTCAGGACAT	CCTGCGGCAG	CAGCTGGCCA	GCGAGGTGCT	CCGTGTGCTC	CACAAGGAGC	3420
-	CAGGCCACCT	CTATGITTGC	GGGGATGTGC	GCATGGCCCG	GGACGTGGCC	CACACCCTGA	3480
	AGCAGCTGGT	GGCTGCCAAG	CTGAAATTGA	ATGAGGAGCA	GGTCGAGGAC	TATTTCTTTC	3540
	AGCTCAAGAG	CCAGAAGCGC	TATCACGAAG	ATATCTTTGG	TGCTGTATTT	CCTTACGAGG	3600
	CGAAGAAGGA	CAGGGTGGCG	GTGCAGCCCA	GCAGCCTGGA	GATGTCAGCG	CTCTGAGGGC	3660
10	CTACAGGAGG	GGTTAAAGCT	GCCGGCACAG	AACTTAAGGA	TGGAGCCAGC	TCTGCATTAT	3720
	CTGAGGTCAC	AGGGCCTGGG	GAGATGGAGG	AAAGTGATAT	CCCCCAGCCT	CAAGTCTTAT	3780
	TTCCTCAACG	TTGCTCCCCA	TCAAGCCCTT	TACTTGACCT	CCTAACAAGT	AGCACCCTGG	3840
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15 seq ID NO: 313 Protein sequence: Protein Accession #: NP_000616

,		1	11	21	31	41	51	
-	20	MACDWKEI'EK	TKFHQYAMNG	RKGTNNNVEK	APCATSSPVT	ODDLOYHNLS	KQQNESPQPL	60
		VETCHKEPES	LUKLDATPLS	SPRHVRIKNW	GSGMTFQDTL	HHKAKGILTC	RSKSCLGSIM	120
		TRESTARGER	DEPTPPDELL	POAIBPVNOY	YGSLKEAKIE	EHLARVEAVT	KEIETTVTYQ	180
		LTCDELTEAT	KQAWRNAPRC	TGRTOWSNLO	VFDARSCSTA	REMPEHICRE	VRYSTNNGNI	240
	25	PRATTUDDOD	SDGKKIDPRVW	NAOLTRYAGY	OMPDGSIRGD	PANVEFTQLC	IDLGWKPKYG	300
•		DEDVALATO	ANGROPELFE	IPPOLVLEVA	MEHPKYEWPR	ELELKWYALP	AVANMLLEVG	360
		CLER DOCUMEN	CMYMGTRIGV	RDFCDVORYN	ILEEVGRRMG	LETHKLASLW	KDQAVVEINI	420
		AVIJESPOKON	VTIMDHHSAA	RSFMKYMONE	YRSRGGCPAD	WIWLVPPMSG	SITPVPHQEM	480
		LMVUL-SPRYY	YOURAWKTRY	WODEKRRPKR	REIPLKVLVK	AVLFACMLMR	KTMASRVRVT	540
- 1	30	TI-PATETCKS	EALAWDLGAL	PSCAPNPKVV	CMDKYRLSCL	EEERLLLVVT	STEGNGDCPG	600
		NORKT-KKST-P	MIJKELNNKPR	YAVFGLGSSM	YPRFCAFAHD	IDOKLSHLGA	SQLTPMGEGD	660
		ELSGORDAFR	SWAVOTEKAA	CETFDVRGKO	HIGIPKLYTS	NVTWDPHHYR	LVQDSQPLDL	720
		· GKAT-SCMHAK	NUPTMRLKSR	ONLOSPIESR	ATILVELSCE	DGOGLNYLPG	EHLGVCPGNQ	780
		PALVOGILER	VVDGPTPHOA	VRLEALDESG	SYWVSDKRLP	PCSLSQALTY	PLDITTPPTQ	840
	35	TATACKLACVA	TERPERORLE	ALCOPSEYSK	WKFTNSPTFL	EVLEEPPSLR	VSAGPLLSQL	900
		DILEPREVAT	SSPRDHTPTE	IHLTVAVVTY	HTRDGOGPLH	HGVCSTWLNS	LKPQDPVPCF	960
		VENASGEHLP	RDPSHPCILI	GPGTGIAPPR	SPWQQRLHDS	QHKGVRGGRM	TLVPGCRRPD	1020
		EDIT LAUERNI	EMAQKGVLHA	VHTAYERLPG	KPKVYVODIL	ROOLASEVLR	VLHKEPGHLY	1080
		VCGDVRMARD	VAHTLKQLVA	AKLKLNEEOV	EDYFFOLKSO	KRYHEDI FGA	VPPYBAKKDR	1140
	40	VAVOPSSLEM						

Seq ID NO: 314 DNA sequence Nucleic Acid Accession #: XM_087254 Coding sequence: 47..2332

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	1	11	21	31	41	51	
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	AGAGTACCTG	TTTACAGATA	AAACTGGTAC	ACTGACAGAA	AATGAGATGC	AGTTTCGGGA	60
50	ATCTTCAATT	AATGGCATGA	AATACCAAGA	AATTAATGGT	AGACTTGTAC	CCGAAGGACC	120
	AACACCAGAC	TCTTCAGAAG	GAAACTTATC	TTATCTTAGT	AGTTTATCCC	ATCTTAACAA	180
	CTTATCCCAT	CTTACAACCA	GTTCCTCTTT	CAGAACCAGT	CCTGAAAATG	AAACTGAACT	240
	AATTAAAGAA	CATGATCTCT	TCTTTAAAGC	AGTCAGTCTC	TGTCACACTG	TACAGATTAG	300
	CAATGTTCAA	ACTGACTGCA	CTGGTGATGG	TCCCTGGCAA	TCCAACCTGG	CACCATCGCA	360
55	GTTGGAGTAC	TATGCATCTT	CACCAGATGA	AAAGGCTCTA	GTAGAAGCTG	CTGCAAGGAT	420
	TGGTATTGTG	TTTATTGGCA	ATTCTGAAGA	AACTATGGAG	GTTAAAACTC	TTGGAAAACT	480
	GGAACGGTAC	AAACTGCTTC	ATATTCTGGA	ATTTGATTCA	GATCGTAGGA	GAATGAGTGT	540
	AATTGTTCAG	GCACCTTCAG	GTGAGAAGTT	ATTATTTGCT	AAAGGAGCTG	AGTCATCAAT	600
	TCTCCCTAAA	TGTATAGGTG	GAGAAATAGA	AAAAACCAGA	ATTCATGTAG	ATGAATTTGC	660
60	TTTGAAAGGG	CTAAGAACTC	TGTGTATAGC	ATATAGAAAA	TTTACATCAA	AAGAGTATGA	720
	GGAAATAGAT	AAACGCATAT	TTGAAGCCAG	GACTGCCTTG	CAGCAGCGGG	AAGAGAAATT	780
	GGCAGCTGTT	TTCCAGTTCA	TAGAGAAAGA	CCTGATATTA	CTTGGAGCCA	CAGCAGTAGA	840
	AGACAGACTA	CAAGATAAAG	TTCGAGAAAC	TATTGAAGCA	TTGAGAATGG	CTGGTATCAA	900
	AGTATGGGTA	CTTACTGGGG	ATAXACATGA	AACAGCTGTT	AGTGTGAGTT	TATCATGTGG	960
65	CCATTTTCAT	AGAACCATGA	ACATCCTTGA	ACTTATAAAC	CAGAAATCAG	ACAGCGAGTG	1020
	TGCTGAACAA	TTGAGGCAGC	TTGCCAGAAG	AATTACAGAG	GATCATGTGA	TTCAGCATGG	1080
	GCTGGTAGTG	GATGGGACCA	GCCTATCTCT	TGCACTCAGG	GAGCATGAAA	AACTATTTAT	1140
	GGAAGTTTGC	AGAAATTGTT	CAGCTGTATT	ATGCTGTCGT	ATGGCTCCAC	TGCAGAAAGC	1200
	AAAAGTAATA	AGACTAATAA	AAATATCACC	TGAGAAACCT	ATAACATTGG	CTGTTGGTGA	1260
70	TGGTGCTAAT	GACGTAAGCA	TGATACAAGA	AGCCCATGTT	GGCATAGGAA	TCATGGGTAA	1320
	AGAAGGAAGA	CAGGCTGCAA	GAAACAGTGA	CTATGCAATA	GCCAGATTTA	AGTTCCTCTC	1380
	CAAATTGCTT	TTTGTTCATG	GTCATTTTTA	TTATATTAGA	ATAGCTACCC	TTGTACAGTA	1440
	TITTTTTTAT	AAGAATGTGT	CCTTTATCAC	ACCCCAGTTT	TTATATCAGT	TCTACTGTTT	1500
	GTTTTCTCAG	CAAACATTGT	ATGACAGOGT	GTACCTGACT	TTATACAATA	TTTGTTTTAC	1560
75	TTCCCTACCT	ATTCTGATAT	ATAGTCTTTT	GGAACAGCAT	GTAGACCCTC	ATGTGTTACA	1620
	AAATAAGCCC	ACCCTTTATC	GAGACATTAG	TARARACCGC	CTCTTAAGTA	TTAAAACATT	1680
	TCTTTATTGG	ACCATCCTGG	GCTTCAGTCA	TGCCTTTATT	TTCTTTTTTG	CATCCTATTT	1740
	ACTARTAGGG	AAAGATACAT	CTCTGCTTGG	AAATGGCCAG	ATGTTTGGAA	ACTGGACATT	1800
	TGGCACTTTG	GTCTTCACAG	TCATGGTTAT	TACAGTCACA	GTAAAGATGG	CTCTGGAAAC	1860
80	TCATTTTTGG	ACTTGGATCA	ACCATCTOGT	TACCTGGGGA	TCTATTATAT	TTTATTTTGT	1920
	ATTTTCCTTG	TTTTATGGAG	GGATTCTCTG	GCCATTTTTG	GGCTCCCAGA	ATATGTATTT	1980
	TGTGTTTATT	CAGCTCCTGT	CAAGTGGTTC	TGCTTGGTTT	GOCATAATCC	TCATGGTTGT	2040
	TACATGTCTA	TTTCTTGATA	TCATAAAGAA	GGTCTTTGAC	CGACACCTCC	ACCCTACAAG	2100
	TACTGAAAAG	GCACAGCTTA	CTGAAACAAA	TGCAGGTATC	AAGTGCTTGG	ACTCCATGTG	2160
85	CTGTTTCCCG	GAAGGAGAAG	CAGCGTGTGC	ATCTGTTGGA	AGAATGCTGG	AACGAGTTAT	2220
	AGGAAGATGT	AGTCCAACCC	ACATCAGCAG	ATCATGGAGT	GCATCGGATC	CTTTCTATAC	2280
	CAACGACAGG	AGCATCTTGA	CTCTCTCCAC	AATGGACTCA	TCTACTTGTT	AAAGGGGCAG	2340

	WO 02/	096443					
	TAGTACTTIG	TGGGAGCCAG	TTCACCTCCT	TTCCTAAAAT	TCAGTGTGAT	CACCCTGTTA	2400
	ATGGCCACAC '	TAGCTCTGAA	ATTAATTTCC	AAAATCTTTG	TAGTAGTTCA	TACCCACTCA	2460
	GAGTTATAAT	GGCAAACAAA	CAGAAAGCAT	TAGTACAAGC	CCCTCCCAAC	ACCCTTAATT	2520
-	TGAATCTGAA	CATGTTAAAA	TTTGAGAATA	AAGAGACATT	TTTCATCTCT	TIGICIGGII	2580
5	TGTCCCTTGT	GCTTATGGGA	CTCCTAATGG	CATTTCAGTC	TGTTGCTGAG	GCCATTATAT	2640 2700
	TTTAATATAA	ATGTAGAAAA	AAGAGAGAAA	TCTTAGTAAA	TATCCTCAAA	arrracerra	2760
	ACRACTORAT	TTTTTTTTATTA	TTAAATCTGC GAGTTATATT	TAAAGCTTTT	CATGGGAAAA	GTTAATGTGA	2820
	ATACTGAGGA	ATTTTTGGTCC	CTCAGTGACC	TGTGTTGTTA	ATTCATTAAT	GCATTCTGAG	2880
10	TTCACAGAGC	ABATTAGGAG	COTTTACTAG	TTATTATO	TACTGCAGTA	TGGGGAGTAA	2940
	ATTTATACCA	ATTCCTCTAA	CTGTACTGTA	ACACAGCCTG	TARAGTTAGC	CATATAAATG	3000
	CAAGGGTATA	TCATATATAC	AAATCAGGAA	TCAGGTCCGT	TCACCGAACT	TCAAATTGAT	3060
	GTTTACTAAT	ATTTTTGTGA	CAGAGTATAA	AGACCCTATA	GTGGGTAAAT	TAGATACTAT	3120 3180
15	TAGCATATTA	TTAATTTAAT	GTCTTTATCA TTTCTCTTTA	TIGGATCTIT	TUCATUCTTT	MATCIGGITA	3240
13	ACATATTTAA	ATTIGCTTT	ATATCAATAA	ANACTORIGGE	CAGTATTTAA	ATATTGCAAA	3300
	TATCTTTAAT	TATACASATC	AGANTAGTAT	GGGTAATTAA	ATGAATACAA	AAAGAAGAGC	3360
	CHAMPINET	AGCCGACTTA	GACATGCTCT	TCCCTTTCTA	TAAGCTAGAT	TTTAGAATAA	3420
	AGGGTTTCAG	TTAATAATYT	TATTTTCAGG	TTATGTCATC	TAACTTATAG	CAAACTACCA	3480
20	CAATACAGTG	AGTTCTGCCA	GTGTCCCAGT	ACAAGGCATA	TTTCAGGTGT	GGCTGTGGAA	3540
	TYPERALAMENT	CTCAACTTCT	ATCAGGTAAT	CTTAGCAATA	AATTAAATGC	TAAGAATGAT	3600 3660
	TAATCGGGTA	CATGTTACTG	TAATTAACTC	ATTGCACTTC	TATTGAAAAG	TTCCATCCTG	3720
	AATTTATCAA	GTAGTTCAGT	ATTGTCATTT TTAGCTTGAG	GTITTIGTT	CRECTOTRAG	CARACTERICA	3780
25	MONOTER TRACET	ATTA ACATA A	TYZGTTT A A TYZ	CCCTTTTACC	MAGTTTTCCC	TTGAAAATGT	3840
	AATTCCTTTA	TGGAGATTTA	TTGTGCAGCC	CTAAGCTTCC	TTCCCATTTC	ATGAATATAA	3900
							3960
	CTTGTTTGCT	TOTABACTAT	TATTTTCTTG	CTAATGTAAC	ATTTGTCTGT	TCCAGTGATG	4020
20	TANGGATATT	AAGTTATTAA	GCTAAATATT	AATTTTCAAA	AATAGTCCTT	CTTTAACTTA	4080
30	GATATTTCAT	AGCTGGATTT	AGGAAGATCT	GTTATTCTGG	CACCARATA	TORROTTA	4200
	CAACGTACAA	TGTCTGCATT	CACTAATTCA GAGGATATGG	ANATTTOOTC	ATABABATCTC	DOLGGEGTETT	4260
	TCCATAGAG	AAAATGACAC	CCAGTAGGCC	TOCATTACAT	TTACATGACC	GTGTTTATTT	4320
	GCCATCAAAT	AAACTGAGTA	CTGACACCAG	ACAAAGACTC	CAAAGTCATA	AAATAGCCTA	4380
35	TGACCAACTG	CAGCAAGACA	GGAGGTCAGC	TCGCCTATAA	TGGTGCTTAA	AGTGTGATTG	4440
	ATCTAATTTT	CTGTACTCAC	CATTTGAAGT	TAGTTAAGGA	GAACTTTATT	TTTTTAAAAA	4500
	AAGTAAATGG	CAACCACTAG	TGTGCTCATC	CIGAACIGIT	ACTCCAAATC	CACTCCGTTT	4560
	TTAAAGCAAA	ATTATCTTGT	GATTTTAAGA	AAAGAGTTTT	CTATTTATTT	AAGAAAGTAA	4620
40	CAATGCAGTC	TGCAAGCTTT	CAGTAGTTTT AAGGAAAGTG	CTAGTGCTAT	ATTCATCCTG	ABBATTCTT	4740
40	ACTACGTAAC	TATCATOR	ATAATTAACT	TACCCCTTATC	TGCCAAAACC	AGAGCAAAAT	4800
	COTABATACC	TTATTYTCTAA	TCAGTGGTCT	CARATCGATT	TGCCTCCCTT	TGCCTCGTCT	4860
	GAGGGCTGTA	AGCCTGAAGA	TAGTGGCAAG	CACCAAGTCA	CTTTCCAAAA	TTGCCCCTCA	4920
	GCTGCTTTAA	GTGACTCAGC	ACCCTGCCTC	AGCTTCAGCA	GGCGTAGGCT	CACCCTGGGC	4980
45	GGAGCAAAGT	ATGGGCCAGG	GAGAACTACA	GCTACGAAGA	CCTGCTGTCG	AGTTGAGAAA	5040
	AGGGGAGAAT	TTATGGTCTG	AATTTTCTAA	CTGTCCTCTT	TCTTGGGTCT	AAAGCTCATA	5100 5160
	ATACACAAAG	GCTTCCAGAC	CTGAGCCACA GAAATACTTG	CCCAGGCCCT	ATCCTGAACA	ACCACCACTO	5220
	CAGAGGCAAA	TCAACCCTAG	GATTGTGAGA	TYPERACTER	CTGATCGCTT	GAGACTCCTA	5280
50							5340
50	TOTAL	AAAAATCTCC	TGAAGGCTGT	AGGAAAAGGG	AGAATCTTCC	ATGTTGGTGT	5400
	TTTTCCTCTA	AAGATCAGTT	TGGGGTATGA	TATAAGCAGG	TATTAATAAA	AATAACACAC	5460
	CAAAGAGITA	CGTAAAACAT	GTTTTATTAA	TTTTGGTCCC	CACGTACAGA	CATTTTATTT	5520
55	CTATTTTGAA	ATGAGTTATC	TATTTTCATA	AAAGTAAAAC	ACTATTAAAG	TGCTGTTTTA	5580 5640
33	TGTGAAATAA	CTTGAATGTT	GTTCCTATAA TTATGAGGAA	TOTAL	GRADATATTOT	ACCRATACTT	5700
	COTTON	TTTTCCACCTC	AGACACTGTG	GCTGTCTAAT	GTAATCCTTT	AAAAATTCTC	5760
	TGCATTGTCA	GTAAATGTAG	TATATTATTG	TACAGCTACT	CATAATTTTT	TAAAGTTTAT	5820
	GAAGTTATAT	TTATCAAATA	AAAACTTTCC	TATAT			
60							
	Seq ID NO:	315 Protein	n sequence:				
	Protein Acc	cession #: 2	XP_087254				
65	1	11	21	31	41	51	
05	ī	1	i -	ī	1	ī	
	MOFRECSING	MKYOEINGRL	VPEGPTPDSS	EGNLSYLSSL	SHLNNLSHLT	TSSSFRTSPE	60
	NETELIKEHD	LFFKAVSLCH	TVQISNVQTD	CTGDGPWQSN	LAPSQLEYYA	SSPDEKALVE	120
70	DANDIGIUPT	CNERETMRVK	TLCKLERYKL	LHILEPDSDR	RRMSVIVQAP	ECEKLLIFAKG	180
70	AESSILPKCI	GGELEKTRIH	VDBFALKGLR	TLCIAYRKFT	SKEYEEIDKR	IPEARTALQQ	240 300
	REEKLAAVFQ	FIEKDLILLG	ATAVEDRIQD SDSECAEQLR	KVRETIEALR	MAGIKVWVLT	GUNHETAVSV	360
	SLSCGHFHRT	MNITERINGK	PLOKAKVIRL	TATODEADLE	1.AVGDGDAVDU	SMIORAHUGI	420
	BETTATA	ADMODVATAD	PKFLSKLLFV	HCHPYYTRIA	TLVOYFFYKN	VCFITPOPLY	480
75	OPVCT.FSOOT	T.VDQUVTAT.V	NICETSLEIL.	IYSLLEOHVD	PHVLONKPTL	YRDISKNRLL	540
	SIKTPLYWTI	LOFSHAFIFF	FGSYLLIGKD	TSLLGNGOMF	GNWTFGTLVF	TVMVITVTVK	600
	MALETHENTW	INHLVTWGSI	IFYFVFSLFY	GGILWPFLGS	QMMYPVPIQL	LSSGSAWPAI	660
	ILMVVTCLFL.	DIIKKVPDRH	LHPTSTEKAO	LTETNAGIKO	LDSMCCFPEG	EAACASVGRM	720
80	LERVIGROSP	THISRSWSAS	DPFYTNDRSI	LTLSTNDSST	C		
δU	Con ID M	316 DNA se	mence				
	Mucleic ac	JEG DNA BE	quence n. #: NM_004	473			
	Coding sem	uence: 661.	,1791				
0.5							
85	1	11	21	31	41	51	
			L	Loroman	GAGGAGGGGG	CTCAGGTCGC	60
	LICGOCAGOG	G-1CCGCGGGG	CIGGAGACCC	ACCCU1GGA	CHOUNCEROC	C. CM001CBC	- 50

	WO 02/	086443					
	aparrament.	cccscscccc	GACCTCGCTG	CCCCCCCCTC	GCCTCTCTGC	COSTGGCGCT	120
	TACCGCCACC	TTGGCCTCGG	GGGCAGGGCA	TGGGCGGCCC	CCGCCAGATC	GCCCAGCGCC	180 240
	AGTACTAACT	GCCCTCGCTC	OCCUPACION	GECCUGARGEE	AGCCACCCCA	ACCCAGGGAT	300
5	CACTTCCGGA	CCCCTCGACC	GCCCGGCACC	AGCGCGCAAG	GGACCCTTCA	GCCGGAGACC	360
-	TRACTCCACT	CCCGGTCGCG	AGGCCACCGC	CGCTGCCCGC	CTCGAGAAGC	ACAACGCGGG	420
	CTGAGCCGTC	GGCTAGCGGG	CGCGCGCCAG	GCCTCTGTCT	TGGGCTCTCC	AGCCCCAGAC GGGCCAGCCC	480 540
		GAGCCTCCAG	CCGCAGAAGG	CCCGACCGTC		ACGCCAGGCC	600
10		CCCCGACAGC	CGCGGGGGATC	CAGAGCCCGG	GGGTGCGGGA	CGCCCGCGCC	660
	ATGACTGCCG	AGAGCGGGCC	GCCGCCGCCG	CAGCCGGAGG	TGCTGGCTAC	CGTGAAGGAA	720
	GAGCGCGGCG	AGACGGCAGC GCCGCAAGCG	AGGGGCCGGG	GTCCCAGGGG	CGCCCTACAG	CTACATCGCG	840
	GGCGGGGGGGC	TGGCCATCGC	GCACGCGCCC	GAGCGCCGCC		CGGCATCTAC	900
15	ADCTTCATCA	CCGAGCGCTT	CCCCTTCTAC	CGCGACAACC	CCAAAAAGTG	GCAGAACAGC	960
	ATCCGCCACA	ACCTCACACT	CAACGACTGC	TTCCTCAAGA	TCCCGCGCGA	GGCCGGCCGC	1020
	CCGGGTAAGG	GCAACTACTG GCCGCCGCAA	GGCGCTCGAC	CCCAACGCGG	TCTCCACCTA		1140
	AUCTICCIGC	CGGCGGCTGC	CGCAGCCGCC	GCTGCCGCAG	CCGCCGCCGC	CCCCCCCCCCC	1200
20	COCCCATOT	TOTORAGEOGE	GGTGCCCGCC	GCGCGCCCCC	CCTACCCGGG	CCCCGTCTAT	1260
	GCAGGCTACG	CGCCGCCGTC	GCTGGCCGCG	CCGCCTCCAG	TCTACTACCC	CGCGGCGTCG	1320
	CCCGCACCGT	GCCGCGTCTT	CGGCCTGGTT	CCTGAGCGGC	CCGCCGGCGC	CCCCGCTACC	1440
	ACCACOGGCT	ACCAGCCCCCC	AGGCTGCACC	GGGGCCCGGC	CGGCCAACCC	CTCTGCCTAT	1500
25	GCGGCTGCCT	ACGCGGGCCC	CGACGGCGCG	TACCCGCAGG	GCGCCGGCAG	TGCGATCTTT	1560
	GCCGCTGCTG	GCCGCCTGGC	GGGACCOGCT	TOGCCCCCAG	CGGGCGGCAG	CAGTGGCGGC	1620 1680
	GTGGAGACCA	CGGTGGACTT ACCCTGGCGG	CTACGGGCGC	GCGCCCAGTG	CAGGGGGCCTA	CCATGCTCGC	1740
	CATGCTGCCG	CTTATCCCCGG	TGGGATAGAT	CCGTTCGTGT	CCGCCATGTG	AGCCAGCGTA	1800
30	GGGAGGAAAA	CTCATAGACA	CATCGGCTGT	TCACACGTTC	CCCGCAACCT	GAGAACGAAC	1860
	AGGAATGGAG	AGAGGACTCA CCGCGCACAG	ACTGGGACCC	ACGTGGAAAA	TGTAAACGGG	BCCACAGAGG	1920
	arangerner.	CAGAGCCCTT	GGACTGGCAC	AGGGACCCTC	GATGGAGCGA	AGCCCTCAAA	2040
	CCCCATCCTT	TCTGGCATTC	TATCGGGGAG	GGTCCTTGGC	GGTAACCAGA	GGGCAGCGTA	2100
35	GTGTCAACAC	CAGAGACCAG	GATCCAAATT	GTGGGGAATC	AGTTTCAGCC	TTCCATGTGC	2160 2220
	TGCCGGAACT	CGGGCCTTTT TGCGGCAGCG	TACGCGGTTC	TANACTCAGG	GCCTTTAACT	TCCABAGGA	2220
	ATACCCTTTT	CALCIPATION	AAATTGGAGA	AATCTCTGCT	CTGGTTGACC	TGGGCTGGTT	2340
	THEORY	CYCAGAACTT	GAGACCTAGC	TCCGAGTTGA	ACTGTGCGTC	AGCACTCCAG	2400
40	TCCCATCACC	TGAACCTTCA	ATTCAGGGCC	TCTGTTACAC	TAGAGGGCTG	CAGGACTCTA	2460 2520
	CCCACCGCCC	CCGGGTTATC	CAGGGCCTCT	GAGTAGCCAC	CCAAAGCCTA	GCCGCTGTTC	2580
	TAGGGAACGG	AAAAGAGTTC	ATGGCCAAGC	GTCTAACCTA	AAGTCCCAGG	ATTGGCTCCA	2640
4.0	GGCAGCAATT	ATATCATAAC	TTATTGAACT	TTTGAGCAGG	ACGTGCTGGT	AATTTCATGG	2700
45	CTGTTACTGC	CCAGTCATAA ACTGTTTCTT	ATCTGCTTTT	CCATTATAAG	CCARAGAGAA	BACTABAGTT	2820
	TARGGRGATG	AGAGGATTCA	AGGAGCCCGT	TGGTGACGCC	TTTCAGTAGC	TGGGGAGGGC	2880
	TOTALCO	CCAGCACCCC	CTGCTACACC	TCAGCAGCCT	CCCCCATGCA	DAAAGGAAAG	2940
50	AGAAAAATTA	AGTTAGGGCA ATCTTGCTTA	GTCAGTAAAG	TGAGCTTTAG	AAAGAAACTG	CCAATTAAC	3000
50	TTCATTTTGT	CCTTGAGAAA	TOTTTAAGTT	TOGATTCTGG	AGCAAAAACT	TTCAGCATTA	3120
	AATATTTCAG	AGGCTCCATT	CACAGCTTTC	AGATAAACTG	GAGTGTTCAG	ATGGACTGTT	3180
	TTAATAAAA	TCTTTGAGCA	AGTGAGTTAT	GGCAAGAGAA	ACTCAGCCTC	TTTCTGTATA	3240 3300
55	AACTTAACAG	GGAAGGGCTG	GGGTGTGAAA	AAGAAGATIG	AGRICATIGNER	ACTEGRATE	3360
33	CTCCAAATGG	ATTTTTGGGA GGATTTGTAT	ARACCAGTGC	TCTCCATTAG	AAATATGGTG	CAAGCCACAT	3420
	ATGTAATTTT	AAATATTCTA	GTAGCCACAT	TAATAAAGTN	AAAAGAAACA	AAAAAAAAA	3480
	AA						
60	a ra m	317 Protei					
00	Protein Ac	cession #: 1	NP 004464				
			-				
	1	11	21	31	41	51	
65	PPUT FUVEOT	DTRANSCRIP	TIONPACTOR	TTPMTARSGP	PPPOPEVLAT	VKEERGETAA	60
05	CACHINGRAMO	DOMOGRAPHY	DI VICKUDANS	YTAT.TAMATA	HAPERRLTLG	GIYKFITERF	120
	DEVEDNERRY	ONSTRUMITI.	NDCFLKIPRE	AGRPGKGNYW	ALDPNAEDMF	ESGSFLRRRK	180 240
	RFKRSDLSTY	PAYMHDAAAA AASPGPCRVF	AAAAAAAAAA	AAAAAIFPGA BI CDADOCDO	OPCARPPYPG COCAPAGAGA	PATTTGYODA	300
70	CCCCADDAND	SAYAAAYAGP	DGAYPOGAGS	AIFAAAGRLA	GPASPPAGGS	SGGVETTVDF	360
, ,	YGRTSPGQFG	ALGACYNPGG	QLGGASAGAY	HARHAAAYPG	GIDRFVSAM		
	Seq ID NO:	318 DNA se	quence	SAR.			
75	Coding seg	uence: 126.	.4439				
	_		21	31	41	51	
	1	11	T.	1	ĺ.	Ĭ-	
80	CCGGGCAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCCTGGAGC	60
	ACCOMPAG	CAATTCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCGCTCAG	120 180
	AGAAGATGAA	GGATATCGAC GAGAACCAGC	ATAGGAAAAG	AGTATATCAT CGCACAGAGA	CCCCAGTCCT	TCCAAGTTCA	240
	CONCRACTO	A CYCPUTYZCZA A	TYTCTARGATY	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
85	TO THE PARTY OF TH	TOTOTOTATO	CATTOTCAGO	TYPERADATY	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420 480
	ACCCAGTGGA	CANTIGCTGGG	CITITICCI	GINIGHCIII	1100100011		- 50

	WO 02/						
	CCCGTGTGGC	CCACAAGAAG TGACGTGAAC	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTETTE	AGACGCTGCT	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600 660
	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720
5	TCATGGTGAA	CATCGTGTGC ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTTAGT	GCTGGGCCTC	CTCCTGACGG	AAATCGTGCG	GTCTTGGTCG	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGCGGGG	GGCCATCCTA	ACCATGGCAT	900
	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
10	TTTGCTCCAA	CGATGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
10	GAGGACCCGT	TGTTGCCATC ATCAGCTGTT	TTAGGCATGA	TTTATAATGT	AATTATTCTG	CCATCACCC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
	AGAGTGTTCA	AAAAATCCGC	GAGGAGGAGC	GTCGGATATT	GGAAAAAGCC	GGGTACTTCC	1320
15	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTG	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTCATAT	GACCCTGGGC	TTCGATCTGA	CAGCAGCACA	TTCAGTAAAG	GTGGTGACAG	1440 1500
	PACCOTCACT	GGCTGTTGAC	ACATTTAACA	CTTTCTTCT	AATGGAAGAG	GTTCACATGA	1560
	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
20	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCCAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCCTCCTGGA	CAGTGACGAG	CGGCCCAGTC	1800 1860
	CCGAAGAGGA	AGAAGGCAAG TCTGGAGATC	CACATCCACC	AACTOCTTOC	AATOTOOGG	AGGACACTGC	1920
25	GTGGGAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
	ACAGCTGCTG	CCTGAGGCCT	GACCTGGCCA	TTCTTCCCAG	CAGCGACCTG	ACGGAGATTG	2160
30	GAGAGCGAGG	AGCCAACCTG CAGGAGCATC	AGCGGTGGGC	AGCGCCAGAG	CAGTGCCTTA	CAMCCCCCAMC	2220
30	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA			2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
20	CCATTTTTAA	TAACCTGTTG	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
35	AAACCAGTGG	TTCACAGAAG	AAGTCACAAG	ACAAGGGTCC	TAAAACAGGA	TCAGTAAAGA	2580 2640
	AGGAAAAAGC CTTCACTGCC	AGTAAAGCCA CTGGTCAGTA	TATCCTCTCT	ACATCCAGGC	TOTTGGGGGG	CCCTTGGCAT	2700
	TOTTGGTTAT	TATGGCCCTT	TTCATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GCTTGACTTA	CTGGATCAAG	CAAGGAAGCG	GGAACACCAC	TGTGACTCGA	GGGAACGAGA	2820
40	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCATG	CTGATCCTGA	AAGCCATTCG	AGGAGTTGTC	TTTGTCAAGG	2940 3000
	GCACGCTGCG	AGCTTCCTCC TTTTGACACG	CGGCTGCATG	ACGAGCTTTT	CAACAGGTTT	TOCALAGEC	3060
	TOTATOMOTT	TGACGTGCGG	CTCCCCCACAG	AGGCCGAGAT	CTTCATCCAG	ABCOTTATCC	3120
45	TGGTGTTCTT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCCTTGT	CATCCTCTTT	TCAGTCCTGC	ACATTGTCTC	CAGGGTCCTG	ATTCGGGAGC	3240
	TGAAGCGTCT	GGACAATATC	ACGCAGTCAC	CTTTCCTCTC	CCACATCACG	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360 3420
50	CTGTGCGGCT	TGACAACCAA GGACCTCATC	ACCATCCCCC	TCATCACCAC	CACGGGGGTTG	ATGATCGTTC	3480
-	TTATGCACGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAACGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTCACCT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCCTT	GGAAGCACCT	GCCAGAATTA	3660
55	AGAACAAGGC	CCGAGAAAAC	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	ACCAMED AAC	3720 3780
"	CTABAGAGA	GATTGGCATT	GTGGGGGGGA	CAGGATCAGG	GARGTOCTOG	CTGGGGATGG	3840
	CCCTCTTCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGCCGAC	CTCCGAAGCA	AACTCTCTAT	CATTCCTCAA	GAGCCGGTGC	3960
60	TGTTCAGTGG	CACTGTCAGA	TCAAATTTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
00	TTTGGGATGC	CCTGGAGAGG AGTGATGGAG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080 4140
	CONTRACTOR	AGCCCTGCTC	AATGGGGATA	ACTICIONGI	TTTAGATGAA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAC GACCATTGCC	TTATTGATTC	AAGAGACCAT	CCGAGAAGCA	TTTGCAGACT	4260
	GTACCATGCT	GACCATTGCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
65	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCCTTCTG	TCCAACGACA	4380
	GTTCCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCGCTGTC	AAGGGCTGAC	4440
	TCCTCCCTGT	TGACGAAGTC CGTCCTCCTA	TCTTTTCTTT	AGAGCATTGC	CATTCCCTGC	TOTCACAGCA	4560
	GTTCCCGATCG	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTOTATTT	4620
70	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTTCTTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	CATGTAAACA ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GITTATTITA	4800
	TATTAAAATA	AGCACTGTGC AGAGATCTGG	TAATAACAGT	GCATATTCCT	TTCTATCATT	TTTGTACAGT	4860
75	TIGCTGTACT	AGAGATCTGG	CTCCCACCTATT	MUNCTUTAGG	CCABAGGESC	ACCRETOTE	4920
15	ATAGTGGGC	CTCCGACAGC	CCCCTCTCCC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	.5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGCAG	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCCTT	5100
	CTGTCCTGGT	GTCACTTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCCT	5160
80	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
ου	TTTCCTGCCT	TCTTCTTTTT	ATTOTTOTT	LIAAACAAGA	ALCAGTCTAT	TCCA AGAGAGAG	5280 5340
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	110	321 Protei					
	Brotein &c	cession #:	NP 005438.1				
	rioccin ne						
75	1	11	21	31	41	51	
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WO 02/086443 Coding sequence: 317-1123

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	Protein Ac	11 PPLAGCSLAG SAPHWNETAE VLDTKARHQQ	NP_003803 21 ASCGPQRGPA KNLGVLADED KHNKAVHLAQ	GSVPASAPAR NTLQQNSSSN ASFQIEAFGS	TPPCRLLLVL ISYSNAMQKE KFILDLILNN MEEDDTPVYM	51 LLLPPLAASS ITLPSRLYY GLLSSDYVEI	120 180 240
	Protein Ac	11 1 PPLAGCSLAG SAPHWNETAE VLDTKARHQQ KGGBHCYYHG KTLAGQYSGBH	NP_003803 21 ASCGPQRGPA KNLGVLADED KHNKAVHLAQ SIRGVKDSKV MKNLTMERGE MKNLTMERGE MTNDTFAKSUV	GSVPASAPAR NTLQQNSSSN ASFQIEAPGS ALSTCNGLHG QWPPLSELOW NLUDSIVEFO	TPPCRLLLVL ISYSNAMQKE KFILDLILINN MFEDDTFVYM LKRKKAVNP LNTRUVLVAV	51 LLLPPLAASS ITLPSRLIYY GLLSSDYVEI IEPLELVHDE SRGIFEEMKY	120 180
50	Protein Ac	11 1 PPLAGCSLAG SAPHWNETAE VLDTKARHQQ KGGBHCYYHG KTLAGQYSGBH	NP_003803 21 ASCGPQRGPA KNLGVLADED KHNKAVHLAQ SIRGVKDSKV MKNLTMERGE MKNLTMERGE MTNDTFAKSUV	GSVPASAPAR NTLQQNSSSN ASFQIEAPGS ALSTCNGLHG QWPPLSELOW NLUDSIVEFO	TPPCRLLLVL ISYSNAMQKE KFILDLILINN MFEDDTFVYM LKRKKAVNP LNTRUVLVAV	51 LLLPPLAASS ITLPSRLIYY GLLSSDYVEI IEPLELVHDE SRGIFEEMKY	120 180 240 300
	Protein Ac	11 1 PPLAGCSLAG SAPHWNETAE VLDTKARHQQ KGGBHCYYHG KTLAGQYSGBH	NP_003803 21 ASCGPQRGPA KNLGVLADED KHNKAVHLAQ SIRGVKDSKV MKNLTMERGE MKNLTMERGE MTNDTFAKSUV	GSVPASAPAR NTLQQNSSSN ASFQIEAPGS ALSTCNGLHG QWPPLSELOW NLUDSIVEFO	TPPCRLLLVL ISYSNAMQKE KFILDLILINN MFEDDTFVYM LKRKKAVNP LNTRUVLVAV	51 LLLPPLAASS ITLPSRLIYY GLLSSDYVEI IEPLELVHDE SRGIFEEMKY	120 180 240 300 360 420 480
50	Protein Activities of the control of	11 PPLAGCSLAG SAPHWNETAE VLDTKARHQQ KGGBHCYYHG KTLAGQYSKQ TYKKHRSSHA EFSKYRQRIK QSLAQNLGIQ CLEPNEPKLF	NP_003803 21 ASCGPQRGPA KNLGVLADED KENKAVHLAQ SIRGVKDSKV MKNLTMERGD HTMNFAKSVV QHADAVHLIS WEPSSKKPK	GSVPASAPAR NTLQONSSSM ASFQIEAPGS ALSTCMGLHG QWPPLSELQW MLVDSIYKEQ RVTPHYKRSS DCTESWGGCI EAGEECDCGF	TPPCRLLLVL ISYSNAMQKE KFILDLILINN MFEDDTFVYM LKRKKAVNP LNTRVVLVAV LSYPGGVCEN MEETGVSHSR HVECYGLCCK	51 LLLPPLAASS ITLPSRLIYY GLLSSDYYE IEPLELVHDE SRGIFEEMKY ETMTEKOQID TRGVGVNEYG KFSKCSILEY KCSLSNGGHC	120 180 240 300 360 420 480 540
50	Protein Active MKPPGSSSRQ RPRANGAAAP INQDSESPYH HYENGKPQYS KSTGRPHIIQ LELMIVNDHK ITTNPVQMLH LPMAVAQVLS RDFLQRGGGA	11 PPLAGCSLAG SAPHWNETAE VLDTKARHOQ KTIAGOYSKQ KTIKHRSSHA EFSKYRORIK QSLAQNLGIQ CLEPREPTKLE	NP_003803 21 ASCGPQRGPA KNLGVLADED KINKAVHLAQ KINKAVHLAQ KINKITMERGD HTMFAKSVV QHADAVHLIS WEPSSRKPKC BPTECONGYV	GSVPASAPAR NTLQQNSSSN ASFQIEAPGS ALSTCNGLHG QWPFLSELQW MLVDSIYKEQ RVTFHYKRSS DCTESWGGCI EAGEECDCGE EAGEECDCGP	TPPCRILLVL ISYSNAMQKE KFILDLIAN MFEDDTFVYM LKRRKRAVNP LNTRVVLVAV LSYFGGVCSR MEETGVSHSR HVBCYGLCCX PDMILHKONGY	51 LLLPPLAASS ITLPSRLIYY GLISDYVEI IEPLELVHDE SRGIFEEMKY ETWIEKOQIO TRGVGVVNEYG KFSKCSILEY KCSISNGAHC	120 180 240 300 360 420 480 540
50	Protein Active MKPPGSSSRQ RPRANGAAAP INQDSESPYH HYENGKPQYS KSTGRPHIIQ LELMIVNDHK ITTNPVQMLH LPMAVAQVLS RDFLQRGGGA	11 PPLAGCSLAG SAPHWNETAE VLDTKARHOQ KTIAGOYSKQ KTIKHRSSHA EFSKYRORIK QSLAQNLGIQ CLEPREPTKLE	NP_003803 21 ASCGPQRGPA KNLGVLADED KINKAVHLAQ KINKAVHLAQ KINKITMERGD HTMFAKSVV QHADAVHLIS WEPSSRKPKC BPTECONGYV	GSVPASAPAR NTLQQNSSSN ASFQIEAPGS ALSTCNGLHG QWPFLSELQW MLVDSIYKEQ RVTFHYKRSS DCTESWGGCI EAGEECDCGE EAGEECDCGP	TPPCRILLVL ISYSNAMQKE KFILDLIAN MFEDDTFVYM LKRRKRAVNP LNTRVVLVAV LSYFGGVCSR MEETGVSHSR HVBCYGLCCX PDMILHKONGY	51 LLLPPLAASS ITLPSRLIYY GLISDYVEI IEPLELVHDE SRGIFEEMKY ETWIEKOQIO TRGVGVVNEYG KFSKCSILEY KCSISNGAHC	120 180 240 300 420 480 540 600
50 55	Protein Ac	11	P_003803 21 ASCGPQRGPA KNLGVLADED KRIKRAVHLAG SIRGVKDSKV MKNLTMERGD HTNNFAKSVV QHADAVHLIS WEPSSRKPKC EPTECGNGVV RDAVMECDIT GSDKFCYKL	GSVPASAPAR MILQUISSSN ASFQIEAFGS ALSTCNGLHG QWPFLSELQW MLVDSIYKEQ RVTFHYKRSS DCTESWGGCI EAGEECDCGF EYCTGDSGQC MTEGTEKGN DCSGRHVVLD	TEPCRILLVL ISYSNAMQKE KFILDLIANN MEEDDTFVYM LKRRKRAVNP LNTRVVLVAV LSYFGGVCSR MEETGVSHSR HVECYGLCCX PPNIHKQDGY GKDGDRWIG DDTDVGYVED	51 LLLPPLAASS ITLPSRLIYY GLLSSDYVEI IEPLELVHDE ERGIFERMKY ETWIEKOLID TRGYGVMEYG KFSKCSILEY KCSISNGAHC SKHUPYCGFL GTPCGPSMMC	120 180 240 300 360 420 480 540 600 720
50	Protein Ac 1 MKPPGSSSRQ RPRAMGAAAP INODESPYH HYENGEPQYS KSTGRPHIIQ LELMIVMDHK ITTHPVOMLH LPMAVAQULS RDFLQRGGA SDGPCCNNTS NGECKTRIN NGECKTRIN LCTNLTRAPR LDPKCLOIDA	11	NP_003803 21 ASCGPQRGPA KNLGVIANED KNIKAVHLAQ SIRGVKDSKV KKNLTMERGD HTMSFRAKSVV QHADAVHLIS WEPSSRKVE EPTECGNGYV RDAVMECDIT TSFYRGGRVI TSFYRGGRVI KGKVCSGRGV	GSVPASAPAR NTLQQNSSSN ASFQIEAPGS ALSTCNGLHG QWPFLSELQW MLVDSIYKEQ RVTPHYKRSS DCTESWGGCI EAGEECDCGF EYCTGDSGQC NTEGTEKGNC DCSGRHVVLD CSNERTCICD	TPPCRLLLVL ISYSNAMQKE KFILDLIANN MFEDDTFVYM LKRRKRAVNP LNTRVVLVAV LSYPGGVCSR MEETGVSHSR HVECYGLCCX PPNLHKQDGY GKDGDRWIQC DDTDVGYVED	51 LLLPPLAAS LLLSDYVEI ITPLEVING SRGIFERMKY ETWIEKO ID TROYGWEYG KESLSNGAK ACKONQGRCY SKHUYPCOFL GTPCOFSMC	120 180 240 300 420 480 540 600
50 55	Protein Ac 1 MKPPGSSSRQ RPRAMGAAAP INODESPYH HYENGEPQYS KSTGRPHIIQ LELMIVMDHK ITTHPVOMLH LPMAVAQULS RDFLQRGGA SDGPCCNNTS NGECKTRIN NGECKTRIN LCTNLTRAPR LDPKCLOIDA	11	P_003803 21 ASCGPQRGPA KNLGVLADED KRIKRAVHLAG SIRGVKDSKV MKNLTMERGD HTNNFAKSVV QHADAVHLIS WEPSSRKPKC EPTECGNGVV RDAVMECDIT GSDKFCYKL	GSVPASAPAR NTLQQNSSSN ASFQIEAPGS ALSTCNGLHG QWPFLSELQW MLVDSIYKEQ RVTPHYKRSS DCTESWGGCI EAGEECDCGF EYCTGDSGQC NTEGTEKGNC DCSGRHVVLD CSNERTCICD	TPPCRLLLVL ISYSNAMQKE KFILDLIANN MFEDDTFVYM LKRRKRAVNP LNTRVVLVAV LSYPGGVCSR MEETGVSHSR HVECYGLCCX PPNLHKQDGY GKDGDRWIQC DDTDVGYVED	51 LLLPPLAAS LLLSDYVEI ITPLEVING SRGIFERMKY ETWIEKO ID TROYGWEYG KCELSNGAKCY ACKONQGRCY SKHUYPCOFL GTPCOFSMC	120 180 240 300 360 420 480 540 600 720
50 55	Protein Ac	11 PPLAGCSLAG SAPHNETAE KYLDTKARKQQ KAGGBICYHIG KYLAGQYSKQ TYKKHRSSHA EPSKYRQRIK QSLAQNLGIQ CLFRPPTKLP CLFQPRGYEC CQYIMGTKAA IGQLQGEIIP LMMSSCPLDS TNLIIGSIAG	ASCGPQRGPA ASCGPQRGPA KNLGVLANED KHNRAVHLAQ SIRGVKDSKV QHADAVHLIS WEPSSRKPKC EPTECGNGFV RDAVMEDIT GSDKFCYEKL TSFYHGGRVI AGKVCSGRGV ALLVAAIVLG	GSVPASAPAR NTLQQNSSSN ASFQIEAPGS ALSTCNGLHG QWPFLSELQW MLVDSIYKEQ RVTPHYKRSS DCTESWGGCI EAGEECDCGF EYCTGDSGQC NTEGTEKGNC DCSGRHVVLD CSNERTCICD	TPPCRLLLVL ISYSNAMQKE KFILDLIANN MFEDDTFVYM LKRRKRAVNP LNTRVVLVAV LSYPGGVCSR MEETGVSHSR HVECYGLCCX PPNLHKQDGY GKDGDRWIQC DDTDVGYVED	51 LLLPPLAAS LLLSDYVEI ITPLEVING SRGIFERMKY ETWIEKO ID TROYGWEYG KCELSNGAKCY ACKONQGRCY SKHUYPCOFL GTPCOFSMC	120 180 240 300 360 420 480 540 600 720
50 55 60	Protein Ac I MKPPGSSSRQ RPRARGAAAP INQDSESTH HYENGROYS RSTGRPHIO LELMIVNOELK LTITNEVOMLH LPMAVAQULS RDFLQRGGGA SDGPCCNNTS NGECKTENNQ LCTMLTRAPR LDRKCLQIQA RDEGREGGA RDEGREGGA RDEGREGGA REGREGGA SEGGLEGGA REGREGGA SEGGLEGGA SEGGLE	11 PPLAGCSLAG SAPMINETAE VIDTKARHQQ KGGBHCYYHG KTLAGQYBKQ TYKKHRSSHA EPSKYKQRIK GSLAGNLGIQ CLPMPTHLIP CLPMPTHLIP CLPGPRGIEC CQYIMGTKAA IGQLQGEIIP LMMSSCPLLS TNLIIGSIAG	SP_003803 21 ASCOPORGPA ASCOPORGPA KNILGVLADED KENNAVHLAQ SIRGVKDSKV QHADAVHLIS WEPSSRKPKC GHADAVHLIS EPTECGNGVV RDAVNECDIT GSDRFCYSRL KGKVCSGRGV AILVAAIVLG	GVPASAPAR MTLQNSSSN MSFQTEAPGS ALSTCNGLHG MPFLSELOM RLVDSIYKEQ RVTPHYKRSS DCTESMGGCI EAGGECDGF EYCTGDSGGC MTEGTEKGNC DCSGAHVULD GTGMGFKNVK	TPPCRLLLVL ISYSNAMQKE KFILDLIANN MFEDDTFVYM LKRRKRAVNP LNTRVVLVAV LSYPGGVCSR MEETGVSHSR HVECYGLCCX PPNLHKQDGY GKDGDRWIQC DDTDVGYVED	51 LLLPPLAAS LLLSDYVEI ITPLEVING SRGIFERMKY ETWIEKO ID TROYGWEYG KCELSNGAKCY ACKONQGRCY SKHUYPCOFL GTPCOFSMC	120 180 240 300 360 420 480 540 600 720
50 55 60	Protein Ac I	11	SP_003803 21 1 ASCGPORGPA ANIGULADED HENRAVHLAQ SIRGYMORSV MENLIMERGD HIDDRAVHLIS WEPSSRKPKG EDTECGNGYV RDAVMECDIT TSPYHOGRWI TSPYHOGRWI AGNUCAGENGE ALLVAAIVLG UM #: AKO744:	GVPASAPAR MTLQNSSSN MSFQTEAPGS ALSTCNGLHG MPFLSELOM RLVDSIYKEQ RVTPHYKRSS DCTESMGGCI EAGGECDGF EYCTGDSGGC MTEGTEKGNC DCSGAHVULD GTGMGFKNVK	TPPCRLLLVL ISYSNAMQKE KFILDLIANN MFEDDTFVYM LKRRKRAVNP LNTRVVLVAV LSYPGGVCSR MEETGVSHSR HVECYGLCCX PPNLHKQDGY GKDGDRWIQC DDTDVGYVED	51 LLLPPLAAS LLLSDYVEI ITPLEVING SRGIFERMKY ETWIEKO ID TROYGWEYG KCELSNGAKCY ACKONQGRCY SKHUYPCOFL GTPCOFSMC	120 180 240 300 360 420 480 540 600 720
50 55	Protein Ac I	11	SP_003803 21 1 ASCGPQRGPA ASCGPQRGPA KNLGVLADED KHNKAVHLAQ SIRGVKOSV KKNLTMERGO HIDNFAKSVV KHNLTMERGO HIDNFAKSVV KHNLTMERGO GEPTECONGVV RDAVMECDIT TSFYHQGRVI TSFYHQGRVI AILVAAIVLG TUGAIVLG TH: AK0744: 1515	GSVPASAPAR NTLQUNSSEN NTLQUNSSEN ASFQTEAPGS ALSTCNGLEG QWPFLSELOW MLVDSIYNEQ RVTPHYKRSS DCTESNGGCI EAGEECDCSP EYCTCNGSGC TEGTEKGNC CSGARVVLD CSNEATCICD GTGWGPRNVK	TPPCRLLLVL ISYSNAMQNE KPILDLILAN MFEDDTFYM LKRRKRAWNE LKTRVLVAV LSYPGGVCSR KWETTOVSHSR HVECYGLCCX GXDGDRWTQC DDTDVGYVCD PTWAGTDCSI KRREDPTQQG	51 LLEPLANSS LLEPLANSS LLEPLANSS LL	120 180 240 300 360 420 480 540 600 720
50 55 60	Protein Ac I	11	SP_003803 21 1 ASCGPORGPA ANIGULADED HENRAVHLAQ SIRGYMORSV MENLIMERGD HIDDRAVHLIS WEPSSRKPKG EDTECGNGYV RDAVMECDIT TSPYRIGRKVI TSPYRIGRKVI AGNUCASGRGV AILVAAIVLG UM #: AK0744:	GVPASAPAR MTLQNSSSN MSFQTEAPGS ALSTCNGLHG MPFLSELOM RLVDSIYKEQ RVTPHYKRSS DCTESMGGCI EAGGECDGF EYCTGDSGGC MTEGTEKGNC DCSGAHVVLD GTGMGFKNVK	TPPCRLLLVL ISYSNAMQKE KFILDLIANN MFEDDTFVYM LKRRKRAVNP LNTRVVLVAV LSYPGGVCSR MEETGVSHSR HVECYGLCCX PPNLHKQDGY GKDGDRWIQC DDTDVGYVED	51 LLLPPLAAS LLLSDYVEI ITPLEVING SRGIFERMKY ETWIEKO ID TROYGWEYG KCELSNGAKCY ACKONQGRCY SKHUYPCOFL GTPCOFSMC	120 180 240 300 360 420 480 540 600 720
50 55 60	Protein Ac New Processing	11 11 11 11 11 11 11 11 11 11 11 11 11	PO03803 21 1 ASCOPORGPA ASCOPORGPA KINLGVILADED KENKRAVHLAG KENKRAVHLAG KENKRAVHLAG KENKRAVHLAG KENKRAKSIV KHANLTMEKGD KEPSERKEKC BPTECONGYV KENKVCSGRGV KGKVCSGRGV ALLVAALIVLG LUCAL LUCALIVLG LUCAL LUCA	GSVPASAPAR NTLQUNSSEN NTLQUNSSEN ASFQTEAPGS ALSTCNGLEG QWPFLSELOW MLVDSIYNEQ RVTPHYKRSS DCTESNGGCI EAGEECDCSP EYCTCNGSCO TEGTEKGNC CSGARVVLD CSNEATCICD GTGMGFRNVK 18.1	TPPCRLLLVL ISYSNAMQNE KPILDLILAN MFEDDTFVYM LKRRGAVNE LKTRYLVAV LSYFOGVCSR KWEFTOYSHSR KVECYGLCCX GKDGDRWIGC GKDGDRWIGC DTDVGYVGC FTWAGTDCSI KRRFDPTQQG	51 LLLEPLAASS ITLESERITYS GLLSSDYVEI IEPLELVHDE SRGIFESMAY ETWICKOLIO TROWGWIETO CS.S.S.S.G.S.G.S.G.S.G.G.G.G.G.G.G.G.G.G	120 180 240 360 360 420 540 660 720 780
50 55 60 65	Protein Ac I	11 11 PPLAGCSLAG PPLAGCSLAG SAPHHNISTAE VLDYKARHQQ KKGBKCYYHG KKGBKCYYHG KKJAGQYSKQ TYKKKRSSKH EPSKYRGRIK GGSAGNIGIG CLEPNPTKLF CLEPORTYKLF LANNSCPLAG 322 ENA 322 ENA 324 ENA 325 ENA 325 ENA 326 ENA 326 ENA 326 ENA 326 ENA 327 ENA 327 ENA 328 ENA	RP_003803 21 4 ASCGPQRGPA ASCGPQRGPA ASCGPQRGPA KINLGVLADED KINLRAVILLAQ SIRGVINSKY KINLGVLADED KINLRAVILLAQ	GSVPASAPAR NTLQONSSSN NTLQONSSSN ASFQTEAPGS ALSTCNGLIG GMPPLSELOR NLVDSIYKEQ RVTPHYKRSS DCTESNGGCT EAGESCOGF EYCTEDSSGC NTEGTEKSNG CSTEANTCICD GTGMGFRNVK 18.1 TCCTCTGCCA	TPPCRLLLVL ISYSNAMCKE KPILDLILIAN MFEDDTPYVM MFEDDTPVVM MFEDDTPVVM LKRRKRAVAP LKRRKRAVAP LKTRVVLVAV LKYPGGVCSR HVBCYGLCCK HVBCYGLCCK FPNLHKQDGY GKDGDRWIGG DIDTDVGYVED DTDVGYVED TWAGTDCSI KRRFDPTQGG	SI LLEPLIASS ITLBERLIVY GLISSIVVEI EINTERVIDE SIGIT EBRUT EINTERVIDE ENGLISSIVAT ACKNORACY SIGIT ENGLISSI SIGIT EGGE SIGIT EGGE SIGIT EGGE SIGIT EGGE FINANCIA EGGE SIGIT EGGE S	120 180 240 360 420 480 540 660 720 780
50 55 60	Protein Ac I I MKPPGSSSRQ MKPPGSSSRQ MKPPGSSSPYH HTMRSRPOYS KSTGRPHIO LELATIVOBUE LITHNYWMHE LITHNYWHHE ITHNYWHH LITHNYWHH LITHNYWH	11 1 PPLACCSLAG PPLACCSLAG SAPHNISTAE VLDYKARHOQ KKIJAGO/SKQ KKIJA	RP_003803 21 4 ASCGPQRGPA ASCGPQRGPA ASCGPQRGPA KRIMAVILADED KRIMAVILA	GSVPASAPAR MILQONSSSM MILQONSSSM ASFQIEAPGS ALSTCNGLING QMPPLSELOM MLVDSIYKEQ EXTERNISCIC EXGENCED EXGENCED EXGENCED GTGMGFRNVK 8.1 1 1 TCCTCTGCCA CCCTCTCCCCCCC	TPPCRLLLVL ISYSNAMKE KPILDLILIAN MFEDDTFYM LKRRKRANL LKSPEGVLSK MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHSR MESTJOVSHS MESTJOVSH MESTJOV	51 LLEPPLAASS TILBSELIVY GLESSOYVEI ISPLELIVIDE SRGIF EBROY KFSCG TLEP	120 180 240 360 420 480 540 660 720 780
50 55 60 65	Protein Ac I I I I I I I I I I I I I I I I I I	DESIGN B: : 1	RE_003803 21 21 21 22 23 23 24 25 26 27 27 27 27 27 27 27 27 27	GSVPASAPAR NTLONISSEN ARPOTRAPS ALSTCNIGHG (MPFISELD MILVOSITKED RYPHTYRES CTESNIGGI EAGRECOGP EYCTUBSQC CSGRAVULD CSGRAVULD CSGRAVULD CSGRAVULD CTGRAFTER 31 1 CCTCTICICA CCCTCTICICA CRICTICICA CRICTICA CRICT	TPPCRILLIVI. ISYSMAMQKE KFILDLILAM KFEDDTPVM KFILDLILAM KFEDDTPVM LATRAVILAM LATRAVILAM KENTOVISH LATRAVILAM KENTOVISH KRETOPTOGG GROGDER IC- DITUGGYVE FRALIKGDOV GROGDER IC- DITUGGYVE FRALIKGDOV GROGDER IC- TAGGACACA CTAMAGTTTA CTAGGACACAC CTAMAGTTTA	51 LLEPPLAASS TILBERLIYY GLESDIYUEI GLESDIYUEI GRANGHORES KYSKCSILBERNAN GRANGHORES GRANGHOR	120 180 240 360 420 540 660 720 780
50 55 60 65	Protein Ac I I I I I I I I I I I I I I I I I I	DESIGN B: : 1	RE_003803 21 21 21 22 23 23 24 25 26 27 27 27 27 27 27 27 27 27	GSVPASAPAR NTLONISSEN ARPOTRAPS ALSTCNIGHG (MPFISELD MILVOSITKED RYPHTYRES CTESNIGGI EAGRECOGP EYCTUBSQC CSGRAVULD CSGRAVULD CSGRAVULD CSGRAVULD CTGRAFTER 31 1 CCTCTICICA CCCTCTICICA CRICTICICA CRICTICA CRICT	TPPCRILLIVI. ISYSMAMQKE KFILDLILAM KFEDDTPVM KFILDLILAM KFEDDTPVM LATRAVILAM LATRAVILAM KENTOVISH LATRAVILAM KENTOVISH KRETOPTOGG GROGDER IC- DITUGGYVE FRALIKGDOV GROGDER IC- DITUGGYVE FRALIKGDOV GROGDER IC- TAGGACACA CTAMAGTTTA CTAGGACACAC CTAMAGTTTA	51 LLEPPLAASS TILBERLIYY GLESDIYUEI GLESDIYUEI GRANGHORES KYSKCSILBERNAN GRANGHORES GRANGHOR	120 180 240 360 420 480 540 660 720 780
50 55 60 65 70	Protein Ac I I I I I I I I I I I I I I I I I I	DESIGN B: : 1	RE_003803 21 21 21 22 23 23 24 25 26 27 27 27 27 27 27 27 27 27	GSVPASAPAR NTLONISSEN ARPOTRAPS ALSTCNIGHG (MPFISELD MILVOSITKED RYPHTYRES CTESNIGGI EAGRECOGP EYCTUBSQC CSGRAVULD CSGRAVULD CSGRAVULD CSGRAVULD CTGRAFTER 31 1 CCTCTICICA CCCTCTICICA CRICTICICA CRICTICA CRICT	TPPCRILLIVI. ISYSMAMQKE KFILDLILAM KFEDDTPVM KFILDLILAM KFEDDTPVM LATRAVILAM LATRAVILAM KENTOVISH LATRAVILAM KENTOVISH KRETOPTOGG GROGDER IC- DITUGGYVE FRALIKGDOV GROGDER IC- DITUGGYVE FRALIKGDOV GROGDER IC- TAGGACACA CTAMAGTTTA CTAGGACACAC CTAMAGTTTA	51 LLEPPLAASS TILBERLIYY GLESDIYUEI GLESDIYUEI GRANGHORES KYSKCSILBERNAN GRANGHORES GRANGHOR	120 180 240 360 420 540 660 720 780
50 55 60 65	Protein Ac KKPPGSSSNO KKPPGSSSNO RPBAMBAN INDOBSSPH INDOSSPH KSTGRPHIO LELMIVNDIK LPMAYAVIJS BEPLAGRGZBA KSTGRPHIO KSTGRP	DESIGN #: PLAGESLAGE SAPHHISTAR VULDTKAREGO KOGSBICTYHO KITLAGY KOGSBICTYHO KITLAGY KOGSBAGHLIGH COLPRETYLIGH COLPRETYLIGH LANGSCHLOS JAC DNA SCHLOS JAC DNA JAC DNA JAC GACCOGG GCCOGG GCCOGG GCCCOGG GCCCOGG ANAMOTICAG ATTACAGGA CALLINGTONA ATTACAGGA CALLINGTONA CALLINGTONA ATTACAGGA CALLINGTONA CALLINGTONA ATTACAGGA CALLINGTONA CALLINGTONA CALLINGTONA CALLINGTONA ATTACAGGA CALLINGTONA CALLINGTO	RE_003803 ASCGPORGIPA ASCGPOR	GSVPASAPAR NTLQONSSEN ARFQIENTES ARFQUENTES ARFQIENTES	TPPCRILLUVL ISYSNANQIE KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KFILDILISM KRIPDFTQQI GTOTCTCCA CTARACTITA TOGRACIAC CTARACTITA TOGRACIAC CTARACTITA GUNCATTIAN GU	51 LLEPILASS TILDERLIVE T	120 180 360 420 480 540 666 720 780
50 55 60 65 70	PROTEIN AC MEPOSSSEQ REPARGAAP INDOSSSPIH HYENGROUS REPARGAS LELATVANIEK LEL	DEPLACESIAGE PPLAGESIAGE PPLA	NE_003803 21 1 ASCGPORGEA INITIAL STATEMENT AND ASCGPORGEA INITI	GSVPASAPAR NTLQUISSEN ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER ARFOTEAPER BLOOM BLO	TPPCRILLVIL ISYSMANQIE	51 ILLEPILASS ITLEBELLYY GLISSYVEI IEPHENYINS SRGIFESHOY EFFTENCON KESISSOAIL KESISSOAIL KESISSOAIL ICANONOCIC TOTALOGA STATE CONCENTRATE 51 ICANOTOTICA CTROCTAGOA TACANGACOA GOANNACAA GOANNACAA GOANNACAA	120 180 240 300 420 480 540 660 720 780 661 120 180 240 366 420 480 480 480 480 480 480 480 480 480 48
50 55 60 65 70	Protein Ac MKEPGSSSRQ REPAMGNAP MKSPGSSSRQ REPAMGNAP MKSPGSSRQ REPAMGNAP MKSPGSSRQ REPAMGNAP MKSPGSSRQ REPAMGNAP MKSPGSSRQ REPAMGNAP MKSPGSSRQ REPAMGNAP MKSPGSRQ RE	COSSION B: : PLAGCSLAG SAPHHNISTAE VUDTKAREGO KOGHEKYHÖR KOGHEKYHÖR KOGHEKYHÖR KOGHEKYHÖR KOGHEKYHÖR KOGHEKYHÖR KOGHEKYHÖR KOGHEKH LINSSCHLER	RE_003803 1 1 1 ASCGPORGPA KNLGVLADED KNLGVLADED KNLGVLADED STRGVFDSKO STRGVFDSKO GNADAVILLS WEFSERNFLA WEFSERNFLA WEFSERNFLA TUBERASSU ALL WEFSERNFLA TUBERASSU TUBE	GSVPASAPAR NTLQONSSEN ASTQUENCE ASTQ	TPPCRILLULL ISYSNANQIE	SILLEPRIAMES ILLEPRIAMES ILLEPRIAMES ILLEPRIAMES INCLEDENCY INCLED	120 180 240 420 480 540 666 720 780
50 55 60 65 70	Protein Ac MKPPGSSRQ RPRAMGAAP MKPPGSSRQ RPRAMGAAP MUNDESSPTI MENOMESST	pplacesian 8: : 11	RE_003803 ASCOPORGEA ANGUALDEE ANGUALDE ANGUALDEE ANGUA	GSVPASAPAR NTLOQUISSEN ASTOTENICA ASTOTENICA ASTOTENICA ASTOTENICA ASTOTENICA ASTOTENICA ASTOTENICA ENCORPTION CONTROL ENCORPTI	TPPCRILLIVIL ISYSNANQIE KYTLDILISM KYTLDILISM KYTLDILISM KYTLDILISM KYTLDILISM KYTLDILISM KYTLDILISM KYTLDILISM KYTLDILISM LSYPGOVER KWETOVSHER KYECYGLOCK PYNLHKODO FYNLHKODO F	SILLEPLIANS ILLEPLIANS	120 180 240 420 480 540 660 720 780 120 120 130 360 480 480 540 660 660 660 660 660 660 660 660 660 6
50 55 60 65 70	Protein Ac MKPPGSSSRQ RPEAMGNAP MKSPGSSSRQ RPEAMGNAP MKSPGSSRQ RECTRIFT MKSPGSSRQ	IN THE PRINCIPLE OF THE	NE_003803 21 1 ASCGPORGEA KOLGVIADED KONLGVIADED LOTTOLOGIA KONLGVIADED LOTTOLOGIA KONLGVIADED LOTTOLOGIA KONLGVIADED LOTTOLOGIA KONLGVIADED LOTTOLOGIA KONLGVIADED LOTTOLOGIA KONLGVIADED LOTTOLOGIA KONLGVIADED LOTTOLOGIA KONLGVIADED LOTTOLOGIA LOTTOLOgia LOTTOLOgia LOTTOLOgia LOTTOLOgia LOTTOLOgia LOTTOLOgia LOTTOLo	GSVPASAPAR NTLOONSEN AFFOLIANCE AFFOLIANCE AFFOLIANCE ONFOLIANCE AFFOLIANCE A	TPPCRILLIVIL ISYENANQIE RYTIDLIENE RYTIDLIENE RABRIANNE RABRIANNE RABRIANNE LSTROGUCS ROTTOGLOX PRILINGOUS ROTTOGLOX ROT	SI ILLEPILANES ITLEPERLIYY GLISSDYVEI IEPLELYNES BRGIFESHOY KFSKCSILKEY KKSISMONIC KKSISMONIC KKSISMONIC COCCTOTA COCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOTA COCCTOT	120 180 300 420 420 480 600 600 720 780 120 120 120 120 424 421 481 481 481 481 481 481 481 481 481 48
50 55 60 65 70	Protein Ac MKPPGSSSRQ RPRAMGAAP MKDPGSSSRQ RPRAMGAAP MUDGESSPTI MUDGESSPTI MUDGESSPTI MUDGESSPTI MUDGESSPTI MUDGESSPTI MUDGESSPTI MUDGESSPTI MUDGES MUDGES 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	IN THE PRINCIPLE OF THE	RP_003803 1 ASCOPORGRA ANGLOVIADED KRITEVIDEN STREVEDSKO STREVEDSKO GNADAVILLS BETSKOGGOT GNADAVILLS BETSKOGGOT GNADAVILLS BETSKOGGOT ANGLOV ALLVAATVA JUBBINA 201 CATGCTCTCC GACCOGTCO GACCOGTGO GACTATOGOC ANGAGGO ACAGTACOC ACAGGAC ACAGCAC ACAC GSVPASAPAR NTLOONGSSH AGUATIONGSSH AGUATIONGSH AGUATIONGSSH AGUATIONGSH TPPCHLLLVL ISYEMMQKE FYTEDLIAW ISYEMMQKE FYTEDLIAW ISYEMMQKE ISYEMMQK ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQKE ISYEMMQK ISYEMMQKE ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK ISYEMMQK IS	1 LLEPLIASS 1 LLEPLIASS 1 LLEPLIASS 1 LLEPLIASS 1 LEPLIASS 1 LEPLI	120 180 300 420 480 600 660 720 780 120 120 120 480 540 660 660 660 660 660 660 660 660 660 6		
50 55 60 65 70	Protein Ac MKPPGSSSRQ RPEAMGNAP MKPPGSSSRQ RPEAMGNAP MCPGSSRQ RPEAMGNAP KSTGRPHIO CTTTCTCOA AANTACAA AANTA	LI 1 PERACESLAGE SAPINENTES VALUE SAPINE	RP_003803 21 1 ASCGPORGPA SILVALIDED SERRAVILLAD SERRA	GSVPASAPAR NTLOONSSEN AFFOLIANCE AFFOLIANCE GWEPLSELOG MILVOSITINE AFFOLIANCE ROTERING RVTPHYKRS DOTTSMIGGE RVTPHYKRS DOTTSMIGGE ROTERING	TPPCRILLUVL ISYENANQIE KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLIENE LSTPGGVCSR KYTLDLIENE KYTLDLIENE LSTPGGVCSR KYTLDLIENE KYTLOL KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLOL KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLIENE KYTLDLI	SILLEPILASS TILLEPILASS TILLEP	120 180 300 420 480 540 660 720 780 120 120 140 424 427 448 540 660 722 780
50 55 60 65 70	Protein Ac MKPPGSSSRQ RERANGANAP MKSPGSSSRQ RERANGANAP MKSTGEPHIO KSTGEPHIO KSTGEPHIO KSTGEPHIO KSTGEPHIO KSTGEPHIO CTNITYOUNG SOGPCORTS SOGPCORTS SOGPCORTS SOGPCORTS SOGPCORTS SOGPCORTS ACCIGNAGA ACCIGNAGA AACCIGNAGA CONTINTOCO TOCOCOCOG TOCOCOCO	11 11 12 13 14 15 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18	RP_003803 21 1 ASCGPORGPA ASCGPOR	GSVPASAPAR NTLOONSEN AFFOLIANCE A	TPPCRILLVL ISYEMANGIE ISYEMANGIE ISYEMANGIE ISYEMANGIE ISTERIA	51 ILLEPILANSS ILLEPILANSS ILLEPILANSS ILLEPILANSS ISOLITERATIVE GLISSDYVEI IEPHELVING ISOLITERATIVE ISOLITERATIVE ISOLITERATIVE ISOLITERATIVE 51 COACTCTCTA CTSCCTAGGA TACCHAGNAC CTCTCATAGA CTCTCCAT CAAAGACCAG CCTCCATCAAA CCTCTCCAT CAAAGACCAG CCTCCATCTAAAACTTTCAA CAGCTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAAACTTTCAAAAACTTTCAAAAACTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAAA	120 180 300 420 480 540 660 720 780 120 120 130 300 342 480 660 660 660 720 780
50 55 60 65 70	Protein Ac MKPPGSSSRQ RERANGANAP MKSPGSSSRQ RERANGANAP MKSTGEPHIO KSTGEPHIO KSTGEPHIO KSTGEPHIO KSTGEPHIO KSTGEPHIO CTNITADAP ROGCCTTROB SOGICTORIO CCNITADAP ROGCCTROB CTNITADAP ACCIGNAGA ACCIGNAGA AACCIGNAGA CONTINACA TOCCCCCCA TCCCCCCCA GOTGATTGAT GOTGATTGAT GOCCCGTAT GOCCGTAT GOCCCGTAT GOCCCGTAT GOCCCGTAT GOCCCGTAT GOCCCGTAT GOCCGTAT GOCCCGTAT GOCCCGTAT GOCCCGTAT GOCCCGTAT GOCCCGTAT GOCCGTAT GOCCCGTAT GOCCCCTAT GOCCCCTAT GOCCCCTAT GOCCC	11 11 12 13 14 15 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18	RP_003803 21 1 ASCGPORGPA ASCGPOR	GSVPASAPAR NTLOONSEN AFFOLIANCE A	TPPCRILLVL ISYEMANGIE ISYEMANGIE ISYEMANGIE ISYEMANGIE ISTERIA	51 ILLEPILANSS ILLEPILANSS ILLEPILANSS ILLEPILANSS ISOLITERATIVE GLISSDYVEI IEPHELVING ISOLITERATIVE ISOLITERATIVE ISOLITERATIVE ISOLITERATIVE 51 COACTCTCTA CTSCCTAGGA TACCHAGNAC CTCTCATAGA CTCTCCAT CAAAGACCAG CCTCCATCAAA CCTCTCCAT CAAAGACCAG CCTCCATCTAAAACTTTCAA CAGCTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAACTTTCAAAAACTTTCAAAAACTTTCAAAAACTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAAA	120 180 300 420 480 540 660 720 780 120 120 130 360 442 480 540 660 720 780 840 860 860 860 860 860 860 860 860 860 86
550 555 660 665 70 75	Protein Ac MKPPGSSSRQ RPRAMGASS RPRAMGAS RPRAMGAS RPRAMGAS RPRAMGAS RPRAMGAS RPRAMGAS RPRAMGAS REST REST REST REST REST REST REST RES	11 1 PEPLAGCSLAG SAPHWINTAN VALOTRABLEGO SAPHWINTAN VALOTRABLEGO KITLAGOYSKO TYLKEKRSKIN KITLAGOYSKO TYLKEKRSKIN KITLAGOYSKO TYLKEKRSKIN KITLAGOYSKO TYLKEKRGRIK CLEPRIPTILI CLEPRIPTI CLEPRIPTILI CLEPRIPTILI CLEPRIPTI C	RP_003803 21 ASCGPORGPA ASCGPORGPA BRINGHALDED BRI	GSSYPAGAPARA NTLOCUSSER ALBERTACHLOR GNEPLESSLOR MUNDSILVES EAGGECOOFE EYCTUSSGO EYCTUS EYCT EYCTUS EYCTUS EYCTUS EYCTUS EYCTUS EYCTUS EYCTUS EYCTUS EYCTUS	TPPCHLLVL ISYSBANGER I	SI ILLEPILANES ITLEPERITY GLISSOYVEI IEPLEVINIO BRGIFESHOY KFSKCSILKEY KKSISMOAIC KKSISMOAIC KKSISMOAIC ACKNOGRCY OFFICIPENS ICACCITOTA CROCKTOSA TACCAGATO GCATOGACA CCTCTCAACA CCTCTCCAAC CCTCTCAACA CCTCTCCAAC CCTCTCAACA CCTCTCCAACAACA CCTCTCCAACAACAACAACAACAACAACAACAACAACAAC	120 180 300 420 480 600 720 780 600 120 120 120 120 120 480 600 600 720 780 600 720 780
50 55 60 65 70	Protein Ac MKPPGSSSRQ RPRAMGNAP MKPPGSSSRQ RPRAMGNAP MCPGSSRQ RPRAMGNAP MCPGSSRQ RPRAMGNAP MCPGSSRQ MCPGSCAPPI MCPGSCAPPI MCCCAPPI CTTTCTCCAA ACCAGAGG AAATGCCGAC GACCTTACC TTCCCCCAG AAATGCCGAC ACCAGGGGG ATCACCGAC ATCACCGAC ATCACCGAC ACCAGGGGGG ACCAGGGGGG ACCAGGGGGAC ACCAGGGGGG ACCAGGGGGAC ACCAGGGGGGAC ACCAGGGGGAC ACCAGGGGGAC ACCAGGGGGAC ACCAGGGGGGCGCAC ACCAGGGGGGCGCAC ACCAGGGGGGCGCAC ACCAGGGGGGCGCAC ACCAGGGGGGCCAC ACCAGGGGGGCGCCAC ACCAGGGGGGCCCAC ACCAGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGC	DEPLACESIAN B: : 11 11 12 11 12 11 12 12 13 14 15 15 16 16 17 17 17 17 17 17 17 17 17 17 17 17 17	SP_003803 21 1 ASCGPORGPA ASCGPORGPORGPA ASCGPORGPA A	GRYPASAPAR NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN SAMMILLOONGSEN SAMINANTINGSEN SAMMILLOONGSEN SAM	TPPCSILLVL ISYSBANGLE	SILLEPLAASS ILLEPLAASS	120 180 300 420 480 540 660 720 780 120 120 130 360 442 480 540 660 720 780 840 860 860 860 860 860 860 860 860 860 86
550 555 660 665 70 75	Protein Ac MKPPGSSSRQ RPRAMGNAP MKPPGSSSRQ RPRAMGNAP MCPGSSRQ RPRAMGNAP MCPGSSRQ RPRAMGNAP MCPGSSRQ MCPGSCAPPI MCPGSCAPPI MCCCAPPI CTTTCTCCAA ACCAGAGG AAATGCCGAC GACCTTACC TTCCCCCAG AAATGCCGAC ACCAGGGGG ATCACCGAC ATCACCGAC ATCACCGAC ACCAGGGGGG ACCAGGGGGG ACCAGGGGGAC ACCAGGGGGG ACCAGGGGGAC ACCAGGGGGGAC ACCAGGGGGAC ACCAGGGGGAC ACCAGGGGGAC ACCAGGGGGGCGCAC ACCAGGGGGGCGCAC ACCAGGGGGGCGCAC ACCAGGGGGGCGCAC ACCAGGGGGGCCAC ACCAGGGGGGCGCCAC ACCAGGGGGGCCCAC ACCAGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGGCCCAC ACCAGGGGGGCCCAC ACCAGGGGC	DEPLACESIAN B: : 11 11 12 11 12 11 12 12 13 14 14 15 15 16 16 17 17 17 17 17 17 17 17 17 17 17 17 17	SP_003803 21 1 ASCGPORGPA ASCGPORGPORGPA ASCGPORGPA A	GRYPASAPAR NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN NTLOONGSEN SAMMILLOONGSEN SAMINANTINGSEN SAMMILLOONGSEN SAM	TPPCSILLVL ISYSBANGLE	SI ILLEPILANES ITLEPERITY GLISSOYVEI IEPLEVINIO BRGIFESHOY KFSKCSILKEY KKSISMOAIC KKSISMOAIC KKSISMOAIC ACKNOGRCY OFFICIPENS ICACCITOTA CROCKTOSA TACCAGATO GCATOGACA CCTCTCAACA CCTCTCCAAC CCTCTCAACA CCTCTCCAAC CCTCTCAACA CCTCTCCAACAACA CCTCTCCAACAACAACAACAACAACAACAACAACAACAAC	120 180 240 300 420 480 540 660 720 780 661 244 362 486 540 665 722 788 844 967 967 967

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		AGCTACATAA					1200
		AATTCATCGC					1260
		TCCACGAAGG					1320
_	AACACTGCAG	GAGGACCTCG	GAATGATGCT	CAATTCAACT	TCTCTGTGCA	AGAGCCAATG	1380
5		ATGTTGTCGT					1440
		AATTTCCACT					1500
		AATAATAAAT					1560
	GAACTATGTT	GTGGTTGCAC	AGACACGGAG	AAAATCAGCG	GAGTTCTTGC	TCCGAATCTT	1620
	CCTGAAAATG	CCAGACAGTG	ACAGGCACCT	GAGCAGCCAT	TTCAACCTCA	GAATGAAGGG	1680
10	AAGCCCTTCA	GAACATGGCT	CCCAACAAAG	CATTTTCAAC	AGATATGCTC	AGCAGGTATG	1740
	GTACCTAGCA	CCCAGGGGCC	TTACGTGGGA	TTGGAGAAAG	GGGACCTGAG	GGAGGGACAG	1800
	CCCTCACAGG	CCCTTACTGG	GATGCAGAGA	GGAGAAGTGA	CTTGATGGAC	TATTTTACCT	1660
	GCCTCTCTTC	CTGGATCGTC	TCCAGAACTG	CTGTGGCTGC	CAAGCTCGGT	AGAGACGTGG	1920
	CGCCCCACCC	AGTCTCATCC	GGGGGACTTC	AAGCTGGAAT	GCAGAGCTTA	GAAAGGGAGG	1980
15	GGATAATTAT	GGGGTGTGAG	GTGCATTGCC	CTCTAAATCT	TTAAACAAGC	AATTGGCAGT	2040
	ACCCCCTGAA	ACCITICCIT	CTCCTACTCG	GCCACCTCCC	ACCAACCTGG	CATCGTTCCT	2100
	CCCGGGAGCT	AGCCAGCTTC	AGAAAGCACA	TACAGCATCC	TTGCTGCCAA	ACCACCTATG	2160
	TGCACACAGG	ATTTCCTTAA	TGGCTTAATA	AACTGTTATA	AAGAACTCCT	TGACTTGTCA	2220
	GAATAAAATA	GCTGCCAGGG	GCTCTGCACA	ATGAGCCTCT	TACCGTTAAA	алалалала	2280
20	AAAAAAAA	AAAAAAAAA	AAAAAAAAA				

Seq ID NO: 327 Protein sequence: Protein Accession #: BAB85075.1

2	5	1	11	21	31	41	51	
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		MAYYORPSVE	TSIIKFKDOD	FITLEDHCLS	MGRTFKDETF	PAADSSIGOK	LLOEKRLSNV	60
		TWKB PODT-PG	GREATING	SRFDIQQGGA	ADCWPLAALG	SLTONPOYRO	KILMVQSFSH	120
		OAVCIABBBBB	MUCAUMARAA	IDDRLPVQGD	KCLFVRPRHO	NOEFWPCLLE	KAYAKLLGSY	180
3	n	SDI'HAGAI'ED	ALVOLTGOVI	TNIHLHSSPV	DLVKAVKTAT	KAGSLITCAT	PSGPTDTAQA	240
_	•	MPMCT.UGT.WA	VTVTGAROTO	YRRGWEETIS	LANDWGWGET	EWRGRWSDGS	OBWEETCDPR	300
		KSULHKKBED	GEPWMSCODE	QQKFIAMFIC	SEIPITLDHG	NTLHEGWSOI	MFRKQVILGN	360
		TACCIDUMDAC	DALESTO EDWE	GTNVVVCVTV	AVTPSNI-KAR	DAKFPLDFOV	ILAGSOKHCP	420
		KLK	THE GREAT CO.					
3	5	KUK						

Seq ID NO: 328 DNA sequence Nucleic Acid Accession #: BC017490.1

40	Coding sequ	sence: 74-21	788				
40	_	11	21	31	41	51	
	1	11	11	3.	7.	ĭ	
	1	TGAACCACTT	mmorrow as a	* CONCOMPON	TOCTOTACTO	GOGGAGAGGA	60
	GTGGGTCACG	GCTATGGCGG	11CGCGCGAA	ACCIONITO	ATGGCATCCA	GCCCGGCCCA	120
45	TCGTGGTACT	GCCAATGATC	ANTONICOUN	ALCOCOTOCC.	CHACCECCC	CCCCCTACTCA	180
43	GCGTCGGCGA	TCCAGCCCTG	CICICACCIC	CAUCCCIOGC	COMMODITOR	COCACCCCCT	240
	TGCCCTCACC	GAGGGGCCCC	GCCGTGACCT	TCCACCATTI	GAGGATGAGT	TTCGAGATGG	300
	CCTAGGCACA	GACTACCGCG	TUGAUGAAUA	AGAGGATGGA	GAGGAGCICA	ACCOACTOO	360
	CATGGAAAGG	GAGGACGTAG	CCATCCCAGA	GCIGGAUGCC	TATGAGGCCG	CACACCCCCC	420
50	TCTGGATGAT	CGTGACCGGG	AGGAGCTGAC	GUCCAGTCAG	AGGGAGGCAG	CHICAGOGGGGGGGG	480
30	CATGCGGCAG	GATGACCGGG	AGGCTGGCCG	GGGCCTGGGC	LGCATGCGCC	*CCMCCTCCT	540
	GTATGACAGC	GATGAGGAGG GACGGCGAGG	ACGAGGAGCG	CCCTGCCCGC	AAGCGCCGCC	AGG I GGAGCG	600
	GGCCACGGAG	CACTCTGTGC	AGGACGAGGA	GATGATCGAG	AGCATCGAGA	MCC1GGMGGA	660
	TCTCAAAGGC	AAGAACTTCC	GCGAGTGGGT	GAGCATGGCG	GGCCCCCGGC	TOUMGRICUM	720
55	CCACCGCTTC	AGGACATGT	TGCGCACTCA	CUTCUACAGE	CACGGCCACA	ACGICITCAA	780
33	GGAGCGCATC	AGCGACATGT	GCAAAGAGAGA	CCGTGAGAGC	CIGGIGGIGA	ACTATOMOGA	840
	CTTGGCAGCC	AGGGAGCACG	TGCTGGCCTA	CFTCCFGCCF	GAGGCACCGG	COGMOCIGCI	900
	GCAGATCTTT	GATGAGGCTG	CCCTGGAGGT	GGTACTGGCC	ATGTACCCCA	AGTACGACCG	960
	CATCACCAAC	CACATCCATG	TCCGCATCTC	CCACCTGCCT	CTGGTGGAGG	AGCTGCGCTC	1020
<i>c</i> 0	GCTGAGGCAG	CTGCATCTGA	ACCAGCTGAT	COSCACCAGT	GGGGTGGTGA	CCAGCTGCAC	1020
60	TGGCGTCCTG	CCCCAGCTCA	GCATGGTCAA	GTACAACTGC	AACAAGIGCA	ATTTCGTCCT	1140
	GGGTCCTTTC	TGCCAGTCCC	AGAACCAGGA	GGTGAAACCA	GGCTCCTGTC	CIGAGIGCCA	1200
	GTCGGCCGGC	CCCTTTGAGG	TCAACATGGA	GGAGACCATC	TATCAGAACT	ACCAGOGTAT	1260
	CCGAATCCAG	GAGAGTCCAG	GCAAAGTGGC	GGCTGGCCGG	CTGCCCCGCT	CCAAGGACGC	1320
ce	CATTCTCCTC	GCAGATCTGG	TGGACAGCTG	CAAGCCAGGA	GACGAGATAG	AGCTGACTGG	1380
65	CATCTATCAC	AACAACTATG	ATGGCTCCCT	CAACACTGCC	AATGGCTTCC	CIGICITIGC	1440
	CACTGTCATC	CTAGCCAACC	ACGTGGCCAA	GAAGGACAAC	AAGGTTGCTG	TAGGGGAACT	1500
	GACCGATGAA	GATGTGAAGA	TGATCACTAG	CCTCTCCAAG	GATCAGCAGA	TCGGAGAGAA	1560
	CATCTTTGCC	AGCATTGCTC	CTTCCATCTA	TOGTCATGAA	GACATCAAGA	GAGGCCTGGC	1620
70	TCTGGCCCTG	TTCGGAGGGG	AGCCCAAAAA	CCCAGGTGGC	AAGCACAAGG	TACGIGGIGA	1680
70	TATCAACGTG	CTCTTGTGCG	GAGACCCTGG	CACAGCGAAG	TCGCAGTTTC	TCAAGTATAT	1740
	TGAGAAAGTG	TCCAGCCGAG	CCATCTTCAC	CACTGGCCAG	GGGGCGTCGG	CIGIGGGCCT	
	CACGGCGTAT	GTCCAGCGGC	ACCCTGTCAG	CAGGGAGTGG	ACCTTGGAGG	Cragaacccr	1800
	GGTTCTGGCT	GACCGAGGAG	TGTGTCTCAT	TGATGAATTT	GACAAGATGA	ATGACCAGGA	1860
	CAGAACCAGC	ATCCATGAGG	CCATGGAGCA	ACAGAGCATC	TCCATCTCGA	AGGCTGGCAT	1920
75	CGTCACCTCC	CTGCAGGCTC	GCTGCACGGT	CATTGCTGCC	GCCAACCCCA	TAGGAGGGCG	1980
	CTACGACCCC	TOGCTGACTT	TCTCTGAGAA	CGTGGACCTC	ACAGAGCCCA	TCATCTCACG	2040
	CTTTGACATC	CTGTGTGTGG	TGAGGGACAC	CGTGGACCCA	GTCCAGGACG	AGATGCTGGC	2100
	CCGCTTCGTG	GTGGGCAGCC	ACGTCAGACA	CCACCCCAGC	AACAAGGAGG	AGGAGGGGCT	2160
	GGCCAATGGC	AGCGCTGCTG	AGCCCGCCAT	GCCCAACACG	TATGGCGTGG	AGCCCCTGCC	2220
80	CCAGGAGGTC	CTGAAGAAGT	ACATCATCTA	CGCCAAGGAG	AGGGTCCACC	CGAAGCTCAA	2280
	CCAGATGGAC	CAGGACAAGG	TGGCCAAGAT	GTACAGTGAC	CTGAGGAAAG	AATCTATGGC	2340
	CACAGGGAGG	ATYCCATTA	CCGCTGCCGCCA	CATCGAGTCC	ATGATCCGCA	TGGCGGAGGC	2400
	CACGOGGG	ATCCATCTGC	GGGACTATGT	GATCGAAGAC	GACGTCAACA	TGGCCATCCG	2460
	COTORTOCTO	GAGAGCTTCA	TAGACACACA	GAAGTTCAGC	GTCATGCGCA	GCATGCGCAA	2520
85	CACTITICCC	CGCTACCTTT	CATTCCGGCG	TGACAACAAT	GAGCTGTTGC	TCTTCATACT	2580
	CARCCACTTA	GTGGCAGAGC	AGGTGACATA	TCAGCGCAAC	CGCTTTGGGG	CCCAGCAGGA	2640
	CACTATTGAG	GTCCCTGAGA	AGGACTTGGT	GGATAAGGCT	CGTCAGATCA	ACATCCACAA	2700

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	CCTCTCTGCA	TTTTATGACA	GTGAGCTCTT	CAGGATGAAC	AAGTTCAGCC	ACGACCTGAA	2760 2820
	AAGGAAAATG TTCTGGTTTG	ATCCTGCAGC	AGTTCTGAGG	COUTATGCCA	CACABARCCA	GAGCACTTGA	2880
	TGAACTCGGG	GTACTAGGGT	CAGGGCTTAT	AGCAGGATGT	CTGGCTGCAC	CTGGCATGAC	2940
5	TOTTTGTTTC	TCCAAGCCTG	CITTGTGCTT	CTCACCTTTG	GGTGGGATGC	CTTGCCAGTG	3000
	TOTOTTACTT	COTTOCTORAL	CATCTTGCCA	CCTCCGAGTG	CTTTGTCTCC	ACTCAGTACC	3060
	TTGGATCAGA	GCTGCTGAGT	TCAGGATGCC	TGCGTGTGGT	TTAGGTGTTA	GCCTTCTTAC	3120 3180
	ATGGATGTCA	GGAGAGCTGC	TGCCCTCTTG	GCGTGAGTTG	CGTATTCAGG	CIGCITITGC	3240
10	TGCCTTTGGC	CAGAGAGCTG	GTTGAAGATG GAGGGCACGA	CAGTGCCAGC	GCAGGGTTCT	GGGCTCCTCA	3300
10	CTCTGTGCCCC	TGTGGTGGGG	GTCATGCGGA	TTATOCACTO	GCCACAGTTA	TCAGCTGCCA	3360
	TTGCTCCCTG	TCTGTTTCCC	CACTCTCTTA	TTTGTGCATT	CGGTTTGGTT	TCTGTAGTTT	3420
	TAATTTTTAA	TAAAGTTGAA	TAAAATATAA	ааааааааа	AAAAA		
1.5							
15	Seq ID NO:	329 Protein	sequence:				
	Protein Acc	ession #: A	CARI /490.1				
	1	11	21	31	41	51	
	ī	Ī	1	1	1	1	
20	MAESSESPTM	ASSPAQRERG	NDPLTSSPGR	SSRRTDALTS	SPGRDLPPPE	DESEGLLGTE	60
	CDLESSEDGE	ELTGDGMRRD	YRAIPELDAY	EAEGLALDDE	DVEELTASOR	EAAERAMKQK	120
	DREAGRGLGR	MRRGLLYDSD	EEDEERPARK NFLRTHVDSH	RRQVERATED	DMCVPWPPCI.	WWANTED BY	240
	SVREWVSMAG	PRESIDENCE	EAALEVVLAM	YPKYDRITNH	IHVRISHLPL	VEELRSLROL	300
25	TIT WOL TREED	IMPROPRIMI.D	OLGMUKYNICH	KCNPVLGPPC	OSONOEVKPG	SCPECOSAGP	360
	DEMMERTTY	ONVODIBLOR	SPGKVAAGRI.	PRSKDAILLA	DLVDSCKPGD	EIELTGIYHN	420
	NYDGGLNTAN	GFPVPATVIL	ANHVAKKONK	VAVGELTDED	VKMITSLSKU	COLGENTANS	480 540
	IAPSIYGHED	IKRGLALALF	GGEPKNPGGK QRHPVSREWT	LEACHLAILAD	DCGDPGTARS	KWNDODRTSI	600
30	SRAIFTTGQG	ASAVGLTATV	QARCTVIAAA	NPIGGRYDPS	LTFSENVOLT	BPIISRFDIL	660
50	CHIPPTINDIV	ODEMLAPEUV	GSHURHHPSN	KEERGLANGS	AAEPAMPNTY	GAELPOEAP	720
							780
							900
35	AEQVTYQRNR	PGAQQDTIEV	PEKDLVDKAR	GINIHNPRAF	ADSRPLEMME	PSHDLKKKMI	900
33	LQQF						
	Sea TD NO:	330 DNA se	ouence				
	Nucleic Ac	id Accession	n #: M17254				
40	Coding seq	uence: 257-	1645				
40		11	21	31	41	51	
	1	11	21	31	1	11	
	GTCCGCGCGT	GTCCGCGCCC	GCGTGTGCCA	GCGCGCGTGC	CTTGGCCGTG	CGCGCCGAGC	60
	CGGGTCGCAC	TAACTCCCTC	GGCGCCGACG	GCGGCGCTAA	CCTCTCGGTT	ATTCCAGGAT	120
45	CTTTGGAGAC	CCGAGGAAAG	CCGTGTTGAC	CAAAAGCAAG	ACAAATGACT	CACAGAGAAA	180
	AAAGATGGCA	GAACCAAGGG	CAACTAAAGC	CGTCAGGTTC	TGAACAGCTG	GTAGATGGGC	240 300
	TGGCTTACTG	GAACCAAGGG	CAACTAAAGC	CCCGGACCCA	GCAGCTCATA GCCTACGGAA	GTAGATGGGC TCAAGGAAGC CGCCACACCT	300 360
	TGGCTTACTG CTTATCAGTT GGCTAAGACA	GAACCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACCG	CAACTAAAGC TTCAGACTGT ACCAGTCGTT CGTCCTCCTC	CCCGGACCCA GTTTGAGTGT CAGCGACTAT	TGAACAGCTG GCAGCTCATA GCCTACGGAA GGACAGACTT	GTAGATGGGC TCAAGGAAGC CGCCACACCT CCAAGATGAG	300 360 420
50	TGGCTTACTG CTTATCAGTT GGCTAAGACA CCCACGCGTC	GAACCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACCG ĆCTCAGCAGG	CAACTAAAGC TTCAGACTGT ACCAGTCGTT CGTCCTCCTC ATTGGCTGTC	CCCGGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCCA	GCAGGTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA	GTAGATGGGC TCAAGGAAGC CGCCACACCT CCAAGATGAG CCATCAAAAT	300 360 420 480
50	TGGCTTACTG CTTATCAGTT GGCTAAGACA CCCACGCGTC GGAATGTAAC	GAACCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACCG ĆCTCAGCAGG CCTAGCCAGG	CAACTAAAGC TTCAGACTGT ACCAGTCGTT CGTCCTCCTC ATTGGCTGTC TGAATGGCTC	CGTCAGGTTC CCCGGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCCA AAGGAACTCT	TGAACAGCTG GCAGCTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA CCTGATGAAT	GTAGATGGGC TCAAGGAAGC CGCCACACCT CCAAGATGAG CCATCAAAAT GCAGTGTGGC	300 360 420 480 540
50	TGGCTTACTG CTTATCAGTT GGCTAAGACA CCCACGCGTC GGAATGTAAC	GAACCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACCG ĆCTCAGCAGG CCTAGCCAGG AAGATGGTGG	CAACTAAAGC TTCAGACTGT ACCAGTCGTT CGTCCTCCTC ATTGGCTGTC TGAATGGCTC GCAGCCCAGA	CGTCAGGTTC CCCGGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCA AAGGAACTCT CACCGTTGGG	TGAACAGCTG GCAGCTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA CCTGATGAAT ATGAACTACG	GTAGATGGGC TCAAGGAAGC CGCACACCT CCAAGATGAG CCATCAAAAT GCAGTGTGGC GCAGCTACAT	300 360 420 480
-	TGGCTTACTG CTTATCAGTT GGCTAAGACA CCCACGCGTC GGAATGTAAC CAAAGGCGGG GGACGAGAGG	GAACCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACCG CCTCAGCCAGG CCTAGCCAGG AAGATGGTGG CACATGCCAC	CAACTAAAGC TTCAGACTGT ACCAGTCGTC CGTCCTCCTC ATTGGCTGTC TGAATGGCTC GCAGCCCAGA CCCCAAACAT	CGTCAGGTTC CCCGGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCA AAGGAACTCT CACCGTTGGG GACCACGAAC	TGAACAGCTG GCAGCTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA CCTGATGAAT ATGAACTACG GAGCGCAGAG TGGCTGGAGG	GTAGATGGGC TCAAGGAAGC CGCACCT CCAAGATGAG CCATCAAAAT GCAGTGTGGC GCAGCTACAT TTATCGTGCC GGGCGGTGAC	300 360 420 480 540 600 660 720
50 55	TGGCTTACTG CTTATCAGTT GGCTAAGACA CCCACGCGTC GGAATGTAAC CAAAGGCGGG GGAGGAGAAG AGCAGATCCT	GAACCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACCG CCTCAGCAGG CCTAGCCAGG AAGATGGTGG CACATGCCAC ACGCTATGCCAC ACGCTATGCCAC ACGCTATGCCAC ACGCTATGCCAC ACGCTATGCCAC ACGCTATGCCAC ACGCTATGCCAC ACGCTATGCAC	CRACTAAAGC TTCAGACTGT ACCAGTCGTT CGTCCTCTC ATTGGCTGTC TGAATGGCTC GCAGCCCAGA CCCCAAACAT TCAACATCTT	CGTCAGGTTC CCCGGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCCA AAGGAACTCT CACCGTTGGG GACCACGAAC TGTGCGGCAG GTTATTCCAG	TGAACAGCTG GCAGGTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA CCTGATGAAT ATGAACTACG GAGCGCAGA TGGCTGGAGT AACATCGATG	GTAGATGGGC TCAAGGAAGC CCCACCCT CCAAGATGAG CCATCAAAAT GCAGTGTGGC GCAGCTACAT TTATCGTGCC GGGCGGTGAA GGGAAGGAACT	300 360 420 480 540 600 660 720 780
-	TEGCTTACTG CITATCAGTT GGCTAAGACT CCCACGCGTC GGAATGTAAC CAAAGGCGGG GGAGGAAAG AGCAGATCCT AGAATATGGC GTGCAAGATG	GARCCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACCG ĆCTCAGCAGG CCTAGCCAGG AAGATGGTGG CACATGCCAC ACGCTATGGA ACTCCAAGGACG ACCAAGGACG ACCAAGGACG	CARCTARAGE TTCAGACTGT ACCAGTGGTT CGTCCTCCTC ATTGGCTGTC TGAATGGCTC GCAGCCCAGA CCCCAGACAT TCAACATCTT ACTTCCAGAG	CGTCAGGTTC CCCGGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCA AAGGAACTCT CACCGTTGGG GACCACGAAC TGTGCGGCAG GTTATTCCAG GCTCACCCCC	TGAACAGCTIG GCAGCTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA ATGAACTACG GAGCGCAGAG TGGCTGAGAT AACATCGATG AACATCGATG AGCTCCATG	GTAGATGGGC TCAAGGAAGC CGCCACACCT CCAAGATGAG CCATCAAAAT GCAGTGTGGC GCAGCTACAT TTATCGTGCC GGGCGTGAA GGAAGGAACT CCGACATCCT	300 360 420 480 540 600 660 720 780 840
-	TEGCTTACTG CITATCAGTT GGCTAAGACA CCCACGCGTC GGAATGTAAC CAAAGGCGGG GGAGGAAAG AGCAGATCCT AGAATATGGC GTGCAAGATG TCTCTCACAT	GARCEARGGG AAGGREATGA GTGAGTGAGG GAGATGACCG ÉCTCAGCAGG CCTCAGCAGG ACGATGCCAC ACGCTATGCAC ACGCTATGGA ACCAGACG CTCCAGACG CTCCAGACG CTCCACTACC CTCCACTACC	CRACTAAAGC TTCAGACTGT ACCAGTCGTT CGTCCTCCTC ATTGGCTGTC GCAGCCCAGA CCCCAAACAT GTACAGACCA TCAACATCTT ACTTCCCAGAGAC TCAGAGAGAC TCAGAGAGAC TCAGAGAGAC TCAGAGAGAC TCAGAGAGAC TCAGAGAGAGAC TCAGAGAGAGAC TCAGAGAGAGAC TCAGAGAGAGAC TCAGAGAGAGAC TCAGAGAGAGAC	CGTCAGGTTC CCCGGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCA AAGGAACTCT CACCGTTGGG GACCACGAAC TGTGCGGCAG GTTATTCCAG GCTCACCCCC TCCTCTCCCA	TGACAGCTG GCAGCTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA CCTGATGAACT ATGAACTACG GAGCGCAGAG TGGCTGGAGT AACATCGATG AGCTACAACG CGTTCAACG CGTTTGACTT	GTRGATGGGC TCAAGGAAGC COCCACACCT CCAAGATGAG CCATCAAAAT GCAGTGTGGC GCAGCTACAT TTATCGTGCC GGGCGGTGAA GGAAGGAACT CCGACATCCT CAGATGATGT	300 360 420 480 540 600 660 720 780 840 900
-	TOGCTTACTG CITATCAGTT GGCTAAGACA CCCACGCGTC GGAATGTAACA CCAAGGGGGG GGAGGAGAAG AGCAGATCCT AGAATATGGC GTGCAAGATG TCTCTCACAT	GARCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACCG CCTCAGCCAGG AAGATGGTGG CACATGCCAC ACGCTATGCA ACGCTATGCA ACGCTATGCA CTTCCAGACG ACCAAGGACG TTCCAGAAGGTATGTACA TTCCAAAACT TTCCAAAACT	CARCTARAGE TTCAGACTGT ACCAGTGGTT CGTCCTCCTC ATTGGCTGTC GCAGCCCAGA CCCCAAACAT GTACAGACCA TCAACATCTT ACTTCCAGAG TCACAGACT TCACAGACT TCACAGACT TCACAGACT TCACAGGTT	CGTCAGGTTC CCCCGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCCA AAGGAACTCT CACCGTTGGG GACCACGAAC TGTGCGGCAG GTTATTCCAG GCTCACCCCC TCCTCTTCAG AATGCATGCT	TGAACAGCTG GCAGCTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA ATGAACTACG GAGCGCAGAG TGGCTGCAGT AACATCCATG AGCTACAACG CATTTGACT AGAACACAG	GTAGATGGGC TCAAGGAAGC CGCCACACCT CCAAGATGAG CCATCAAAA GCAGTGTGGC GCAGGTACAT TTATCGTGCC GGGCGGTGAA GGAAGGAACT CCGACATCCT CAGACATCCT ATTTACCATA	300 360 420 480 540 600 660 720 780 840
-	TOGCTTACTE CITATCAGTT GGCTAAGACA CCCACGCGTC GGAATGTAAC CAAAGGCGGG GGAGGAGAAG AGCAGAATACT AGAATATGGC GTGCAAGATA TCATCACAT TGATAAAGCC TGAGCCCCC TGCTCAACCA	GAACCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACCG CCTCAGCAGG CACATGCCAG ACGATATGCAA CTTCCAGAGG ACCAAGGACG TTACAAAACT AGGAATACA TTACAAAACT AGGAATACG	CARTAAGC TTCAGACTGT ACCAGTCGTT GGTCCTCCTC GGAGCCGAG CCCCAAACAT GTACAGACA TCAACATCTT ACTTCCAGAG TCAGAGAGAC CCCAAGAGT CCAGGGGGCCAG CCCCAAGAGT CCAGGGGGCCAG CCCCAAGAGT CCAGGGGGCCAG CCCCAGGGT CCAGGGGCCAG CCCAGGGT CCAGGGCCCA	GOTCAGGTTC CCCGGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCCA AAGGAACTCT CACCGTTGGG GACCACGAAC GTTATTCCAG GCTCACCCCC TCCTCTTCCA AATGCATGCT TCACGGCCAC AATGCATGCT TCACGGCCAC	TGAACAGCTEG GCAGCTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA CCTGATGAAT ATGAACTACG TGGCTGGACT AACATCGATG AGCTCAACACC CCATTTAACTTACT AGAACACCG CCACCCCC CAGCCTCCC CAGCCTCCC	GTAGATGGGC TCAAGATGAA CCACCACCT CCAAGATGAA CCATCAAAAT GCAGTGTGGC GGCGGTACAT TTATCGTGCC GGGCGTGAA GGAAGGAACT CCGACATCCT ATTTACCATA AGTTGAAAGC AGTTGAAAGC	300 360 420 480 540 660 720 780 840 900 960 1020
55	TOGCTTACTE CITATCAGTT GGCTAAGACA CCCACGGGTC GGAATGTTAAC CAAAGGGGGG GGAGAGAAA AGCAGATCCT AGAATATGGC GTGCAAGAT TCTCTCACAT TGATAAAGAC TGAGCCCCC TGGCCCCC TGGCCACCC	GAACCAAGGG AAGGACATGA GTGAGTGAGG GAGATGACGG CCTAGCCAGG AAGATGGTGAG CCTATCCAGCCG ACGATGCAC ACGCTATGGA CTTCCAGACG TCCACTACC TTACCAAAACT AGGAGATCAG TCTCCTTCCA	CARTHANGE TTCAGACTGTT ACCAGTCGTTT GTCCTCCTC GTAGCTGTC TGAATGGCTC GCAGCCAGA CCCCAAACAT TCAACACTCT TCAACACTCT TCAGAGAGGC CTCCACGGTT CTGGACCGG CCTGGACCGC CAGTGCCCAA	GOTCAGGTTC CCCGGACCOA GTTGAGTGT CAGCGACTAT TCAACCCCCA AAGGAACTCT CACCGTTGGG GACCACGAAC GTTATTCCAG GCTCACCCCC TCCTCTTCCA AATGCATGCT TCACGGCCAC AACTGAAGAC CCTTGTAGAAC CCTTCTAGAAC CCTTCTACAAC CCTTCTACA	TGAACAGCTIG GCAGCTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA CCTGATGAAT ATGAACTACG TGGCCAGAG TGGCTGAGTT AACATCGATG AACTCGATG AACATCGATG AACAACG CATTTGACTT AGAACACAG CCCACGCCCC CAGCTCCT CCAGGCGCTCCCCCCCCCC	GTAGATGGGC TCAAGAAGC CGCACACCT CCAAGATGAG CCATCAAAAT GCAGTGTGGC GGAGCTACAT TTATCGTGCC GGGGGGTGAA GGAAGGAACT CCGACATCCT CAGATGATGATGATGATGATGATGATGATGATGATGATGAT	300 360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140
55	TGGCTTACTE CCTTATCAGTT GGCTAAGACA CCCAGGGTC GGAATTAAAC CAAAGGCGGG GGAGGAAGA AGCAGATCCT AGAATATGGC GTCCACAT TGATAAAGCC TGAGCCCCC TGCTCAACAT TGATTCAGATT TGATTCAGATT TGATTCAGATT TGATTCAGATT TGATTCAGATT TGATTCAGATT TGATTCAGATT TGCTTTGGCAG	GANCCANGGG ANGGACATOA OTGAGTGAGG GAGATGACCG CCTCAGCAGG CCTAGCAGG ACGATGCAA ACGATACCAA ACGATACCAA ACGATACCAA CTTCCAGACG TTACAAAACT ACGAGTACC TTACAAAACT ACGAGTACC TTACAAACT ACGAGTCAC TTACAAACT ACGAGTCAC TTACAACT ACGAGTCAC TTACACCATACC TTACACCATACC TTACACCATACC TTACACCATACC TTACACCATACC TTACACCATACC TTACACCATACC TTACACCATACC TTACACCATACC TTACACCATACC TTACACCATACC TTACACCATACC	CARTIANAGE THE AGAINST ACCAGNOST ACCAGNOST CONTROL CON	GOTCAGGTTC CCCGGACCCA GTTTGAGTGT CAGCGACTAT TCAACCCCCA AAGGACTCT CACCGTTGGG GACCACGAAA GTTATTCCAG GCTCACCCCC TCCTCTTCCA AATGCATGCT TCACGGCCAG AATGCATGCT TCACGGCCAG CCTTGCAAAT CCTTGCAAAT CGTTGCAAAT CGTTGCAAGCCC CCTTGCAAAT CGACAGCCTAC CGACAGCCTAC CGACAGCCAC CCTTGCAAAT CGACAGCCTAC CGACAGCTAC CGACAGCTCC CGACAGCTAC CGACAGCTCC CGACAGCTAC CGACAGCTCC CGCAGCTCC CGACAGCTCC CGACACCTC CGACAGCTCC CGACAGCTCC CGACAGCTC	TGAACAGCTEG GCAGGTCATA GCCTACGGAA GGACAGACTCA GCCAGGGTCA CCTGATGAAT ATGAACTACG AAGCCCAGAA AGCTCGAGT AACATCGATG AACATCGATGAAT AGCTACAACG CCATTGAACT AGAACACG CCATGGACT AGAACACG CCAGGCCCC CCAGGCAGCC CCAGGCAGCA AACTCAGGCAGCA	GTARATGGGC TCARACT TCARGARAC CCCACACCT CCARGATGAG CCATCAAAAT GCAGTGTGGC GGAGGTACAT TTATCGTGCC GGAGGGAACT CCGACATCCT ATTTACCATA ATTTACCATA AGTCAAGA AGTTAGATCC GCACGAGTCCG GCACTACCT GCACGACCCG GCACCACCCT GCACACCCT GCACACCCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCT GCACCACCCT GCACCACCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCCT GCACCACCACCT GCACCACCCT GCACCACCT GCACCACCCT GCACCACCT GCACCA	300 360 420 480 540 600 720 780 840 900 960 1020 1080 1140
55	TGGCTTACTE GCTANGACT GCTANGACT GCAGGGTGT GGAATTAAC CAAAGGGGGG GGAGGAGAAG AGCAGATCCT AGAATATGGC TGTCAAGAT TCTCTACAT TGATAAAGC TGAGCCCCC TGGTCAAGAT GCTTTGCAGAT GCTTTTGCAGAT GCTTTGCAGAT GCTTTTGCAGAT GCTTTTTCAGAT GCTTTTTTTTTT	GANCCANGGG AAGGACATGA GAGATGACGG GCTCAGCAGG CCTAGCAGG CCTAGCAGG AAGATGCCAG AAGGATGCCAG ACGCTATGGA CTCCAGAG CTCCACTACC TTACAAAACT TCCCTCCA TCCTCCTCCA TCCCTCCA TCCCCTCCA TCCCCCCAG TCCCCCCCAG TCCCCCCCAG TCCCCCCCAG TCCCCCCCAG TCCCCCCCAG AACGGGGACAA	CARTARAGE TTCAGACTGT ACCAGTGGT ACCAGTGGT ACCAGTGGT ATGGCTGTC TGAATGGTC GCAGCCCAGA CCCAAACAT GTACAGACCA TCACAGACT ACTTCCAGAG TCAGAGCAG CTCCAGGGTC CCTGGACCGG CAGTGCCCAA CAGTTGCCCAA CAGTTCCTCAGGTTCAGACTGT TCAAGATGAC	GGTCAGGTTC CCCGGACCCA GTTTGAGTGT CAGCGGCATAT TCAACCCCA AAGGACTCT CACCGTTGGG GTTATTCCAG GCTCACCCC TCCTCTCCA AATGCATGCT TCACGGCCAC ACTGAACAGCCC CCTTGCAAC GGACCACCCGGATCCAACGGCCAC CCTGCAACAGCTCC GGATCCCGAACAGCTCC GGATCCCGAAC	TGAACAGCTIG GCAGCTCATA GCCTACGGAA GGACAGACTT GCCAGGGTCA CCTGATGAAT ATGAACTACG GAGCCAGAG TGGCTGAGAT AGCATGAACG CCATTGACTT AGAACACAG CCCAGGCCC CCAGGCCCC CCAGGCAGT AACATCCAGCT CCAGGCAGT AACATCCAGCT CCAGGCAGT AACATCCAGCT CCAGGCAGT AACATCCAGCT CCAGGCAGT AACATCCAGCT CCAGGCAGT AACATCCAGCT CCAGGCAGT AACATCCAGCT CCAGGCAGT AACATCCAGCT CCAGGCAGT AACATCCAGCT CGAGGCAGT AACATCCAGCT CGAGGCAGT CGAGGCAGT AACATCCAGCT CGAGGCAGT AACATCCAGCT CGAGGCAGT CGAGGCAGT CGAGGCAGT CGAGGCAGT CGAGGCAGT CGAGGCAGT CGAGGCAGT CGAGGCAGT CGAGGCAGC CGAGGCAGT CGAGGCAGT CGAGGCAGC CGAGGCAGT CGAGGCAGC CGAGGCAGT CGAGGCAGC CGAGGCAGT CGAGGCAGC CGAGGCAGT CGAGGCAGC CGAGCAGC CGAGCACC CGAGCACC CGAGCC CGAGCACC CGAGCCC CGAGCACC CGAGCACC CGAGCC CGAGCC CGAGCC CGAG	GRARTGGGC COCACACCT TCANGGANGC CCACACCT CCAGACTANA CCACTCAAAAT GCAGTTOGGC GGCGGTGAA GGAGGACT CCGACATCCT CCGACATCCT CAGTTAGATCC ATTTACATCC CAGATGATGT ATTTACATCC CGGCGTTAA AGTCGAAAGC GCTGAAAGC GCCACACTC GCACACCT GGCGTGGG	300 360 420 480 540 600 720 780 840 900 1020 1080 1140 1200 1200
55	TGGCTTACTG GGTAAGCAC CCACGCGTC GGARTGTAAGCC GAAGAGAGAG AGAGAGAGAGAGAGAGAGAGAGA	GANCCANGGG ANGGACATOA OTGAGTGAGG GAGATGACCG CCTCAGCAGG CCTAGCAGG ACGATGCACA ACGCTATGGA CTTCCAGACG CTCCAGACG TCTCCAGACG TCTCCAGACG TCTCCAGACG TCTCCAGACG TCTCCATACCA ACGAGATCAC TTACAAAACT ACGAGATCAG TCTCCTCCAG TCTCCCTGGACCAA TCCCCCTGGACCAA ACGAGGACCA ACGAGGACCA TCCCCTGGACCAA TCCCCCTGGACCAA TCCCCCTGGACCAA TCCCCCTGGACCAA ACGAGGGACT ACGAAACCCA ACGAGGACA ACGAGACCA ACGAGGACA ACGAGACA ACGACA ACGACAC ACGAGAC ACGACA ACGACAC ACGACA ACGACAC ACGACAC ACGACA ACGACAC ACGACA ACGACAC ACGACA ACGACAC ACGACA ACGACAC ACCAC ACGACAC ACCAC ACC	CARTIANAGO TTCAGACTOT ACCAGTOST ACCAGTOST ACCAGTOST ATTGACTOTC GARGCCAGA CCCAAACAT TCAACATCT ACTTCCAGAG TCAGAGACA TCAGCAGG TCAGGAGAC CCCAGGTT CCTGAGCCG CAGTTGCCCAA AGCTCCTGTC TCAAGATAGCA AGCTCTGTC TCAAGATAGA	GOTCAGGITIC CCCGGACCCA GTTTGAGTOT CAGCGACCA TCAACCCCCA AAGGAACTCT CACCGTTGGG GACCACGAAC GTTATTCCAG GCTCACCCCC AATGCATCCAC AATGCATGCT TCACCGGCAG AACTGAAGAC CTTGCAAGAC CGTTGCAGACC GGATAGGCCC GCATAGGCCC GCATAGGCCC GGATAGGCCC GGATAGGCCC GGATAGGCCC GCATAGGCCC GCATAGGCCC GCATAGGCCC GCATAGGCCC GCATAGGCCC GCATAGGCCC GGATAGGCCC GCATAGGCCC GCATAGCCC GCATAGGCCC GCATAGGCCC GCATAGGCCC GCATAGCCC GCATAGCCC GCATAGCCC GCATAGCCC GCATAGCC GCATAG	TGAACAGCTEG GCAGGTCATA GCCTACGGAA GGACAGGGTCATA ATGAACTACGA GAGGCCAGAGA TGGCTGGAGT AACATGAATG AACTGAATG AACTGAATG CCCAGGCCC AGGCCCC AGGCCCC AGGCCCC AGCCCC CC	GRAGATGGGC TCAGATGAAT TCAGATGAAT CCACCACACT TCAGATGAAAT TCAGTGCC GCAGCTACAT TTATCGTGCC GGGCGGTGAA GGAAGGAACT CCGACATCCT CCGACATCCT ATTTACATA AGTCGAAGC GCCAGATCCT GCAGATCCT GCAGATCCT AGTCGACACT GCCAGATCCT GCAGATCCT AGTCGACT GCAGATCCT AGTCGACT GCAGATCCT AGTCGACT GGCCTGGGG TCCGTTACTA AGTTCGACT TCGGTTACTA TCAGACT TCGGTTACTA TCAGACT TCGGTTACTA TCAGACT TCGGTTACTA TCAGACT TCGGTTACTA TCAGACT	300 360 420 480 540 660 720 840 900 1020 1080 1140 1200 1260 1380
55	TGGCTTACTG GCTTATCAGTT GGCTAAGCAG GCACCGGTC GGACTGTAC CAAAGCCGG GGAGGAGAAG AGCAGATCCT TCTCTACAT TGATAAAGCC TGCTCAACA TTATCAGAT TGCTTTGGCAG GGAAGGCACC CAAGGGAAG CAAGGGAAG CAAGGGAAG CAAGGGAAG CAACGGAAG CAACGGAAG CAACGGAAG	GANCCANGGG AAGGACATGA AGGACATGA AGGACAGG AGATGACGC CCTAGACAGG AGATGACGC CACACAGG AAGATGCAC CTCCAGACG CTCCAGACG CTCCAGACG CTCCAGACG CTCCAGACC CTCCAGACC CTCCAGACC CTGGACCAA ACGATACCA ACGACACAC ACGACACAC AACATACACA AACATACAA	CARTIANAGE TICAGACTOTI ACCAGTOGIT ACCAGTOGIT COTCCTCCTC ATTGGTGTC CARGCCCAAA CCCCAAACAT GTACAGACCA TCAACATCTT ACTTCCAGAG TCAGACACCT CCACGGTT CCAGGACCAG CAGTTGCCCA CAGTTACCAG ACATCT TCAAGATGACCA CAGTTACCAG CAGAGTACCA CAAGGTCCCA CAAGGTCCA CAAGGTCCCA CAAGGTCCCA CAAGGTCCCA CAAGGTCCA CAAGGTCCAAGGTCCA CAAGGTCCAAGGTCCAAC CAAGGTCCAAGGTCCAAC CAAGGTCCAAGGTCCAAC CAAGGTCCAAGGTCCAAC CAAGGTCCAAGGTCCAAC CAAGGTCCAACAC C CAAG	GOTCAGGITIC CCCGGGACCA GTTTGAGTGT TCAACCCCCA AAGGAACTAT TCACCCCCA AGGAACTAT TCACCCCCA TGTGCGGCAG GTTATTCCAG GTTATTCCAG GTTATTCCAG AATGCATACCCCC TCCTCTTCCA AATGCATAGAC CCTTGCAAAT GGACAGGCTC GGATCCCGAG CGATAAGGCTC TGGAAAT CGATAAGCTC TGGAAAT CGATAAGCTC TGGAAAT CCATAAGCTC TGGAAAT CCATAAGCTC TGGAAAT CCATCAGAAGCTC TGGAAAT CCATCAGAAGCTC TGGAAAT CCATCAGAAGCTC TGGAAAT CCATCAGAAGCTC TGGAAAT CCATCAGAAGCTC TGGAAACCCC CCCCCCGAAA	TGAACAGCTE GCAGGTCATA GCTACGGAA GGACCAGGGTCATA AGACTACGA GACCACAGGTCAACACGACCAGCAGCAGACACAGCAGCAGAGAGAACACAGGAGAGAACACGAGCAG	GTAGATGGGC TCAAATGGAC TCAAAGATGAC CCATCAAAAT CCATCAAAAT TTATCGTGC GGGGGTTAAA GGAAGGAC CCACACCT CCGACATCCT CCGACATCCT CCGACATCCT CAGATGATGC AGTTAGATCC GGCGGGTGAA GGTCGAAAGC TCCGTCAAAGC TCCGTCAAAGC TCCGTCAAAGC TCCGTCAAAGC TCCGTCAAAGC TCCGTCAAAGC TCCGTCAAAGC TCCATCACCT GGCCTCGGGC TCCGTTACTA AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTTCGACTT AGTATCACCT AGTTCGACTT AGCACTACCCC	300 360 420 480 540 660 720 840 900 900 1020 1140 1260 1320 1320
55	TGGCTTACRG GCTTATCAGTI GGCTAAGACA CCCAGGGGGGAGAAA GCAAGGGGGGAGAAA AGCAAGATCTAA CAGATTTAGC GTTCAAGATG TTCTCTCACAT TGATAAAGAC TTAGAGAT GCTTTAGCAG GTTTTGCAGA GCAAGAGGAAG GCAAGGGAAG CCACGGGAC CCACGGACC CTTACACAA CCACGGACC CTTACACAA CCACGGACC CTTACACAA CCACGGACC CTTACACAA CCACGGACC CTTACACAA CCACGGACC CTTACACAAG CCACGGACC CTTAGACAAG CCACGGACC CTTAGACACC CTTAGACCT CTTAG	GANCCANGGG AAGGACATGA AGGACATGA GAGATGACGG CCTCAGCAGG CCTCAGCAGG CACATGCCAG AGGATATGGA CTCCAGACG TTCCAGACG TTACAAAACT AAGGAGATCAG TCTCCTTCCA AACGAGACCA TTCCTCTTCA AACGAGACCA TCCCCTTCA AACGAGACCA AACGAGACCA CCCAGAGCCC CCCAGAGCCC	CARTINANGE TTCAGACTOTT ACCACTOTT ACCACTOTT COTCCTCCT ATTGCTTOT CGAGCCAGA CCCCAACAT TCAACATCTT ACTTCCAGAG TCAGACAGCT CAACATCTT CCTGGACCGA CCAGGOTT CCTGGACCGA CAAGTGCCA ACATGCCT TCAAGAGTACA CAAGTGACT TCAAGATGACT TCAAGATGACT TCAAGATGACT TCAAGATGACT TCAAGGCCA TCAAGGCCCA TCCAGGCCCA TCCAGGCCA TCCAG	GOTCAGOTTIC COCGAGACCA GTTTGAGTGT TCAACCCCA ANGGAACTCT CACCGTTGGG GACCACGAAC GTTATTCCAG GCTCACCCCC TCCTCTTCCC TCACGCCAC AACTGAACTG	TGAACAGCTIC GCAGGTCATA GCTTACGGAA GGACAGGGTCATA ATGAACTACG GAGGGTCATA ATGAACTACG GAGGCAGAA AGCTACAACG CATTTTAACTT AGAACACAGC CCAAGGCCC CAAGCCCC CAAGCCCC AGCCCGCCC	GTAGATGGGC CUCACACCT TCAAGGAAGC CUCACACCT CCAAGATTAG CCATCAAAAT TATCGTTGCC GGGGGTTACA TATACCTTGCC GGACATCCT AGTTAGATGA AGTTAGATGA AGTTAGATGA GCAGATCCA GCAGATCCA GCAGTACAT GCAGATCCA GCAGTACCT GCAGTACCT GGGGGTGGGG TCGGTTACTAGATCC AGTTGACTCC AGATGACTCA CAGTAGATCCA CAGTAGATCCA CAGTAGATCCA CAGTAGATCCA CAGTAGATCCA CAGTAGATCA CAGTAGATCA CAGTAGATCA CAGTAGATCA CAGTAGATCA CAGTAGATCA CAGTAGATCA CAGTAGATCA CAGTAGTGGGC CAGTAGTGGGC CAGTTGGGGC CAGTTGGGC CAGTTGGGGC GGGG	300 360 420 480 540 660 720 840 900 1020 1140 1200 1320 1380 1440 1500
55	TGGCTTACTG GCTTATCAGTT GGCTAAGACT GCTATCAGTT GGAATGTAAG CCAAGGGGGAGAAG AGCAGATCCT AGAATATGAC GTGCAAGATT TGTTAAGACT TGATAAAGC TGATCAACA TTATCAACA TTATCAGATT GCTTTGGCAG GGAAGGGCCCCC AGAGGGGAGC CCAGGGGAGC CCAGGGGACC CCAGGCCTC CCAGCCTC CCCACCCCC CTTATCAGATT CCAGGCCTC CCAGCCTC CCCACCCCC	GANCOAGGGG AAGGACATGA ATGAATGAGG GAGATGACG CCTAGCAGG AAGATGATGA ACGATGACAGG ACGATGCAG ACGATGCAG ACGATGCAG ACCAAGGAGG CTCCACTACC TTACAAGAG TCTCCTAGCAG TCTCCTACTACC TTGAACAAA TCTCCCTTCCA TTACCAAAACT TAGAACAA ACGACAGAGACG CCTGACACAC CTGGACCAA AACATCATGA AACATCATGA AACGAGGACC CCGTACATGC CCGTACATGC CCGGCCCCC CCGTACATGC CCAGCCCCCC CCGTACATGC CCAGCCCCCCC CCGTACATGC CCAGCCCCCCC CCGTACATGC CCAGCCCCCCCCCC	CARTIMAGE TICAGACTOTI ACCAGTOTI ACCAGTOTI COTCCTCCTC ATTGGTTGTC TGAATGGTC TGAATGGTC TGAACACAT TTACAGACCA TCAACAT TTACAGACCA TCACAGCCAC TCACAGGTC TCAGGACCAG TCAGGACCAG TCAGGACCAG AGATTAGCCC AGATTAGCCC AGATTAGCCC TCAAGATTAC CCAAGGTCCAC GCTCCTATCC GCTCCTATCC CCOTTGACCAG CCCCTCTC TCCAAGCCCC CCCCTCTC TCCAAGCCCC CCCCCTCTC CCACCC CCCCCTCTC CCACCC CCCCCCCC	OSTERGETTE COCCOCCOGNA TOTAGOSTA TOTAGCOCCA ANGGARACTET CACCOCCA TOTAGCOCCA GOTTAGCOCCA GOTTAGCOCCA GOTTAGCOCCA TOTACTCCA ANTGCATGCOCCA TCACCOCCA TCACCOCCA TCACCOCCA TCACCOCCA TCACCOCCA GOTTAGAAAT GOTTAGAAAT COCCCCCCOGNA COCCCCCCOGNA COCCCCCCOGNA COCCCCCCCA TICCAGTTTI	TGAACAGCTIG GCAGGTCATA GCCTACGGAA GGACAGGGTCAT GCCAGGGTCAT ATGAACTACO AACATCGATG AACATCGATG ACATCGATG CAGAACATCAT CAGACATCAT CAGACAT CAGACATCAT CAGACATCAT CAGACATCAT CAGACATCAT CAGACATCAT CAGACATCAT CAGACATCAT CAGACATCAT CAGACATCAT CAGACAT CAG	GRAGATGGGC TCAAAGATGGC CCACACCT TCAAAGATGAC CCATCAAAAT TTATCGTTGCC GGGCGTTGAC GGAGGGACCCT TCATCATCAC GGAGGACCC CCAACACCT CCAACACCT CCAACACCT CCAACACCT ACTTATCACCT ACACTTATCACCT ACACTTATCACCT ACACTTATCACCT ACACTTATCACCC ACTTATCACCC ACTT	300 360 420 480 540 660 660 720 780 900 960 1080 1140 1260 1380 1440 1560
55 60 65	TGGCTTACRG GCTTATCAGTI GGCTAAGACA CCCAGGGGGGAGAAA GCAAGGGGGGAGAAA AGCAAGATCTA AGAATATGGC GTGCAAGATG TTCTCTCACAT TGATAAAGCC TGCTCAACAC TTATCAGAT GCTTTGGCAG GCAAGGGGAGA GCAAGGGGAGA GCAAGGGGAG CCACGGGAC GCCCCCCCC	GANCOAGGGG ANGGACTAN ATGIAGAGGA AGAGTAN ATGIAGAGGA AGAGTAN AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	CAACTIAAGGC TTCAGACTGT ACCAGTGGTT ACCAGTGGTT COTCCTCCTC ATTGGCTGTC CTGAATGGCTGTC CCAGCCCAAA CAT TCACAGCCCAA TCACACACT TCACAGCCAC ACTTCCAGAGG TCAGAGGCG CAGTGCCCAA ACATTCTCAGAGGC AGTCCCTGTG ACTCCTGTG ACTCCTG ACTCCTGTG	OSTCAGSTIC CCCGGACCCA GTTTGAGTGT TCAACCCCCA AAGGAACTAT CACCGTTGGG GCTCACCCCC ACTTTCCA AATGCAGCAC ACTTTCCAG GCTCACCCCC AATGCAGCAC ACTGCAGCCC TCCCGGAAC CCTTGCAAT CCTTGCAAT CCTTGCAAT CCTTGCAAT CCACCCCCCCAA CCTCCCCCCCAA CCCCCCCCAAC TCCCCCCCAAC TCCCACTCCC TCCCACCCCC TCCCACCCCC TCCCACCCCC TCCCACCCCC TCCCACCCCCCACCC TCCCACCCCCCCACCCC TCCCACCCCCCCACCCC TCCCACCCCCCCC	TOAACAGCTIC GCAGGTCATA GCTTACGGAA AGACTAC GCAGGGTCAT ATGAACTACG AGACCAGGGTCAT AGACTACGATA AGACTACGATA AGACTACGATA AGACTACGATA AGACTACGATG CCAGGGCCC CAGGGCCC CAGGGCCC CAGGCCC CAGGCCC CAGGCCC CAGGCCC CAGGCCC CAGGCCC CAGGCCC CAGGCCC CAGCCC CC CAGCCC AGCCC AGCCC CAGCCC CAGCCC CAGCCC CAGCCC CAGCCC CAGCCC CAGCCC CAGCC GTAGATGGGC CUCACACCT TCAAGGAAGC CUCACACCT CCAGAGTTAG CCATCAAAAT GCAGTTGGC GGCGGTTACA GGAGGTACAT ATTATCGTGC CAGATACT ATTACCATA ATTACAATA ATTAGATCC GCAGATCCA GCAGTCCAT GCAGTACCT GCAGTCCAT CCGAGTCCAT CCAGATCCAT CCGAGTCCAT C	300 360 420 480 540 660 720 840 900 1020 1140 1200 1320 1380 1440 1500	
55	TGGCTTACRG GCTTATGAGT GGCTANGACA CCCAGSGGTC GGAATTTAAC CANAGGCGGG GGAGGAGAAG AGCAGATATGAC GTGCAGGAGTAG GTGCAGGAGTAG TCTCTCACAT TGATAAAGC TGGCCCCC TGGCAGGGGAGAG GGAGGCCCCC GGGGGGAGGCCCCCC CTGGAATCCC CTCAGACCCCCC CTGGAATCCC	GANCOANGIGO ANGGACATRA GTGAGTAGGA GAGATGACCA GAGATGACCA CCTAGCAGG ACGATGCAG ACCATACCA ACCATACCA ACCATACCA TTACAAAACT TTACAAAACT TTACAAAACT TTACACAAG ACCAAAGGACCA ACCATACC TTACACAAG ACCAAAGACCA ACCAAAGACCA ACCAAAGACCA ACCAAAGACCA CTGGACCA ACCAAAGACCA ACCAAAGACCA ACCAAAGACCA ACCAAACACCA ACCAAACACCA ACCAAACACCA ACCAACACCA ACCAACCACC	CAACTAAGC TCCAACGAC ACTGACACAC ACTGACACAC CACTACACAC CACTACAC CAC	GFTCAGGFTC COCGAGCCC GTTGAGTGT CACCAGGTT CACCAGGTT CACCAGGTT CACCAGGTTGG GCCACCAG GTTATTCAG GCCACCAG GGCACCAG GGCACCAG GGCACCAG GGCACCAG GGCACCAG GGCACCAG GGCACCAG GGCACCAG GGCACCAG GGCACCAC GGCACCAG GGCACCAC GGCCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCACCAC GGCAC	TOAACRACTI GOCAGGCATA GCCTACOGRA GCCTACOGRA GCCACOGRA GCCCACOGRA AGCACACAC TTTCCCCACC TTTCCCCACC TTTCCCATC CARACATTCC TCCCCACCAC TTTCCCCATC CARACATTCC TTTCCCATC TTTCCCATC TTTCCCATC TTTCCCATC TTTCCCATC TTTCCCATC TTTCCCATC TTTCCCATC TTTCCCATC TTTCCATC TTTCCCATC TTTCCATC	GRAGATGGGC COAGACCT TCAAGGAAGC COAGACCT COAGACCT COAGACCT COAGACCT COAGACCT TTATCGTGCC COGCCTACA TTATCGTGCC COGCATCAC TATTCGTGCC COGCATCAC TATTCACAT AGTCGAAGCC GCCAGATCCT GCCAGATCCT GCCAGATCCT GCCAGATCCT GCCAGATCCT GCCCTCAGACCC AGTTAGATCC GCCAGATCCA AGTTAGATCC GCCAGATCCA AGTTAGATCC GCCAGATCCA AGTTAGACC AGTTAGACC CAAACCCATA AGTTAGACC CAAACCCATAC CCCAGATCCA CCCAGATCCA CCCAGATCCA CCCAGATCCA CCCAGATCCA CCCAGATCCA CCCAGATCCA CCCAGATCCA CCCAGATCCA CCCATACCC CCAAACCCATA CCCATATCC CCAAACCCATAC CCAGATCCA CCCAGATCCA CCCACA CCCACAC CCCACAC CCCACA CCCACAC CCCCACAC CC	300 360 420 480 600 600 720 780 900 1020 1140 1200 1320 1320 1440 1500 1500 1620 1620 1740
55 60 65	TOGETTACHE GCTTATCAGTT GCCTAAGACA CCCAGGCGTAGACA CCAAGGCGGA GGAGGAGAA GCAGGTCCC AGCAGGAGCAGA TCATTAAAGCC TGTCACAT TTATAAAGCC TGTCACAC TTATCAGAT GCTTTGGCAG GGAAGGGAGA GCAAGGGAGA GCACGGGAGC CCCACCCT TCTCACAT TTATCACAG TTATCACAG TTATCACAG TTATCACAG TTATCACAG TTATCACAG TTATCACAG TTATCACAG TTATCACAG TTCTCACAG TTCTCACCAG TTCTCACCAG TTCTCACCAG TTCTCACCAG TTCTCACCAG TTCTCACCAG TCCCACCCC TTCGACAGCCC TCCCACCCC TTCTCACCAG TTCTCACCAG TCCCACCCC TCCCACCCC TTCTCACCAG TCCCACCCC TCCCACCCC TTCTCACCAG TCCCACCCC TCCCACCC TCCCACCC TCCCACCC TCCCCC TCCCCC TCCCCC TCCCCCC TCCCCCC	БАЛСОМОВО АЛОВОСТВОЕМ В В В В В В В В В В В В В В В В В В В	CARCTRANGE THORACTOR TOTAL TOT	GSTCARGSTC CCCGGACCC GTTGAGTGT CACCGCATA TTCAACCCCA AAGGAACTT CACCGCATA GTTATCAG GTCATGGGGG GTCACCGGA AATGATCA CACCGCA AATGATCA CACCGCA AATGATCA CACCGCA CACCACCA CACCGCA CACCGCA CACCGCA CACCGCA CACCACCA CACCA CACCGCA CACCA	TOAACRAGHTO COCACAGA GOCACAGA GOCACAGA GOCACAGA GOCACAGA AGACACACA	GRAGATGGGG CONGACCT COMMINGTON COMMINGTON GRAGATGAT COMMINGTON GRAGATGAT THATCOTIGGC GRAGATGAT COGACATCAT ATTACOTIGGC COGACATCAT ATTACOTIGGC COGACATCAT ATTACOTIGGC COGACATCAT CAGACATCAT CAGACAT CA	300 360 420 480 600 660 720 780 900 900 1020 1140 1200 1320 1320 1340 1560 1560 1560 1560 1680 1740 1800
55 60 65	TOGCTTACTG GCTTATCAGTT GGCTANGACA GCAGGCGTC GGAATGTAAA GCAAGATGTAAA AGCAAATGTAAA AGCAAATGTAAA AGCAAATGTAAA TCTATCACAT TCATAAAAGCC TCTGAGCCC TCTGACCC TCTGACCC TCTGACCC TCTGACCC TCTGACCC TCTGACCC TCTGACCC TCTGACCC TCTGACCC TCTGACCT TCTCACCAC TCTCACCAC TCTCACCAC TCTCACCAC TCTCACCAC TCTCACCAC TCTCACCAC TCTCACCAC TCTCACCC TCTGAATTCA CACCCC TCTGAATTCA C	GAACCAMGGG AAAGGACATAG GTGAAGTGAGG GGAATGACCG CCTCAGCAGG CCCAGGCCC CCTCAGCCC CCTCAGCCC CCTCAGCCC CCTCAGCCC CCAGCCCC CCAGCCCCC CCAGCCCC CCAGCCCCC CCAGCCCCC CCAGCCCC CCAGCCCCC CCAGCCCCC CCAGCCCCC CCAGCCCCC CCAGCCCCC CCACCCC CCAGCCCCC CCACCCC CCACCCC CCACCCC CCACCCC CCACCCC CCACCCC CCACCCC CCACCCC CCACCC CCACCC CCACCCC CCACCC CACCC CACCC CCAC	CARCTAAGE TICAGACHT ACCAGTGTT TICAGACHT ACCAGTGTT TICAGACHT ACCAGTGTT TICAGACHT TICAGA	GETCAGGETC COCCAGAGETC GETCAGGETC GETCAGGETC GETCAGGETC COCCAGGETC GETCAGGETC COCCAGGETC GETCAGGETC GETCAGGETC GETCAGGETC GETCAGGETC GETCAGGETC GETCAGGETC GETCAGGETC GETCAGGETC TCAGGGETC GETCAGGETC GETCAG	TORACE/RECTI GOAGGTCAN GCCTA/COSEAN GCCTA/COSEAN GCCTA/COSEAN GCCTA/COSEAN GCCTA/COSEAN GCCCA/COSEAN TTTCCCA/CCCA/CCCA TTTTCCCA/CCCA/CCCA GCCCA/CCCA/CCCA TTTTCCCA/CCCA/CCCA GCCCA/CCCA/CCCA/CCCA GCCCA/CCCA/	GRAGATOGUE TENAGGAGE CUCCACACCE CUCAGATOGUE CONGATOGUE	300 360 420 480 600 720 780 900 900 1020 1140 1260 1320 1340 1560 1620 1620 1740 1860
55606570	TOGCTTACTE TTTTACAGT GGCTAGAGAGA GGCAAGGAGA GGAAGGAGA GGCAAGGAGA TTTTACAGAT TTTTTACAGAT GCTTTGGCA GGCGAGAGAG GCCAAGGAGAG TTTTTTTTGGCA GCTTTTTGGCA GCAAGGAGAGA CCACGGAAC TTTTTTGGCA GCAAGGAGAGA CCACGGAAC TTTTTTGGCA GCAAGGAGAC TTTTTTGGCA GCAAGGAGAC TTTTTGGCA GCAAGGAGAC TTTTTGGCAAG CCACGGAAT TTTTTGGCAA GCAAGGAGAC TTTTTGGCAAG CCACGGAAT TTTTTGGCAAG CCACGGAAT TTTTTGGCAAG CCACGGAAT TTTTTGGCAAG CCACGGAAT TTTTGGCAAG CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAT CCACGGAAG CCACGGAAT CCACGAAT CCACGGAAT CCACGAAT CCACGGAAT CCACGAAT CCACGGAAT CCACGAAT CCACG	GAACCAMGGG AAAGGACATA GTUAGTTGAG GTUAGTTGAG GTUAGTTGAG GTUAGTTGAG GTUAGTTGAG GTUAGTTGAG GTUAGTTGAG GTUAGTTGAG GTUAGTTGAG GTUAGTTGAG GTUAGTGAG GUAGTGAG GUAGTGAG GUAGTGAG GUAGTGAG GUAGTTGAG GUAGTGAG GUAGTTGAG GUAGTGAG GUAGTTGAG GUAGTGAG GUAGTTGAG GUAGTGAG GUAGTTGAG GUAGTGAG GUAGTGAG GUAGTTGAG GUAGTGAG G	CARCTARAGE TECHNOLOGY TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACTOR TOTAGACT TOTAGACTOR TO	GETCAGGTTC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TOAACEASCTIS GOAGETCATA GCCTACOGRA GCCTACOGRA GCCTACOGRA GCCTACOGRA ACATCACA GRAGATOGOC TCAAGGAAC COCCAACC	300 360 420 480 540 660 720 840 960 1020 11200 1200 1380 1440 1560 1560 1680 1740 1800 1800 1800 1800 1800 1800 1800 1800 1800 1800 19	
55 60 65	TOGGTTACTO TTTTACAGT GGCTAAGAGA TTTTACAGT GGAGGAGAGA AGAGAGTCAT AGAATATAGA TTTTTACAGAT TTTTTACAGAT GCTTTACAGA TTTTTACAGAT CCTTACAGA TTTTTACAGAT CCTTAGACAG TTTTTACAGAT CCTTAGACAG TTTTTACAGAT CCTTAGACAG TTTTTACAGAT CCTTAGACAG TTTTACAGAT CCTTAGACAG TTTTACAGAT CCTTAGACAG CCTTAGACAG TTTTACAGAT CCTTAGACAG CCTTAGA	GAACCAAGGG AAAGGACAAGGG AAAGGACAAGG GAACAACGC CCTAAGCAGG AAGGACAAGG CCTCAAGCAGG AACAAGCAGC CCTCAAGCAGG AACAAGGACACAG CCTCAAGCAGAGAGACAGC CCTCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CARCTANAGE TRANSCOTOR ACCAGNOTORT ACCAGNOT	GETCAGGETC COCCAGAGETC GETCAGAGETC GETCAGAGETC GETCAGAGETC GETCAGGETC CACCAGGETC TCAGCAGGETC GACCAGGETC GACCAGGETC GACCAGGETC GACCAGGETC GACCAGGETC GACCAGGETC GACCAGGETC GACCAGGETC TCACGGETC TCACGGETC GACCAGGETC GAC	TOAACRICTIE GOAGGTCAN GOCTACANA GOCTACAGA GOACAGACT GOCAGGTCA CCCAGAGACA GAGACACAC AAACTCAGAC AAAACTCAGAC AAACTCAGAC C AAACTCAGA	GRAGATOGUE TONAGGNAU TONAGGNAU TONAGGNAU TONAGGNAU TONAGGNAU GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE GRAGATOGUE AGTOGNAU AGTOG	300 360 420 480 600 720 780 900 900 1020 1140 1260 1320 1340 1560 1620 1620 1740 1860
55606570	TOGGTTACTS CTTATCAGTT GGTTACTAGT GGTTACTAGT GGTTACTAGT GGTTACTAGT GGTTACTAGT GGTTACTAGT GGTTACTAGT TAGTAGT GGTTACTAGT TAGTAGT	GAACCAMGGG AAAGGCATTAG GTGAGTGAGG GCAGGCAGG CCCCAGGCAGG CCCCAGCAGGCAG	CARCTAAGC TICAGACTGT ACCAGTGTT TICAGACTGT ACCAGTGTT TICAGACTGT ATTOGACTGTT ATTOGACTGTT ATTOGACTGTT ATTOGACTGTT ATTOGACTGTT CARCCCTGT TICAGCCTGT TICAGCCTGT TICAGCCTGT TICAGCCTGT TICAGCTGTT CARCGTT CARCGTT ACTCCAGAGTT CARCGTGT ACTCCAGAGTT CARCGTGT ACCAGGTT CARCGTGT TICAGCTGT TICAGCT TI	COTCAGGTTC CONCAGGTTC CONCAGGTC	TOAACAGCTT GOACAGCTT GOACAGCT	GRAGATOGUE TOMOGRAGE COMMANDA	300 420 480 480 600 720 780 960 1020 1140 1260 1380 1440 1560 1620 1620 1380 1440 1560 1620 1740 1860 1740 1860 1980
55606570	TOGCTTACTO TOTACTACTO OTACTACT TOTACTACT TOTACT TO	GAACCAMGGG AAAGGCATTAG GTGAGTGAGG GCAGGCAGG CCCCAGGCAGG CCCCAGCAGGCAG	CARTENAMIC THORACTOR ACCIONTONT ACCIONTONT ACCIONTONT TO ACCIONT TO ACCIONTONT TO ACCIONTONT TO ACCIONTONT TO ACCIONTONT TO ACCI	GETCAGGTTC COCCOGNACO TTTAGGAGGGG COCCOGNACO ANGGAACTCT CACCOTTOG CACCOTTOG ANGGAACTCT CCCCCCCCOGNAC ANGGAACTCT CCCCCCCCCAG ANGGAACTCT CCCCCCCCCAG ANGGAACTCT CCCCCCCCAG ANGGAACTCT CCCCCCCCAG ANGCACC CCCCCCCAG ANGCACC A	TOALGERETTE GOOGLEGE TO TOALGERETTE GOOGLEGE TO TOALGERETTE GOOGLEGE TO TOALGERETTE GOOGLEGE	GRAGATOGUE TOMAGRAGUE COCCACACA COCCACACA GRAGATOGUE THAT GRAGATOGUE COCCACACACA AGATOGAA 300 420 480 540 660 720 840 960 1020 1020 1180 1260 1320 1440 1560 1560 1560 1680 1740 1800 1800 1800 1800 1900 2040 2040 2160	
55 60 65 70	TOGGTTACTO TTTTACAGTT GOCTAGAGTACTO TTTTACAGTT GOCTAGAGTACTO TOGGTAGT GOCTAGAGTACT TAGAGTACT TAGAGT	GAACCAAGGG AAGGGATAGAG GTGAATGAGG AAGGAATGAGG AAGGAATGAGG AAGGAATGAGG AAGGAATGAGGAGG GGGAATTAGG GGGAATGAGG GGGAATTAGG TTGAATGAGGAGG GGGAATTAGG TTGAATGAGGAGG GGGAATTAGG TTGAATGAGGAGG GGGAATTAGG TTGAATGAGGAGG GGGAATTAGG TTGAATGAGGAGG GGGAATTAGGT TTGAATGAGGAGT TTGAATGAGGAGG GGGAATTAGGT TTGAATGAGGAGT TTGAATGAGGAT TTGAATGAGGAT TTGAATGAGGAT TTGAATGAGGAT TTGAATGAGGAT TTGAATGAGGAT TTGAATGAGGAT TTGAATGAGGAT TTGAATGAGGAT TTGAATGAGAATGAGAGT TTGAATGAATGAGAATGA	CARCTARAGE GARGESTER ACTORDATE TORANGES GARGESTER GARGESTER TORANGES COCCARACT COCCARACT TORANGES COCCARACT COCCARACT TORANGES COCCARACT COCCARACT COCCARACT COCCARACT COCCARACT COCCARACT TORANGES COCCARACT COCCARACT TORANGES COCCARACT COCCARACT TORANGES	GETCAGGTEC COCCAGGTEC CACCATTAGA	TOALGERGTE GOOGGEGET TO TO TO THE TOTAL TO T	GRAGATOGUE COMMATTOGUE COMMAT	300 420 420 480 540 660 720 840 900 900 1020 1140 1120 11320 11320 11320 11440 1500 1680 1740 1860 1980 2040 2140 2100 2120 2120
55606570	TOGCTTACTO TOTALTACTO	GAACCAAGGG AAGGGACTAG CTCAAGGGACAAGGGACAAGGGACAAGGGACAAGGGACAAGGGACAAGGGACACAAGGGACACAAGGGACACAAGGGACACAAGGGACACAAGGGACACAAGGACACAAGGGACACAAGCACAAGGACACAAGGACACAAGGACACAAGGACACAAGGACACAAGGACACAAGGACACAAGGACAAGACACAAGGACACAAGGACACAAGACACAAGGACACAAGACACAAGGACACAAGACACAAGACACAAGACACAAGACACAAGACACAAGACACAAGGACAAGACACAAGGACAAGACACAAGGACAAGACAACA	CARTENAMIC THORACTOR ACCAPTORIA A	COTCAGGATTC COCCAGGATTC OCCAGGATTC COCCAGGATTC COCCAGGATTC COCCAGGATT COCCAGATT COCCAGGATT CO	TOALCASCTIC CONGENITY CONCENTRATION CONCENTR	GRAGATOGUE TOMAGRAMO TOMAGRAMO CONNENTRA GENETTOGE GONOCTACH GONOC	300 420 480 540 660 720 840 960 1020 1080 1260 1380 1440 1380 1440 1500 1500 1680 1780 1780 1880 1780 1880 1980 20
55 60 65 70	TOGGTTACTS TTTTTGGTAG GRAGITAGAG AGGAGGTAGAG GAG	GAACCAMGGG AAGGGATGAG GTAAGTGAGG GAAGTAGTGAG ACCAMGGAGG GAAGTAGTGAG ACCAMGGAGG GTAAGTGAGGAG ACCAMGGAGG GTAAGTGAGG ACCAMGGAGG TTCCACTTCCAC TTCACACTAGG ACCAMGGAGG GTAACTAGG GGCAACTAGG GGCAACTAGG GGCAACTAGG GGCACTTAGGAGGAGG GGCAACTAGG GCCAACTAGG	CARTARAGE THORSESS TO THE CONTROL OF	GETCAGGTEC COCCOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TOALGERETTE GOOGLEGE TO THE TOALGERETTE GOOGLEGE TO THE TOALGERETTE GOOGLEGE TO THE TOALGERETTE GOOGLEGE TOALGE TOALGERETTE GOOGLEGE TOALGERETTE GOOGLEGE TOALGERETTE TOALGERETTE GOOGLEGE TOALGERETTE TOALGERETTE GOOGLEGE TOALGERETTE GOOGLEGE	GRAGATOGUE TOMAGRAMO TOMAGRAMO CONTRACTOR GRAGATOM GRAGAT	300 420 480 540 660 660 780 900 1020 1140 1220 1380 1440 1500 1520 1620 1620 1620 1620 1740 1860 1980 2040 2040 2040 2120 21
55 60 65 70	TOGGTTACTS TTTTTGGTAG GRAGINATACTS GRAGINATACTS GRAGINATACTS GRAGINATACTS GRAGINATACTS GRAGINATACTS GRAGINATACTS GRACIA GRAGINATACTS GRACIA G	GAACCAAGGGA AAGGGATA CTCAAGGGATA CTCAAGGGATA CTCAAGGATA CCCAAGGATA CCCAAGGATA CCCAAGGATA CCCAAGGATA CCCAAGGATA CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGGATA CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGGATA CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGGAT CCCAAGTAGGAT CCCAAGTAGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGGAT CCCAAGTAGAT CCCAAGTAG	CARCTARAGE TOGAGE GETCAGGETCE CONGROUNT CONG	TOALGERGETE GOAGGETOTA CONTROL OF THE CONTROL OF TH	GRAGATOSIC TOMAGEMAC TOMAGEMAC COMMANTES CONTENANT CONTENANT THAT COPTO GOOGLOTTOM COMMANT COM	300 420 480 540 660 720 840 960 1020 1080 1260 1380 1440 1380 1440 1500 1500 1680 1780 1780 1880 1780 1880 1980 20	
55 60 65 70 75 80	TOGETHATE TOTALING TO	GAACCANGGG AAGGACAAGGACAAGGACAAGGACAAGGACAAGGACAAGGACAAGAAAAAA	CANTENAME THOMASTER TOTALOGATER GOTCAGGTEC COCCOGGACTA COCCAGGTEC	TRANACRISCHE GONGETONE GON	GRAGATGGGC TOMAGRAGA CONTONADA CONTO	300 420 480 544 600 660 660 780 900 1020 1140 1200 1260 1380 1500 1500 1500 1500 1500 1500 1500 15	
55 60 65 70	TOGGTTACTS CTTTACAGE TOTTACAGE TOTTA	GANCACAGO GANCACAGO ANGORACIO GANCACAGO GANCACAGO ANGORACAGO ANGORACAGO CHARACAGO CANTENAME THOMSONE TO THE TOTAL THE	GOTCAGOTEC COCCAGOTEC CACCACCAC CACCACCAC CACCACCAC CACCACCA	TOALGERGETE GOOGLOCK AND TO THE TOALGE TO THE TOALGE TO THE TOALGE TO THE TOALGE GRAGATOGUE CONAGRAMO CONAGRATOGUE CONAGRATOGUE CONAGRATOGUE CONAGRATOGUE CONAGRATOGUE GRAGAGGAC GRAGAGGAC AGTICAL AGTICAL AGTICAL AGTICAL AGTICAL CONAGRATOCUE AGTICAL AGTICAL AGTICAL AGTICAL AGTICAL CONAGRATOCUE ACTICAL AGTICAL CONAGRATOCUE ACTICAL AGTICAL CONAGRATOCUE ACTICAL CONAGRATOCUE ACTICAL CONAGRATOCUE ACTICAL CONAGRATOCUE	300 420 480 544 600 660 660 672 780 900 1020 1140 1132 1132 1132 1132 1132 1132 1132 113		
55 60 65 70 75 80	TOGGETTACHS TOTTACHS OTTACH TOT	GAACCAAGGG AAGGGAAGGG AAGGGAAGGGAGGGAGGG	CANCENARIO THORAGENER TO TO TO TO TO TO TO TO TO TO TO TO TO T	GOTCAGGTEC COCCAGGTEC COCCAGGTEC CAGGGTEC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTT CAGGGT CAGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGT CAGGGT CAGGGT CAGGGT CAGGT CAGGGT CAGGT CAGGGT CAGGT CAGGGT CAGGT CAGGT CAGGGT CAGGT	TOALGERETE GOOGLEGE TO TO THE TOALGERETE GOOGLEGE TO THE TOALGERETE GOOGLEGE TO THE TOALGERETE GOOGLEGE TOALGE TOALGE TOALGE TOALGE TOALGE TOALGE TOALGE TOALGE TOALGE	GRAGATOGUE TOMAGRAMO TOMAGRAMO CECNATORA CECNA	300 420 480 544 600 660 660 780 950 1080 1080 1140 1200 1320 1320 1560 1560 1520 1580 1590 1590 1590 1590 1590 1590 1590 159
55 60 65 70 75 80	TOGGETTACHS TOTTACHS OTTACH TOT	GAACCAAGGG AAGGGAAGGG AAGGGAAGGGAGGGAGGG	CANCENARIO THORAGENER TO TO TO TO TO TO TO TO TO TO TO TO TO T	GOTCAGGTEC COCCAGGTEC COCCAGGTEC CAGGGTEC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTTC CAGGGTT CAGGGT CAGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGGT CAGGT CAGGGT CAGGGT CAGGGT CAGGT CAGGGT CAGGT CAGGGT CAGGT CAGGGT CAGGT CAGGT CAGGGT CAGGT	TOALGERETE GOOGLEGE TO TO THE TOALGERETE GOOGLEGE TO THE TOALGERETE GOOGLEGE TO THE TOALGERETE GOOGLEGE TOALGE TOALGE TOALGE TOALGE TOALGE TOALGE TOALGE TOALGE TOALGE	GRAGATOGUE CONAGRAMO CONAGRATOGUE CONAGRATOGUE CONAGRATOGUE CONAGRATOGUE CONAGRATOGUE GRAGAGGAC GRAGAGGAC AGTICAL AGTICAL AGTICAL AGTICAL AGTICAL CONAGRATOCUE AGTICAL AGTICAL AGTICAL AGTICAL AGTICAL CONAGRATOCUE ACTICAL AGTICAL CONAGRATOCUE ACTICAL AGTICAL CONAGRATOCUE ACTICAL CONAGRATOCUE ACTICAL CONAGRATOCUE ACTICAL CONAGRATOCUE	300 420 480 544 600 660 660 672 780 900 1020 1140 1132 1132 1132 1132 1132 1132 1132 113

	ACANTCAGAN	ATCACGCAGG	CATTTTGGGT	AGGCGGCCTC	CAGTTTTCCT	TTGAGTCGCG	2760
	AACCCTCTCC	GTTTGTCAGA	ATGAAGTATA	CAACTCAATG	TTTTTCCCCCC	TTTTTTATATA	2820
	ATAATTATAT	AACTTATGCA GACAATCGAT	TTTATACACT	ACGAGTTGAT	CTCGGCCAGC	CAAAGACACA	2880 2940
5	TACAATATGA	AGTTATTAGT	TCTTAGAATG	CAGAATGTAT	GTAATAAAAT	AAGCTTGGCC	3000
,	TAGCATGGCA	AATCAGATTT	ATACAGGAGT	CIGCATTIGC	ACTITITITA	GTGACTAAAG	3060
	TTGCTTAATG	AAAACATGTG	CTGAATGTTG	TGGATTTTGT	GTTATAATTT	ACTITGTCCA	3120
	GGAACTTGTG	CAAGGGAGAG	CCAAGGAAAT	AGGATGTTTG	GCACCC		
10	Sec ID NO.	331 Protei	semience				
10	Protein Ac	cession #:	AAA5239	8			
	1	11	21	31	41	51	
15	1	HIKEALSVVS	PROOF PROFA	CTDUT NUTSM	#Acceptive	TOUNGDOUGG	60
13	ODMI-SODDAR	VTIKMECNPS	OVNGSRNSPD	ECSVAKGGKM	VGSPDTVGMN	YGSYMEEKHM	120
	DDDNMTTNED	RVIVPADPTL	WSTDHVROWL	EWAVKEYGLP	DVNILLFONI	DGKELCKMTK	180
	DDFORLTPSY	NADILLSHLH	YLRETPLPHL	TSDDVDKALO	NSPRLMHARN	TDLPYEPPRR	240
	SAWTGHGHPT	POSKAAOPSP	STVPKTEDOR	POLDPYQILG	PISSRLANDG	SGQIQLWQFL	300
20	LELLSDSSNS	SCITWEGTNG	EFKMTDPDEV	ARRWGERKSK	PHMNYDKLSR	ALRYYYDKNI	360
	MTKVHGKRYA	YKFDPHGIAQ APNPYWNSPT	ALQPHPPESS	LYKYPSDLPY	MGSYHAHPQK	MNFVAPHPPA	420
	LPVTSSSPPA	APNPYWNSPT	GGIIPNIKDP	IShineshiasi	**		402
	Seg ID NO:	332 DNA se	quence				
25	Nucleic Ac	id Accession	#: NM_0000	20			
	Coding seq	uence: 283-	1794				
		11	21	31	41	51	
	î	1	1	1	1	Ĭ.	
30	AGGAAACGGT	TTATTAGGAG	GGAGTGGTGG	AGCTGGGCCA	GGCAGGAAGA	CGCTGGAATA	60
	AGBARCATTT	TTGCTCCAGC	CCCCATCCCA	GTCCCGGGGAG	GCTGCCGCGC	CAGCTGCGCC	120
	GAGCGAGCCC	CTCCCCGGCT	CCAGCCCGGT	CCGGGGCCGC	GCCGGACCCC	AGCCCGCCGT	180
	CCAGCGCTGG	CCCGCCACCC	GCGGCCGCGC	GGTGGAGGGG	AGGTGGCCCC	COCCCCCCC	300
35	AGGCTAGCGC	TTCTGATGCT	COMMISSION	TTCCTCACCC	AGGGAGACCCTT	TGTGAAGCCG	360
55	TCTCGGGGCC	CGCTGGTGAC	CTGCACGTGT	GAGAGCCCAC	ATTGCAAGGG	GCCTACCTGC	420
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40	CACTACTGCT	GCGACAGCCA CGGAGCAGCC	CCTCTGCAAC	CACAACGTGT	CCCTGGTGCT	GGAGGCCACC	600 660
40	CAACCTCCTT	TGGCCCTGGT	GGCCCTTGGGT	GTCCTGGGC	TOTOGCATOT	CCGACGGAGG	720
	CAGGAGAAGC	AGCGTGGCCT	GCACAGCGAG	CTGGGAGAGT	CCAGTCTCAT	CCTGAAAGCA	780
	TCTGAGCAGG	GCGACACGAT	GTTGGGGGAC	CTCCTGGACA	GTGACTGCAC	CACAGGGAGT	840
	GGCTCAGGGC	TOTOTTOT	GGTGCAGAGG	ACAGTGGCAC	GGCAGGTTGC	CTTGGTGGAG	900
45	TGTGTGGGAA	AAGGCCGCTA	TGGCGAAGTG	TGGCGGGGCT	TGTGGCACGG	TGAGAGTGTG	960 1020
	GCCGTCAAGA	TCTTCTCCTC	GAGGGATGAA	CAGTCCTGGT	TCCGGGAGAC	CARCACCTAT	1080
	COCKACTCGA	CCACCCACCT	GTGGCTCATC	ACGCACTACC	ACGAGCACGG	CTCCCTCTAC	1140
	GACTTTCTGC	AGAGACAGAC TGGCGCACCT	GCTGGAGCCC	CATCTGGCTC	TGAGGCTAGC	TGTGTCCGCG	1200
50	GCATGCGGCC	TGGCGCACCT	GCACGTGGAG	ATCTTCGGTA	CACAGGGCAA	ACCAGCCATT	1260
							1320
	GCCGACCTGG	GCCTGGCTGT TGGGCACCAA	GATGCACTCA	CAGGGCAGCG	ATTACCTGGA	CATCGGCAAC	1380 1440
							1500
55	GAGATTGCCC	GCOGGACCAT	CGTGAATGGC	ATCGTGGAGG	ACTATAGACC	ACCCTTCTAT	1560
	GATGTGGTGC	CCAATGACCC	CAGCTTTGAG	GACATGAAGA	AGGTGGTGTG	TGTGGATCAG	1620
	CAGACCCCCA	CCATCCCTAA	CCGGCTGGCT	GCAGACCCGG	TCCTCTCAGG	CCTAGCTCAG	1680 1740
	ATGATGCGGG	AGTGCTGGTA AAAAAATTAG	COCAAACCCC	CACAACCCTA	AAGTGATTCA	ATAGCCCAGG	1800
60	AGCACCTGAT	TCCTTTCTGC	CTGCAGGGGG	CTGGGGGGGT	GGGGGGCAGT	GGATGGTGCC	1860
••	CTATCTGGGT	AGAGGTAGTG	TGAGTGTGGT	GTGTGCTGGG	GATGGGCAGC	TGCGCCTGCC	1920
	TGCTCGGCCC	CCAGCCCACC	CAGCCAAAAA	TACAGCTGGG	CTGAAACCTG	ATCCCCTGCT	1980
	GTCTGGCCTG	CTCAAAGCGG	CAGGCTCCCT	GACGCCTGGC	TCTCTCCCCA	CCCCTATGGC	2040
65	CAGCATGGTG	CACCCCCTAC AGGGAATCCC	AGTCCCAGAC	TCAGAGCCCC	GGCCTGCACT	TTGCCCCCTG	2160
05	CCCTTGATCA	ACCCCACTGC	CCCACCAGAG	CTGCCAGGGT	GGCACAGGGC	CCTGTCCAGC	2220
	CCCTGGCACA	CACTTCCCTG	CCAGGCCTCA	GCCTCTAGCA	TAAGCTCCAG	AGAGCCAGGG	2280
							2340
70	TCCTCAACAA	GAGTGCAGCT	TGCTGAATGT	CAGCTGCCTG	AGAGAGCTGG	GGCCTGACTT	2400 2460
70	ACTAGGGCAT	GTCAGATGGG	CARCOCCAC	CACTTTCAGA	TTAACTGAGA	CCATATOGAG	2520
	GCCAAGCATG	GCAGGGGGAA	GGTCAGTGGG	TGTCAAGAGA	CCCAGGTCTG	ACCCCGGATG	2580
	TTTGCTCCAT	GTYGACAAAAG	CAGGCCTGTC	TCAGGACCTT	TTCTTTTCTT	TTTTCCTTCT	2640
7.	TITTTTTTT	GACACGGAGT	TTCGCTCTTG	TTGTCCAGGC	TAGAGTGCAA	TGGCATGATC AGACTCCCGA	2700
75	CCAGCTCACC	GCAACGTCTA	CCTCCCAGGT	TCAAATCATT	CTCTTGCCTC	AGACTCCCGA	2760
	GTAGCTGGGA	TTACAGGCAC	ATGCCACCAT	GCCTGGCTAA	TITTGTATAT	TIAGTAGAAA	2820 2880
	A CONCACOOT	CCCABAGTGC	TGGGGTTACA	GGTGTGAGCC	ATCGCGCCTG	GCCAGGACCT	2940
	THETHRETTA	TCTACATATT	GGAAGATTTG	GTCCTGATGT	CCTTTGAGGC	TTCTTTAGCT	3000
80	CTAGTTCTCT	GACACTTCAG	CCTATATCAC	AGCTAACTTC	YTCAGTCTCA	TCTATTCCTT	3060
	ATTICTOCAGO	CCCCCCCAAT	TTGCCTCAAG	ATCCCCCCTTT	GAAAATAACT	TTACCTGACT	3120
	CAAGGAGTGT	CTGGAGCACC	TCCTAGTCTA	AGTCTGCAAG	CICCAGTTCT	TGCCTAAAAC	3180 3240
	CATGCCAGTG	GCCACCCTTG	GUCTUAGACA	CCCCAGGACT	GCAGGGGGGG	TTCCTCCAAC	3300
85	GCTTCCAAGG	CTCAAAAGAA	ATTTGGCTCC	ATCCAAGAAG	GCTCCAGCTC	TTCCTCCAAG CCCTACTGGC	3360
	CCCTGGCTTC	AGGCCCACAC	CCCTGGGCCA	GGSCCAGAGA	GTGTGTCTCA	GGAGAATTCA	3420
	ATGGGCTCTA	GAGAGACACA	CAGAAAGTTT	GGGCATTTGG	GAAATTTTCA	AGGRTGTATG	3480

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	TATGGYTCAC GAAGTGGATT GACAAGGACA	GTATGGWGCA GGAGGGGAGC GCCCCAAGGT	TTGAGGAATA TGGGAAGACC	TAAGGAGCGG TGGCCTTAGT	GGGTGGAGAC CGTCCTCAGC	TCAGGCTATG CTAGGGCAGG CCCCAGGCCG	3540 3600 3660 3720
5	GCATCTTATG CATTGTGCAA TGGATGGGCT AATCCACCCA	TGTGTCTTCC	ACCATECTCA AGAACCAGGA ATCATTAGGG CATCTCCCTC	TGGTGGCACT AGTGAAACTG CAGAGTTTGC TTTGAAGGAT	TTTCTAGGCC GGTGAAAACA ACGTCCTCTG TTTWATTTCT	TGTCTCCCAG GAAAGCTCAA GTTCACTGGG ACTGGGTTTT	3780 3840 3900 3960 4020
10	TGGAAAATCC GAGAAGGGGG ATGCTTCTGT AGACGCTGTT	CTAAGAGAAG CCCAATGGCC CTGAGTGCAG TGTGGGAGCA	GCCTGGGGGA AGGGAGTGAA GAAGGTGTTC CTGGGCTCAT	MAGGAAKTGG GGAGGTGGCG CAGGGTCGAA	AGTGACAGGG TTGCTGAGAG ATTACACTTC	GACAGGTAGA CAGTCTGCAC TCGTACCTGG	4080 4140 4200 4260
15		CCTGAAAAAA					
	Seq ID NO: Protein Acc	333 Protein ession #:	NP_0000	11			
20	1	11	21	31	41	51	
		 LMLLMALVTQ NLHRELCRGR ALVALGVLGL					60 120 180
25	DCTTGSGSGL RETEIYNTVL	PFLVQRTVAR LRHDNILGFI AHLHVEIFGT GTKRYMAPEV NDPSFEDMKK	QVALVECVGK ASDMTSRNSS OGKRATAHRD	GRYGEVWRGL TQLWLITHYH PKSRNVLVKS	WHGESVAVKI EHGSLYDFLQ NLOCCIADIG	ROTLEPHLAL LAVMHSOGSD	240 300 360 420 480
30	TALRIKKTLQ	KISNSPERPR 334 DNA 800	VIQ	IPRRIBADEV	130BM2-FIRE	CHIPHIOTEC	
	Nucleic Act	d Accession	1 #: NM_0041	.26.1			
35		ience: 108-					
	1	11	21 .	31	41	51 i	
	GGCACGAGCT	CGTGCCGGCC	TTCAGTTGTT	TCGGGACGCG	CCGAGCTTCG	CCGCTCTTCC	60 120
40	ACATCGAAGA	CTGCCAGAGC TTTGCCAGAG	AAGGAAAAAC	TGAAAATGGA	AGTTGAGCAG	CTTCGCAAAG	180
	AACTGAACTT	GCAGAGACAA	CAAGTGTCTA	AATGTTCTGA	AGAAATAAAG	AACTATATTG	240 300
	AAGAAAAAGG	TGGAGAGGAT CAGCTGTGTT	ATTTCATAAA	TAACTTGGGA	GAAACTGCAT	CCTAAGTGGA	360
45							420 480
43	ACAATTATGG	AGGAGACTTT TCTTTGCTCA AAATAAGAAC AAGTTTTGTC	ATTACTTGAG	TTTTTTAGA CATGACACTT	GAGCAGAGAG CTTTCAGTAT	TATCAGATGT ATTGCTTGAT	540 600
50	Seq ID NO: Protein Acc	335 Protein cession #:	n sequence NP_0041	117.1			
	1	11	21	31	41	51	
55	MPALHIEDLP KNPFKEKGSC		QLRKEVKLQR	OGASKCRERI	KNYIEERSGE	DPLVKGIPED	60
60	Nucleic Ac	336 DNA se id Accession uence: 555-	n #: NM 005	795			
	1	11	21	31	41	51	
65	GCACCIAGGGA	ACAACCTCTC	TCTCTSCAGC	AGAGAGTGTC	ACCTCCTGCT	TTAGGACCAT	60
05	CAAGCTCTGC	TAACTGAATC	TCATCCTAAT	TGCAGGATCA	CATTGCAAAG	CTTTCACTCT	120
	TOAGAATATT	TCACAAAGAA	TTTCCTTAAG	ACCTGGACTG	GGTCTTGACC	AGTTCCATCC CCTGGAATTT	240
70	AAGAAATTCT	TARAGACAAT	GTCAAATATG	ATCCAAGAGA	AAATGIGATI	TGAGTCTGGA AACAATATTT	300 360
70	CARTARTARA	BACCCATACT	ACCUTATACA	AAACAATATT	TGAAAGATTG	CTACCACTAA	420
	BABGAAAACT	ACTACAACTT	GACAAGACTG	CTGCAAACTT	CAATIGGTCA	CCACAACTTG AGCATATTTC	480 540
	ATTTGGGGTT	DARRETAR	AAAAAGTGTA	CCCTGTATTT	TCTGGTTCTC	TTGCCTTTTT	600
75	TTATGATTCT	TOTTACAGCA	GAATTAGAAG	AGAGTCCTGA	GGACTCAATT	CAGTTGGGAG	660 720
	CONTROLACA	ACCRONAGOC	CTTTA CTGCA	ACAGAACCTG	GGATGGATGG	CTCTGCTGGA	780 840
	ATCCATCAGA	AAAAGTTACA	AAGATCTGTG	ACCAAGATGG	AAACTGGTTT	CAGGACTTTG AGACATCCAG	900
80	CANGCAACAG	BACATOGACA	AATTATACCC	AGTGTAATGT	TAACACCCAC	GAGAAAGTGA ATTGCATCAC	960 1020
	TOCTTATCTC	GCTTGGCATA	TTCTTTTATT	TCAAGAGCCT	AAGTTGCCAA	AGGATTACCT	1080
	TROSCASAAA	TOTOTAL	TOATTTOTT	CTAACTCTGT	TOTANCARTO	ATTCACCTCA	1140
85	AGTTCATTCA	TCTTTACCTG	ATGGGCTGTA	ATTACTTTTC	GATGCTCTGT	GAAGGCATTT	1260
	ACCTACACAC	ACTCATTGTG	GTGGCCGTGT	TTGCAGAGAA	GCAACATTTA	ATGTGGTATT GCTAGAAGCT	1320 1380
	ATTICING	CLUGGGGTTT	·			_ ,	

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	TATATTACAA	TGACAATTGC TGCTGCTTTA	TGGATCAGTT	CTGATACCCA	TCTCCTCTAC	ATTATCCATG	1440
	GCCCAATTTG	TGCTGCTTTA	CTGGTGAATC	TTTTTTTCTT	GTTAAATATT	GTACGCGTTC	1500 1560
	TCATCACCAA	GTTAAAAGTT TATCTTGGTG	CCATTCCTTC	CCATTCAATT	TOTGOTACATO	CCATGGGGG	1620
5							1680
	AGGGTCTTTT	GATTCAATAC GAATCAATAC	ATTTTCTGCT	TCTTTAATGG	AGAGGTTCAA	GCAATTCTGA	1740
	GAAGAAACTG	GAATCAATAC	AAAATCCAAT	TTGGAAACAG	CTTTTCCAAC	TCAGAAGCTC	1800
	TTCGTAGTGC	GTCTTACACA	GTGTCAACAA	TCAGTGATGG	TCAGGTTAT	CTCTTABAAC	1920
10	CAGAAAATTT	ACACTTAAAT ATATAATTGA	AAATAGAAGG	ATGGTTGTCT	CACTGTTTGG	TGCTTCTCCT	1980
							2040
	GGGAATGTCA	TAAAGAAGAG ATGTGGGAAA GATGTGACGC	CCTTCACATG	AAATTAGTAG	TGTGTTGATA	AGAGTGTAAC	2100
	ATCCAGCTCT	ATGTGGGAAA	AAAGAAATCC	TGGTTTGTAA	CTYTTGGAATT	GGAGAAAAGC	2220
15	ACAATCAACT	TTTCTGAGCT	GGTGTAAGCC	AGTTCCAGCA	CACCATTGAT	GAATTCAAAC CSCCCCAAGA AAACTCTTTA	2280
	AAATGGCTGT	AAAACTAAAC	ATACATGTTG	GGCATGATTC	TACCCTTATT	CSCCCCAAGA	2340
	GACCTAGCTA	AGGTCTATAA	ACATGAAGGG	AAAATTAGCT	TTTAGTTTTA	AAACTCTTTA	2400 2460
	TCCCATCTTG	ATTGGGGCAG CTCAAATGGA	TTGACTTTTT	ACTEAATTAT	CCCTGCTGGG	TTTCTTTTCT	2520
20							2580
	ATCTTGTGGC	ATATCCATTG TTAGGAAAAC	TGGAAACTGG	ATGAACAGGA	TGTATAATAT	GCAATCTTAC	2640
	TTCTATATCA	TTAGGAAAAC	ATCTTAGTTG	ATGCTACAAA	ACACCTTGTC	AACCTCTTCC	2700
		AACAGTGGGA AAACAAATTA					2760 2820
25	A TETTETICA	AATTTTTTAA	PTTTAKADAAA	TGAAAAATGA	CCTTGTAAAT	ACTCCATTAT	2880
20	THETTATHETAT	AGTOTCAAAT	CARATACATA	CAACCTATGT	AATTTTTAAA	GCAAATATAT	2940
	AATGCAACAA	TGTGTGTATG	TTAATATCTG	ATACTGTATC	TGGGCTGATT	AATAAATTT	3000
	AATAGAGTCT	GGAATGCT					
30	Sea ID NO:	337 protein	sequence				
50	Protein Ac	cession #:	NP_0057	86.1			
	_				41	51	
	ļ	11	21	31	11	1	
35	MERKCTLYPL	UT.T.DPPMTT.U	TABLEESPED	SIQLGVTRNK	INTAQYECYQ	KIMQDPIQQA	60
	EGVYCURTWD	GWI CWNDVAA	GTESMOLCPD	YFODFDPSEK	VTKICDQDGN	WFRHPASNRT	120
	WINYTOCHVN	THEKVKTALN TIIHLTAVAN	LFYLTIIGHG	LSIASLLISL	GIFFYFKSLS	CORITLHENL	180 240
	TIMESTER PVO	DI MUYYUI CH	CEPT-TRACTH	CHYV-12844A	NCWISSDITHL.	LYTIHGPICA	300
40	ALLVNLPPLL	NIVRVLITKL	KVTHQAESNL	YMKAVRATLI	LVPLLGIEFV	LIPWKPEGKI	360
	AREVYDYIMH	ILMHFOGLLV	STIPCFFNGE	VOAILRRNWN	QYKIQFGNSF	SNSEALRSAS	420
	YTVSTISDGP	GYSHDCPSEH	LNGKSIHDIE	NVLLKPENLY	N		
	Seq ID NO:	338 DNA sec	quence				
45	Nucleic Ac	id Accession	n #: NM_001:	195			
45	Nucleic Ac	338 DNA sec id Accession wence: 25-2	n #: NM_001:	195			
45	Nucleic Ac	id Accession	n #: NM_001:		41	51	
	Nucleic Ac Coding seq	id Accession mence: 25-2	n #: NM_001: 379 21	31 	1	1	
45 50	Nucleic Ac Coding seq	id Accession	#: NM_001: 379 21 	31 -	TECTCCTCSC	CACATCGGGC	60
	Nucleic Ac Coding seq 1 GCACGATCTG GCCTGCCTGG	id Accession mence: 25-2: 11 TTCCTCCTGG GCCTGCTGGC	#: NM_001: 379 21 GAAGATGCAG AGTGGCAGCA	31 AGGCTCATGA GTGGCAGCAG	TGCTCCTCGC CAGGTGCTAA	CACATCGGGC CCCTGCCCAA GATTTGGAAC	120
	Nucleic Ac Coding seq 1 GCACGATCTG GCCTGCCTGG	id Accession mence: 25-2: 11 TTCCTCCTGG GCCTGCTGGC	#: NM_001: 379 21 GAAGATGCAG AGTGGCAGCA	31 AGGCTCATGA GTGGCAGCAG	TGCTCCTCGC CAGGTGCTAA	CACATCGGGC CCCTGCCCAA GATTTGGAAC	120 180 240
50	Nucleic Ac Coding seq 1 GCACGATCTG GCCTGCCTGG	id Accession mence: 25-2: 11 TTCCTCCTGG GCCTGCTGGC	#: NM_001: 379 21 GAAGATGCAG AGTGGCAGCA	31 AGGCTCATGA GTGGCAGCAG	TGCTCCTCGC CAGGTGCTAA	CACATCGGGC CCCTGCCCAA GATTTGGAAC	120 180 240 300
	Nucleic Ac Coding seq 1 GCACGATCTG GCCTGCCTGG GGGGACACCC CAGATGCACA TCAAGCGTGA	id Accession nence: 25-2: 11 TTCCTCCTGG GCCTGCTGGC ACAGCCTGCT TTGATGAAGA GTCGCAAGAA	#: NM_001: 379 21 GAAGATGCAG AGTGGCAGCA GCCCACCCAC GAAAACAC TGCCAAGAC	31 AGGCTCATGA GTGGCAGCAG CGGCGCCAAA TCACTTCCCC CTGCTCAAAG	TGCTCCTCGC CAGGTGCTAA AGAGAGATTG ATCATGTAGG GAGAATATGT	CACATCGGGC CCCTGCCCAA GATTTGGAAC CAAGATCAAG GGGCAAGGTC	120 180 240 300 360
50	Nucleic Ac Coding seq 1 GCACGATCTG GCCTGCCTGG GGGGACACCC CAGATGCACA TCAAGCGTGA	id Accession nence: 25-2: 11 TTCCTCCTGG GCCTGCTGGC ACAGCCTGCT TTGATGAAGA GTCGCAAGAA	#: NM_001: 379 21 GAAGATGCAG AGTGGCAGCA GCCCACCCAC GAAAACAC TGCCAAGAC	31 AGGCTCATGA GTGGCAGCAG CGGCGCCAAA TCACTTCCCC CTGCTCAAAG	TGCTCCTCGC CAGGTGCTAA AGAGAGATTG ATCATGTAGG GAGAATATGT	CACATCGGGC CCCTGCCCAA GATTTGGAAC CAAGATCAAG GGGCAAGGTC	120 180 240 300 360 420
50	Nucleic Ac Coding seq 1 GCACGATCTG GCCTGCCTGG GGGGACACCC CAGATGCACA TCAAGCGTGA	id Accession nence: 25-2: 11 TTCCTCCTGG GCCTGCTGGC ACAGCCTGCT TTGATGAAGA GTCGCAAGAA	#: NM_001: 379 21 GAAGATGCAG AGTGGCAGCA GCCCACCCAC GAAAACAC TGCCAAGAC	31 AGGCTCATGA GTGGCAGCAG CGGCGCCAAA TCACTTCCCC CTGCTCAAAG	TGCTCCTCGC CAGGTGCTAA AGAGAGATTG ATCATGTAGG GAGAATATGT	CACATCGGGC CCCTGCCCAA GATTTGGAAC CAAGATCAAG GGGCAAGGTC	120 180 240 300 360
50 55	Nucleic Ac Coding seq 1 	id Accession uence: 25-2 11 TTCCTCCTGG GCCTGCTGCT TTGATGANGA ATGCANGAN ATGCANGAN ACCACCTCAC GCTTCACCAT TCAATGGGTC TGGATGGAGAA TTCAATGGGTC TGGATGGAGAA	n #: NM_001: 379 21 GAAGATGCAG GCCCACCAC GAAAACACC TGCCAAGTAC AGGAGACATG TGCTTCATT CAAGTTCAT CAAGTCCTAG CGACCCCACT	31 AGGCTCATGA GTGGCAGCAG CGGGCCAAA TCACTTCGCC CTGCTCAAAG TTCGCCATTG GTGGACAAGG GACGTGAACG TCGTCGGCTG GTGGGAGCC	TGCTCCTCGC CAGGTGCTAA AGAGAGATTG ATCATGTAGG GAGAATATGT AGAGGCTGGA ACACTGGTGA ACACTGGCC TGGGGACCTC ACGCCTCTGT	CACATCGGGC CCCTGCCCAA GATTTGGAAC CAAGATCAAG GGGCAAGGTC CCCGGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCTCT CATGTACCAA	120 180 240 300 360 420 480 540
50	Nucleic Ac Coding seq 1 GCACGATCTG GCCTGCCTGG GGGGACACCC CAGATGCACA TCAAGCGTGA ATTCCGGGTG ATCTCAGAAT ACTCCTTCCA ACTCGTTGT GGACAGCAG	id Accession uence: 25-2: 11	n #: NM_001: 379 21	31 	TGCTCCTCGC CAGGTGCTAA AGAGAGATTG ATCATGTAGG GAGAATATGT AGAGGCTGGA ACACTGGTGA ACACTGGTGC TGGGGACCTC TGGCCCTCTGT GACCTTATTAT	CACATCGGGC CACATCGGGCCAA GATTTGGAAC CAAGATCAAG GGGCAAAGGTC CCGGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCTCT CATGTACCAA ACACAATAACG	120 180 240 300 360 420 480 540 600 660
50 55	Nucleic Ac Coding seq 1 GCACGATCTG GCTGCTGG GGGRACCCC CAGATCACA TCAGCGTGA TTCCGGGTTGA ACTCCTTCCA ACTCGTTGT GTGACAGCAG ANAGCTTGAAGG	id Accession uence: 25-2. 11 11 TTCCTCTGG GCCTGCTGGC ACAGCTGGT TGATGAAGA ATGCAAGAA ATGCAAGAA ATGCAGAGAC TCACCTCAC GCTTCACCAT TCAATGCGTC TGGATGCAGA GGAAGAGAA ACCGAGAGAA	n #: NM_001: 379 21	31 AGGCTCATGA GTGGCAGCAG CGGCGCCAAA TCACTTCOCC CTGCTCAAAG GTCGTCAAAG GACCTGAAAG TCGTCGGCTG GTGGGAGAC GTGGGAGAC GATAATTCTG TATGAGATCG	TGCTCCTCGC CAGGTGCTAA ACAGAGATTG ATCATGTAGG GAGAATATGT ACAGGCTGGA ACACTGGTGA ACACTGGCC TGGGGACCTC GACGTATTAT TGGTGGAAGC	CACATCGGGC CACATCGGGC CACATCGGAG GATTTGGAAC CAAGATCAAG GGGCAAGGTC CCGGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCTCT CACATGACCAA CACAATAACG GCGAGATGCA	120 180 240 300 360 420 480 540
50 55	Nucleic Ac Coding seq 1 GCACGATCTG GCTGCTGG GGGRACCCC CAGATCACA TCAGCGTGA TTCCGGGTTGA ACTCCTTCCA ACTCGTTGT GTGACAGCAG ANAGCTTGAAGG	id Accession uence: 25-2. 11 11 TTCCTCTGG GCCTGCTGGC ACAGCTGGT TGATGAAGA ATGCAAGAA ATGCAAGAA ATGCAGAGAC TCACCTCAC GCTTCACCAT TCAATGCGTC TGGATGCAGA GGAAGAGAA ACCGAGAGAA	n #: NM_001: 379 21	31 AGGCTCATGA GTGGCAGCAG GGGCGCCAAA TCACTTCOCC CTGCTCAAAG GACCTGAAAG GACCTGAAAG TCGTCGGCTG GTGGGAGAC GATAATTCTG GATAATTCTG TATGAGATCG	TGCTCCTCGC CAGGTGCTAA ACAGAGATTG ATCATGTAGG GAGAATATGT ACAGGCTGGA ACACTGGTGA ACACTGGCC TGGGGACCTC GACGTATTAT TGGTGGAAGC	CACATCGGGC CACATCGGGC CACATCGGAG GATTTGGAAC CAAGATCAAG GGGCAAGGTC CCGGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCTCT CACATGACCAA CACAATAACG GCGAGATGCA	120 180 240 300 360 420 480 540 600 720 780 840
50 55 60	Nucleic Ac Coding seq 1 1 GCACGATCTG GCGACACCC CAGATCACA TCAAGGTGA ATTCCGGTGG ATTCCAAAG ACTCCTTCCA ACTCGTTGT GTGACAGCAG ATTCGAAG ATTCGGAAG ATTCGGAAG AAAGGTTGG CAGGGCTTGG	id Accession uence: 25-2. 11 11 TTCCTCCTGG GCCTGCTGGC ACAGCTGGT TTGATGAAGA ATGCAAGAA ATGCAAGAA ATGCAAGAA ATGCAAGAA ATGCAAGAA ATGCAAGAA AGGATGCAAGA GGATGCAAGA AGGAGGAAGAA ACGAGGAGGAAGAA ACGAGAGGAAA ACGAGGAAGAA ACGAGGAACA	n #: NM_001: 379 21 GAAGATGCAG GCCCACCAC GCCACCAC GCCAGTAC TGCTGTCATT CAAGTCAT CGTGCCTGAG CGACCCAGT TTTTGCATC GCAGCCAG GGGCAGGC CGAGCCAG GGGCAGGC CCAACCAG	31 AGGCTCATGA GTGGCAGCAG GGGGCCAAA TCACTTCACC GTGGCACAG GACGTGAACG GACGTGAACG GTGGGAGACC GATAATTCTG TATAGATCG ACCGTCCTGG TACACATTCA	TGCTCCTGG CAGGTGCTAA AGAGAGATTG AGAGATTGT AGAGCTGGA ACACTGGTGA ACACTGGTGA ACACTGTGTGA ACGCCTCTTT GACGTATTAT TGGTGGAAGTC TCGTGCTGA TCGTCTGCTGA ATGAGCCCCA	CACATCGGGC CACATCGGGC GATTTGGAAC CAAGATCAAG GGCAAGGTC CCGGGGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCTCT CATGTACCAA CACAATAACG GCGAGATGCC GCGAGATGCC TGTGTCCATCTCT TATGTACCAA AGACACCCGTT AAACCTGGATG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	Nucleic Ac Coding seq 1 1 GCACGATCTG GCGACACCC CAGATCACA TCAAGGTGA ATTCCGGTGG ATTCCAAAG ACTCCTTCCA ACTCGTTGT GTGACAGCAG ATTCGAAG ATTCGGAAG ATTCGGAAG AAAGGTTGG CAGGGCTTGG	id Accession uence: 25-2. 11 11 TTCCTCCTGG GCCTGCTGGC ACAGCTGGT TTGATGAAGA ATGCAAGAA ATGCAAGAA ATGCAAGAA ATGCAAGAA ATGCAAGAA ATGCAAGAA AGGATGCAAGA GGATGCAAGA AGGAGGAAGAA ACGAGGAGGAAGAA ACGAGAGGAAA ACGAGGAAGAA ACGAGGAACA	n #: NM_001: 379 21 GAAGATGCAG GCCCACCAC GCCACCAC GCCAGTAC TGCTGTCATT CAAGTCAT CGTGCCTGAG CGACCCAGT TTTTGCATC GCAGCCAG GGGCAGGC CGAGCCAG GGGCAGGC CCAACCAG	31 AGGCTCATGA GTGGCAGCAG GGGGCCAAA TCACTTCACC GTGGCACAG GACGTGAACG GACGTGAACG GTGGGAGACC GATAATTCTG TATAGATCG ACCGTCCTGG TACACATTCA	TGCTCCTGG CAGGTGCTAA AGAGAGATTG AGAGATTGT AGAGCTGGA ACACTGGTGA ACACTGGTGA ACACTGTGTGA ACGCCTCTTT GACGTATTAT TGGTGGAAGTC TCGTGCTGA TCGTCTGCTGA ATGAGCCCCA	CACATCGGGC CACATCGGGC GATTTGGAAC CAAGATCAAG GGCAAGGTC CCGGGGGAGAAT AAACCTGGAG TGTGTTCACG AGTCATCTCT CATGTACCAA CACAATAACG GCGAGATGCC GCGAGATGCC TGTGTCCATCTCT TATGTACCAA AGACACCCGTT AAACCTGGATG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	Nucleic Ac Coding seq 1 GCACGATCTG GCTGCTTGG GCTGCTTGG GCTGCTTGG ATCACGGTTGA TCCGGGTTGA ACTCCTTCCA CATCGGTTGA ACTCCTGAAGA ACTCCTGAAGA ACTCCTGAAGA ACTCCTGAAGA ACTCCTGAAGA ACTCCTGAAGA ACACTTGAAGA ACACTGAAGA ACACTGAAGA ACACTGAAGA ACACTGAAGA ACACTGAAGA ACACTGAAGA ACACAGTACA ACCAAGTACA	id Accession uence: 25-2: 11 TTCCTCCTGG GCCTGCTGGC ACAGCCTGGT TTGATGAAGA ATGCAGAGAA ATGCAGAGAA ATGCAGAGAA ATGCAGAGAA ACCAGAGTCA GCTTCACCAT TCAATGCGTC TCAATGCAGC CCTTCACCAT CCTTCACCAT CCTTCAC CCTTCACGCTC CCTTCACGCTC CCTTCACGCTC CCTTCACGCTC CCTTCACGCTC CCTTCACGCTC CCTTCTCAC CCTTTCACG	n #: NM_001: 3799 21	31 	TGCTCCTCGC CAGGTGCTAA AGAGAGATTG AGAGATATGT AGAGCTGGA ACAACTGGCC TGGGGACCTC TGGGGACCTC TGGTGAAGC TGGTGAAGC TCACTCTGCA ACACTGCCTACA TCACCCCCACACACCACCACCACCACCACCATCA	CACATOGGGC CACATOGGGCAAGATCTAGAAGAGATCAAG AGATTCAAG GGGCAAGATC CAGGGAGAAT AAACCTGGAG AGTCATCTC CACATTACCAA AGACATCAAT AGACACCGT AGACACCGT GAACCGGAT GAACCGGAT GAACCGGAT CACACACACCAC CACACACACACCAC CACACACAC	120 180 240 300 360 420 480 540 600 720 780 840 900 960
50 55 60	Nucleic Ac Coding seq 1 GCACGATCTG GCTGCTTGG GCTGCTTGG GCTGCTTGG ATCACGGTTGA TCCGGGTTGA ACTCCTTCCA CATCGGTTGA ACTCCTGAAGA ACTCCTGAAGA ACTCCTGAAGA ACTCCTGAAGA ACTCCTGAAGA ACTCCTGAAGA ACACTTGAAGA ACACTGAAGA ACACTGAAGA ACACTGAAGA ACACTGAAGA ACACTGAAGA ACACTGAAGA ACACAGTACA ACCAAGTACA	id Accession uence: 25-2: 11 TTCCTCCTGG GCCTGCTGGC ACAGCCTGGT TTGATGAAGA ATGCAGAGAA ATGCAGAGAA ATGCAGAGAA ATGCAGAGAA ACCAGAGTCA GCTTCACCAT TCAATGCGTC TCAATGCAGC CCTTCACCAT CCTTCACCAT CCTTCAC CCTTCACGCTC CCTTCACGCTC CCTTCACGCTC CCTTCACGCTC CCTTCACGCTC CCTTCACGCTC CCTTCTCAC CCTTTCACG	n #: NM_001: 3799 21	31 	TGCTCCTCGC CAGGTGCTAA AGAGAGATTG AGAGATATGT AGAGCTGGA ACAACTGGCC TGGGGACCTC TGGGGACCTC TGGTGAAGC TGGTGAAGC TCACTCTGCA ACACTGCCTACA TCACCCCCACACACCACCACCACCACCACCATCA	CACATOGGGC CACATOGGGCAAGATCTAGAAGAGATCAAG AGATTCAAG GGGCAAGATC CAGGGAGAAT AAACCTGGAG AGTCATCTC CACATTACCAA AGACATCAAT AGACACCGT AGACACCGT GAACCGGAT GAACCGGAT GAACCGGAT CACACACACCAC CACACACACACCAC CACACACAC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60 65	Nucleic Ac coding seq 1 GCACGATCTG GCCTGCTTGG GCTGCTTGG GCTGCTTGG TCAAGCGTGA TTCAGGGTGA ACTCCTTCCA ACTCGTTGT GGACAGCGC ACAAGTTGAAGG AAAAGCTTGA ACTCGTTGAAGG AAAAGCTTGA ACAGCAGC GACAACTTCC GACAACTACC ACCAAGTACA ACCACAACG TACAAGCAACG TACAAACG TACAAACC TAC	id Accession uence: 25-2: 11	n #: NM_001: 379 21	31 I I AGGCTCATGA GTGGCAGCAG GGCACCAAA TACACTTCCCC CTGCTCAAAG GACTCAACGACCATT GTGGACAAGG GACTGAACGACCAACACTCACACACTCAACACACACACAC	TGCTCCTCGC CAGGTGCTAA AGAGAGATTG ATCATGTAGG GAGAATATT AGAGGCTCGA ACACTGCTGA ACACTGCTGA ACACTGTGTGA ACACTGTGTGA ACACTGTGTGA ACACTGTGTGA ACACTCTGCA ATGAGCCCCA ATGAGCCCTA ATGAGCCCCA ATTAGAATA ATTATGAATA ATTATGAATA TCCGATACAT TGGAGAGAGCCCCT GAGAGAGCCCCT GAGAGAGCCCCA ATGAGCACA ATGAGCACA ATGAGCACA ATGAGCACA AGAAGCCCCA AGAAGCCTCT AGAGAGCACCA AGAAGCCCCCA AGAAGCCCCCA AGAAGCCCCCC AGAACCCC AGAACCCCCC AGAACCCCCCC AGAACCCCCCC AGAACCCCCCCC	CACATTOGGGC CACATOGGGC CACATOGGGA GATTTGGAAC CAGAGATCAAG GGGCAAGGTC CCGGGAGAAT AAACCTGGAG TGTGTTCACC AGTCATCTGT CATGTACCAA CACAATAACG GCGAGAATGCC AGACATCACT GACAACCCGT GAACACCGGT GAACACCGCT CACCAGCAA GAGCCCTCCC CCCCATTTC	120 180 240 300 360 420 540 600 660 720 780 840 900 1020 1080 1140 1200
50 55 60	Nucleic Ac coding seq 1 GCACGATCTG GCCTGCATGG GCACGATCTG GCACGATCTG GCACGATCTG GCACGATCTG ATCTCGAGT ATCTCGAGT ATCTCGAGT ATCTCGAGT ATCTCGAGT ATCTCGAGT ACTCTTCCA GATCGGTTG AGGGCTTCG GCACAACT GCACAACT GCGAGAACT GCGGAAACT GCGGGAAACT GCGGAGAG GCGGGAACT GCGGGAACT GCGGGAGACT GCGGGAGACT GCGGGAACT GCGGAGAT GCGAGAT GCGGAGAT	id Accession uence: 25-2: 11 Total Control	n #: NM_001: 379 21 MAGATICAG AGTOCACCA AGTOCACCA AGTOCACCA TOCALOTIAC AGGAGACCTG TGCTTCATT TGTTGCTTCA TTTTGCCTTCA GGAGCCAGG GGGCAGGCC CCAGACCACT TCTTGCCTCAC CCAGACCACC CCACACC 311 AGGCTCATGA GTGGCAGCAG GTGGCAGCAG GTGGCACAAG TCACTTCOCC CTGCTCAAAG GACCTGACAG GACCTGACAG GACTGACAG ATCACTCAGCTG ATCACTCAGCTG ATCACAGCAT AGGCACCCAG AGGACCCTA AAGCACCAG ACCATCAGCA ACCACTCAGCAG ACCACCAGAG ACCACCACCAG ACCACCACCAC ACCACCACCAC ACCACCACCAC ACCACC	TGCTCCTGG CAGGTGCTAA AGAGAGATTG ATCATGTAGG GAGAATATGT ATCATGTAGG ACACTGGTAG ACACTGGTAG ACACTGGTAG ACACTGTATAT TGGTGGAGCTC TGGTGGTATAT TGGTGGTATAT TGGTGCTGAA ATTATGCCTGA ATTATGACCATTGA ATTATGAATA TCCGATACAT TGGAGGAGCC AGAAGCTCT	CACATOGGGC CACATOGGGC CACATOGGAGA CACAGATCAAG GGGCAAGGT CAGGGAGAAT CAGGAGAGAA AACCTGGAG AGTCATCACT CACAGTAAAG GCGAAGATCAAT AGACACCAGT AACACCAGT AACACCAGT AACACCAGT CACACAAAACCCC CATCCAGCAA AGGCCTCCC CATCTGGCAAA CACCCCCCATTTTC GATTGGCACA CCGCCAGGACC CCCCATTTTC GATTGGCACA CCGCCAGGACC CCCCATTTTC CATTGGCACA CCGCAGGACC CCCCATTTC CATTGGCACA CCCATTTC CATTGGCACA CCCCATTTC CATTGCACA CCCCATTTC CATTGCACA CCCCATTTC CATTGCACA CCCCATTTC CATTGCACA CCCCATTTC CATTGCACA CCCCATTTC CATTCCACT CCCCATTTC CATTGCACA CCCCATTTC CATTCCACT CCCCATTTC CATTCCACT CCCATTTC CATTCCACT CCCCATTTC CATTCCACT CCCCATTTC CATTCCACT CCCCATTTC CATTCCACT CCCCATTTC CATTCCACT CCCCATTTC CATTCCACT CCCATTTC CATTCCACT CCCATTCCACT CCCA	120 180 240 300 360 420 540 600 720 780 900 900 900 1080 1140 1260	
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50 55 60 65 70	Nucleic Ac Coding meg CACANTCTE GEACANTCTE GEACANTCTE GEACANTCTE GEGACACCC CACANTCCACA TYCCOGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ACANTTCC GACGACTTCC GACGACTTCC GTGTCGCCA ATTCCCGGTOS	11 Interest of the control of the co	a B : NM _ OO1: 779 21 21 GANGATGCAG GANGATGCAG GCCACCCAC GCCACCCAC GCCACCAC TGCCAAGTAC AGGAGAGCAT TTTTTGCATT TCCTTTTTTTTTT	JI AGGCTCATGA GTGGCACGA GTGCACGAC GTGGCACGT GTGGCACGAC GTGGCACGT GTGGCACGAC GTGGCACGT GTGGCACGAC GTGGCACGT GTGGCACGAC GTGGCACGT GTGCACGAC GTGGCACGT GTGCACGAC GTGCACAC GTGCAC	I TEGTOCTOSC CAGGIGGOTAN A MORAGAGATHT OF THE TOTAL TO	CACATCGGGC CACATCGGGC CACATCGGAC GATTTGGAAC CAGAGATCAAG GGGCAAGGTC CCGGGGAGAT CATTTGGAC CACATCACC CACATCACC CACATCACC CACCACC CACCACC CACCACC CACCACCAC CACCAC	120 180 240 300 420 480 600 600 720 780 900 900 1020 1080 1140 1200 1260 1360 1360 1360
50 55 60 65	Nucleic Ac Coding meg CACANTCTE GEACANTCTE GEACANTCTE GEACANTCTE GEGACACCC CACANTCCACA TYCCOGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ATTCCCGGTOS ACANTTCC GACGACTTCC GACGACTTCC GTGTCGCCA ATTCCCGGTOS	11 Interest of the control of the co	a B : NM _ OO1: 779 21 21 GANGATGCAG GANGATGCAG GCCACCCAC GCCACCCAC GCCACCAC TGCCAAGTAC AGGAGAGCAT TTTTTGCATT TCCTTTTTTTTTT	JI AGGCTCATGA GTGGCACGA GTGCACGAC GTGGCACGT GTGGCACGAC GTGGCACGT GTGGCACGAC GTGGCACGT GTGGCACGAC GTGGCACGT GTGGCACGAC GTGGCACGT GTGCACGAC GTGCACAC GTGCACGAC GTGCACAC GTGCAC GTGCACAC GTGCACAC GTGCACAC GTGCACAC GTGCACAC GTGCACAC GTGCACA	I TEGTOCTOSC CAGGIGGOTAN A MORAGAGATHT OF THE TOTAL TO	CACATCGGGC CACATCGGGC CACATCGGAC GATTTGGAAC CAGAGATCAAG GGGCAAGGTC CCGGGGAGAT CATTTGGAC CACATCACC CACATCACC CACATCACC CACCACC CACCACC CACCACC CACCACCAC CACCAC	120 180 300 300 480 540 600 600 780 900 900 1080 1140 1200 1260 1320 1440 1560
50 55 60 65 70	Nucleic Ac Coding meg 1 1 1 CARACTER C	11 Interest of the control of the co	a B : NM _ OO1: 779 21 21 31 GANGATGCAG GANGATGCAG GCCACCCAC GCCACCCAC GCCACCACCAC TGCCAAGTAC AGGAGAGGTAC GCCACCCAC TGCCAAGTAC GANGAAGAGTAC GANGAGCAGT GCCACCCAC TTTTTGCATT GGGCACGGCC GCCACCCAC TTTTTTGCATT GGGCACGGCC GCCACCCAC CAGGTATACAC CCAGGTTAGAC CCAG	AGECTATAA AGECTATAA AGECTATAA AGEGTACAA ATAATTACCC CATGCTAAAA ATAATTACCC ATGCCAATA ATGCCATTA AGCCATTA AGCCATTA AGCCATTA AGCCATTA AGCCATTACA ATCACAGATC AAAAAAGGGGA CTACACATACA ATCACAGATC AAAAAAAGGGA CTACACATTACAAAAAAAAAA	TRETTCOTOSE CAGGITGCTAN AGRAGAGATT AGRAGACT TCACCATTAG ATTAGATT TGGACAGACT AGRAGACC AGRAGAC AGRAG	CACHTGGGC ACATTGGAC ACATTGGAC CACATCAGC CACATCAGC CACATCAGC CACATCAGC CACATCAGC CACATCAGC CACATCAGC ACACCAGC ACACCAGC ACACCAGC CACCAGC CACCAC CACCAC CACCAC CACCAC CACCAC CACCAC	120 180 240 300 420 480 600 600 720 780 900 900 1020 1080 1140 1200 1260 1360 1360 1360
50 55 60 65 70	Nucleic Ac coding neg 1 OANTON GOOD TO THE CONTROL GOOD TO TH	11 TICCTTUARGE CONCRETA	a B : NM _ 001:79 21 1 GANGATGCAG GCCACCCAC GCCACCCAC GCCACCCAC GCCACCCAC	31 AGGCTCATGA GOGGGGCCAAA TOACTTCCCC GGGGGCCAAA TOACTTCCCC CTCATGA GAGGGGGGGGA GAGGATGAACA GAGGACCAGGGACAAA GAGGGGGGGGACAA AGCATGAGGAGGGGGAGAAA AGCATGAGGAGGCTT AACAGGGGGGGAAACATGAGGAGGCTT TACAGGAGGACCAGGAACACATGAGGAGACCAGGAACACATGAGGAGGACCAGGAACACATGAGGACCATTAGAGAGACCAGGAACACATGAGAGACCAGGAACACATGAGAGACCAGGAACACATGAGAGACCAGGAACACATGAGAGAGA	TRICTICOTOSC CAGGITGCTAN AGAGAGATTA AGAGAGATTA AGAGAGATTA AGAGAGATTA AGAGACTIGGA ACACTIGGAC TOSC TOSC TOSC TOSC TOSC TOSC TOSC TOS	CACATOGGGC COCCIOCOM ANTOGGAC CACATOGGAC CACATOGGAC CACATOGGAC CACATOGGAC CACATOGGAC CACATOGGAC CACATOGGAC CACATOGGAC CACATOGAC CACATACAC 120 180 240 300 420 540 660 720 840 960 1020 11200 1260 1320 1350 1350 1500 1500 1540	
50 55 60 65 70	Nucleic Ac coding see Coding see Coding	11 TOTAL COLOR OF THE COLOR O	a B: NM_001:779 21 1 GANGATOCAG	31 AGGCTCATGA GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG TOGCCATGAG TTGGCCATTG GTGGCATGAG TTGGCCATTG GTGGCATGAG TTGGCCATTG GTGGACAAG GAGGAGCAG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATTG TATGGCATGC TATGCAGT TATGCAGT TATGCAGT TTGGCAGT TTGGCAGT TTGGCAGT TTGGCAGT TTTGCAGT TTGGCAGT TTTGGCAGT TTTGGCAGT TTTGGCAGT TTGGCAGT TTG	TRETECTORSE CAGGITGCTAN ARGAGANTITO ARGANTITO ARGAGANTITO ARGANTITO CACHTOSIGE CCCTICOCCHA GARTISSAN ANACCTIGAR GGCAAGGTC CCGGGGGGAAT ANACCTIGAR ATTORITICAGE GGCAAGTC CCGGGGGAAT ANACCTIGAR ATTORITICAGE ATTORITICAGE ATTORITICAGE CCGAATATACA AGACACCATT AGACACCATT AGACACCATT AGACACCATT CACATATACA CACA	120 180 240 300 420 480 540 660 720 960 1080 1140 1260 1380 1440 1560 1560 1680 1740	
50 55 60 65 70	Nucleic Ac coding seq 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	11 Trecreating and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second a second and a second a s	a B : NM _ 001:779 21 GANGATGCAG GANGATGCAG GANGATGCAG GANGATGCAG GANGATGCAG GANGAGCAG ANAGAGCAG ANAGAGC	31 ASSOCIATION OF THE PROPERTY OF THE PROPE	TRUCTOCTOSE CAGGATGATA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACATTA AAGACAATTA	CACATOGGE COCCIOCOCA A CACATOGGE CACATOGGE CACATOGGE CACATOGGE CACATOGGE CATOGGE CATOGGE CATOGGE CACATOGGE CATOGGE CACATOGGE CATOGGE CACATOGGE CAC	120 180 240 300 420 600 660 720 900 900 1020 1020 1120 1200 1320 1380 1560 1560 1560 1620 1620 1620 1620 1620 1620 1620 16
50 55 60 65 70	Nucleic Ac coding seq 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	11 Trecreating and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second a second and a second a s	a B : NM _ 001:779 21 GANGATGCAG GANGATGCAG GANGATGCAG GANGATGCAG GANGATGCAG GANGAGCAG ANAGAGCAG ANAGAGC	31 ASSOCIATION OF THE PROPERTY OF THE PROPE	TRUCTOCTOSE CAGGATGATA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACAATTA AAGACATTA AAGACAATTA	CACATOGGE COCCIOCOCA A CACATOGGE CACATOGGE CACATOGGE CACATOGGE CACATOGGE CATOGGE CATOGGE CATOGGE CACATOGGE CATOGGE CACATOGGE CATOGGE CACATOGGE CAC	120 120 240 300 420 600 600 780 900 900 900 1020 1140 1260 1320 1440 1560 1560 1560 1680 1740 1800 1800 1800 1800 1920
50 55 60 65 70	Nucleic Ac Coding seg Coding	11 Troctorios	a B : 3M _ 001: 21 34 35 36 37 37 37 37 37 37 37 37 37	31 AGGCTCATGA GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG GTGGCAGCAG AACCCAG AACCCAG AACCCAG AACCCAGCAG AACCCAG AACCCAG AACCCAG AACCCAG AACCCAG AACCCAG AACCCAG AACCCAGCA AACCCAGCA AACCCAGCA AACCCAGCA AACCCAGCA AACCCAGCA AACCCAGCAC CCAGCACCAGCA CCAGCACCAGCAC CCAGCACCAGCAC CCAGCCACCAC CCAGCCACCACCAC CCAGCCACCACCACCACCACCCCCCACCCCCCACCCCCCC	TRETECTORSE CAGGATGCTAN AGGACGATA AGGACATA AGGACA	CACATTOGGE CONTROLLANGE CONTROLLANGE CONTROLLANGE CONTROLLANGE CONGRETA ANACTERIA ANAC	120 180 240 300 420 600 660 720 900 900 1020 1020 1120 1200 1320 1380 1560 1560 1560 1620 1620 1620 1620 1620 1620 1620 16
50 55 60 65 70 75	Nucleic Ac coding see Coding see Coding	LIGHT STATE OF THE	a B: NM_001: 21 12 13 13 13 14 15 15 15 15 15 15 15 15 15	31 AGENTATION AG	TREFECTORE CARGERICATAN A TRANSPORT OF THE PROPERTY OF THE PRO	CONTROLLAR OF THE CONTROLLAR O	120 180 240 300 360 420 480 540 660 780 900 1080 1140 1140 1140 1150 1150 1162 1162 1174 1186 1198 1198 1198 1198 1198 1198 1198
50 55 60 65 70	Nucleic Ac Coding seg Coding	11 Trecreation Trecreation Trecreation Trecreation Trecreation Trecreation Trecreation Treation Treatio	a B 1 M 001: 719 21 1 GANGATOCAG AGTOCAGAG AGTOCAGAG AGTOCAGAG AGAGAGAG AGAGAGAGAG AGAGAGAGAG AG	31 ACCIOCATA NA CONTROL CONT	TRETTECTORE CARGAGETTA ANTANTAL ANTANTANTAL ANTANTAL ANTA	CACATOGGE COCTOGGE CACATOGGE CACATOG	120 180 240 300 480 540 660 780 840 960 1020 1140 11320 1140 11560 1440 1560 1620 1740 1560 1740 1800 1740 1800 1800 1920 1920 1920 1920 1920 1920 1920 19
50 55 60 65 70 75	Nucleic Ac coding seg Coding	11 Control C	a B 1 MM CO11-7979 21 121 221 232 234 235 236 237 237 237 237 237 237 237	31 AGENTATIAN AG	I CONTROL OF THE PROPERTY OF T	CALATICOSIC CANAGRAMA CANAGRAMA CANAGRAMA CANAGRAMA GGCANGGA CANAGRAMA GGCANGGA CANAGRAMA AGACACCA CANAGRAMA AGACACCA CANAGRAMA AGACACCA CANAGRAMA AGACACCA CANAGRAMA AGACACCA CANAGRAMA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA AGACACCA ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACACAC ACACACACACAC ACACACACACACACAC AC	120 120 130 130 130 140 140 140 140 160 160 160 160 160 160 160 16
50 55 60 65 70 75	Nucleic Ac coding seg Coding	11 Control C	a B 1 MM CO11-7979 21 121 221 232 234 235 236 237 237 237 237 237 237 237	31 AGENTATIAN AG	I CONTROL OF THE PROPERTY OF T	CACATOGGE COCTOGGE CACATOGGE CACATOG	120 180 240 300 480 540 660 780 840 960 1020 1140 11320 1140 11560 1440 1560 1620 1740 1560 1740 1800 1740 1800 1800 1920 1920 1920 1920 1920 1920 1920 19

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_		GACTCCCCAG					2520
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		GCCTGTCAAG					3000
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15		GTGACAGATC					3180
		GAGCTGAGAC					3240
		GATGTTCCCG					3300
		GCTCTCTTTC					3360
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		AAGGAAGGCC					3540
		TTCACTGCAA					3600
		ACACCAAGCT					3660
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25		GATTTTTTTA					3780
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Seq ID NO: 339 Protein sequence Protein Accession #: NP 001786

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	KPYOPKYCEN	AVHGQLVLQI	SAIDKDITPR	NVKFKFTLNT	ENNFTLTDNH	DNTANITVKY	540
45	COFDREKTKY	HPLPVVISDN	CMPSRTCTST	LTVAVCKONE	QGEFTFCEDM	AAQVGVSIQA	600
	VVAILLCILT	ITVITLLIFL	RRRLRKOARA	HGKSVPEIHE	QLVTYDEEGG	GEMDTTSYDV	660
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	ELLY						

Seq ID NO: 340 DNA sequence Nucleic Acid Accession #: NM_003088

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Coding sequence: 112-1593 55 21 31 GCGGAGGGTG CGTGCGGGCC GCGGCAGCCG AACAAAGGAG CAGGGGCGCC GCCGCAGGGA CCCGCCACC ACCTCCCGGG GCCGCGCAGC GGCCTCTGT CTACTGCCAC CATGACCGCC
AACTGCACAG CCGAGGGGGT GCAGATCCAG TTCGGCCTCA TCAACTGCCAC CAACAAGTAC 120 60 CTGACGGCCG AGGCGTTCGG GTTCAAGGTG AACGCGTCCG CCAGCAGCCT GAAGAAGAAG 240 300 360 65 480 . 540 720 70 GCGCGCCCCQ AGCCGGCAC TGGCTACAG CTGGAGTTC GCTCGGCAA GGTRGCCTTC
CGCGACTTGC AGGCGCGTTA CCTGGGCGC TCGGGGCCA GCGCCAGGTC CAAGGCGCAA
AGGCCACCA AGGTGGGCAA GGACGAGCTC TTGGCTCTGG AGCAGAGCTC GCCCAGGTC 780 840 900 GTGCTGCAGG CGGCCAACGA GAGGAACGTG TCCACGCGCC AGGGTATGGA CCTGTCTGCC AATCAGGACG AGGAGACCGA CCAGGAGACC TTCCAGGTGG AGATCGACCG CGACACCAAA 960 1020 75 ANTICAGRACI AGRAGACCIA CONGAGNACI TECHNOLOGO MATERICAS CONGAGOGOTO
ANGTIGUECT TECHTACECA CACGGGENAG TACTIGGAGE TRACGGCAC COGGGGOTO
CAGTECACCO CETECAGENA GANTGECAGE TGETACTITG ACATEGAGTG GEGTGACEGG 1140 CSCATCACAC TRAGSGCOTT: CAATGACAAG TTTGTGACCT CCAAGAAGAA TGGGCAACCTG GCCGCCTCGG TGGGAACAGC AGGGGACTGA GAGCTCTTGC TCAAGAAGGT CATCCAACCAC CCCATCATCG TGTTCCGCGG GGAGCATGGC TTCATCAGGGT CATCCAACCAC 1200 1320 80 CTGGACGCCA ACCGCTCCAG CHATGACGTC TTCCAGCTGG AGTTCAACGA TGGCGCCTAC AACATCAAAG ACTCCACAGG CAAATACTGG ACGGTGGGCA GTGACTCCCG GGTCACCAG AGCGGGGGAA CTCCTTGTGA CTTCTTCTC GAGTTCTGC ACTATAACA GTGGGCCATC 1380 1440 AAGGTGGGCG GGCGCTACCT GAAGGGCGAC CACGCAGGCG TCCTGAAGGC CTCGGCGGAA 1560 ACCOTOGACE COSCETOGET CTGGGAGTAC TAGGGGGGGG COGTCCTTCC CCGCCCCTGC
CCACATGGGG GCTCCTGCCA ACCOTCCCTG CTAACCCCTT CTCCGCCAGG TGGGCTCCAG 1620 85 1680 GGCGGGAGGC AAGCCCCCTT GCCTTTCAAA CTGGAAACCC CAGAGAAAAC GGTGCCCCCA CCTGTCGCCC CTATGGACTC CCCACTCTCC CCTCCGCCCG GGTTCCCTAC TCCCCTCGGG

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	PODORYSVOT	ADHRPLRHDG	RLVARPEPAT	GYTLEPRSGK	VAFRDCEGRY	LAPSGPSGTL	240 300
	DWWW CA DDWG	DELFALEQUIC	COMPORTACON	MASCVEDTEW	PARATTERNS	NOKPUTSKKN	360
. 30	201 3 3 MITTER	COCCUT OF MOST	TATE DIT TATE DC	PUODICCPIO	TYTTIDANDSS	VIDVEOLEPNID	420
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26							
35	Seq ID NO:	342 DNA sec d Accession	quence	nrodiated			
	Coding seg	ience:660	1 #1 FUSINSSI 1705	predicted			
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	ACCORTGOGTG	CGGGCGCCGA	GCTGCGCGCT	GTGCTCGCGC	TCCTGCGGGC	AGGCCCAGGG	480
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	ESDPEPAALG	SSSAHCTNNG	VKVGDCDLRD	RAEGALLAES	PLGSSDA		

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_							420 480
.5							540
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							3060 3120
60							3180
OU	TGAACGGGA	ATGATGCAC	ACCATCCTG	GATTTTAAA	CCTGAAGTG	TTAGCACAGT GGGTGGCGCA TCTGTCTCTT	3240
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	TCATTTGGG	G TGAAGGAGA	CATTTCTGTC	C TIGGCTICC	C ACAGCCCCA	A CGCAGTCTGT	4260
00	GTATGATTO	C TGGGATCCA	A CGAGCCCTC	C TATTTTCAC	A GIGITCIGA	C CTTGCCCTTA A CGCAGTCTGT T TGCTCTCACA G GGAGGTCATG	4320 4380
80	GCCCAGGCC	C ATCGTCTGT	T CTCTGAATG	AGCCCTGTT	T ARAGAATC	A GTTCCTCAAA	4440
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0.5	AACCACIG	AG CTCAAACAC	O IGCILIALI	C ICCIOITIN		a agreement	4600
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			_				
	1	11	21	31	41	51	
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45	TPGGFRCECW	VGYEPGGPGE CVGPGGPLCD	GACQDVDECA SLCFNTQGSF	LGRSPCAQGC HCGCLPGWVL	THTDGSFHCS APNGVSCTMG	PVSLGPPSGP	420 480
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· -	TPGGPRCECW DGTQCQDVDE	VGYEPGGPGE CVGPGGPLCD	GACQDVDECA SLCFNTQGSF SDTRGDEGTP	LGRSPCAQGC HCGCLPGWVL KATPTTSRPS	TNTDGSFHCS APNGVSCTMG LSSDAPITSA	PVSLGPPSGP PLKMLAPSGS	420 480 540
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50 55 60	TPGGFRCEN DTTCQDVDE PDEEDKGEKE SQVMREPSIH LGLLVYRKRR Seq ID NO: Nucleic Ac Coding sequ 1	VGYEROGOGE CVORGGPLCO GSTVPRANTA HATAASGPQE AKREBKKEKK 346 DNA sei did Accession Lence: <1- 11 GCATGTACAA GCGCGGGGGGGGCTCAAGGG CCCAGGGAGA AACTITIGTC TGCACATGAT TGAACAAGGA CGAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGAGAGGAGGAGA	GACQUVEEA SLCENTQGSF SPTRGPEATP PAGGDSSYN Quence 1 #: 231560 966 21	LGRSPCAGGE RGGLPGWVI KATPTSRPS QNNDGTDGGW VPERAESRAM 31 ACOGAGCTCA GCGGCGGGG GCCTTCATGG CACAACTCGG AAGCGGCCTG AGCAGCTCA AGCAGCGCCTG AGCAACGGCG AAGCGCCTG AGCAACGGCAAACGGCAAACGGCAAACGGCCTG AGCAACGGCAAACGGCAAACGGCAAACGGCAAACGGCAAACGGCAAACGGCAAACGGCAAACGAAACGGCAAACGCAAACGGCAAAACAAACAAACAAAACAAAACAAAAAA	TATTOGERICS APROYSCTIMG LSSBAPTTSA LSSBAPTTSA LLLEFILLOT ENQYSPTPGT 41 AGCCGCCGGG CCGGCGGCAA TGTGGTCCCG GGTGTGTGCCG GGTGCTGGC GGCGGGCG	CERGYVLAGE PVSLGPPSGP PLIMILAPSGS VATILLIAIA DC 51	420 480 540 600 120 180 240 350 420 480 540 600
50 55 60	TPGGFRCEN DTTCQDVDE PDEEDKGEKE SQVMREPSIH LGLLVYRKRR Seq ID NO: Nucleic Ac Coding sequ 1	VGYEROGOGE CVORGGPLCO GSTVPRANTA HATAASGPQE AKREBKKEKK 346 DNA sei did Accession Lence: <1- 11 GCATGTACAA GCGCGGGGGGGGCTCAAGGG CCCAGGGAGA AACTITIGTC TGCACATGAT TGAACAAGGA CGAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGAGAGGAGGAGA	GACQUVEEA SLCENTQGSF SPTRGPEATP PAGGDSSYN Quence 1 #: 231560 966 21	LGRSPCAGGE RGGLPGWVI KATPTSRPS QNNDGTDGGW VPERAESRAM 31 ACOGAGCTCA GCGGCGGGG GCCTTCATGG CACAACTCGG AAGCGGCCTG AGCAGCTCA AGCAGCGCCTG AGCAACGGCG AAGCGCCTG AGCAACGGCAAACGGCAAACGGCAAACGGCCTG AGCAACGGCAAACGGCAAACGGCAAACGGCAAACGGCAAACGGCAAACGGCAAACGGCAAACGAAACGGCAAACGCAAACGGCAAAACAAACAAACAAAACAAAACAAAAAA	TATTOGERICS APROYSCTIMG LSSBAPTTSA LSSBAPTTSA LLLEFILLOT ENQYSPTPGT 41 AGCCGCCGGG CCGGCGGCAA TGTGGTCCCG GGTGTGTGCCG GGTGCTGGC GGCGGGCG	CERGYVLAGE PVSLGPPSGP PLIMILAPSGS VATILLIAIA DC 51	420 480 540 600 120 180 240 300 420 480 540 660
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50 55 60 65 70 75	TROUGRECON DOTTOCOUNDS PRINGENEER PRINGENEER PRINGENEER Seq ID NO NUCLEIC AC: COCKING Seq 1 1 CACAGGGCCC CACAGGGCCC AATRICACAG COCAGAGACC AATRICACAGC AATRICACAGC AATRICACAGC CTCGGCCC CTGGCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCCC TGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCC TGCCC TGCCC TGCCC CTGCCC CTGCCC CTGCCC CTGCCC CTGCC CTGCCC CTGCCC CTGCC	VOTEBOGICIE CVIDEGGILO GETVERANTA AKREBICKER 346 DNA 8E GONTOTACAA GONTO	GACGIVIDECA SILENTAGEN SPITAGEPORTE SPITAGEPORTE SPITAGEPORTE SPICACE	LGRSPCAQCE LGRSPCAQCE	THITDISPICS ANNOYSCING	CEROTYLAGE PPELAPPSOP S1 CONDUCATION CONSTITUTION S1 CONSTITUTION CONSTITUTION GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO	420 480 540 600 120 180 240 300 420 480 480 480 480 480 660 670 780 780 900 900 900 1020 1080
50 55 60 65 70 75	TROUGRECON DOTTOCOUNDS PRINGENEER PRINGENEER PRINGENEER Seq ID NO NUCLEIC AC: COCKING Seq 1 1 CACAGGGCCC CACAGGGCCC AATRICACAG COCAGAGACC AATRICACAGC AATRICACAGC AATRICACAGC CTCGGCCC CTGGCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGGCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCCC TGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCC TGCCC TGCCC TGCCC CTGCCC CTGCCC CTGCCC CTGCCC CTGCC CTGCCC CTGCCC CTGCC	VOTEBOGICIE CVIDEGGILO GETVERANTA AKREBICKER 346 DNA 8E GONTOTACAA GONTO	GACGIVIDECA SILENTAGEN SPITAGEPORTE SPITAGEPORTE SPITAGEPORTE SPICACE	LGRSPCAQCE LGRSPCAQCE	THITDISPICS ANNOYSCHIB ANNOYSCHIB LESDAFTIBA ANNOYSCHIB LESDAFTIBA LESDAFTIBA LESDAFTIBA ANNOYSCHIB LESDAFTIBA ANDOYSCHIB	CEROTYLAGE PPELAPPSOP S1 CONDUCATION CONSTITUTION S1 CONSTITUTION CONSTITUTION GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO GOSTMAGGO	420 480 540 600 120 120 120 480 540 420 480 540 660 660 720 840 960 960 1020 1080
50 55 60 65 70 75	TROUGRECOM DOTTOCOMONE DOTTOCOMONE SOURCE SO	VOTEBOGREE VOTEBOGREE	GACQUYDECA SILPHYGABY SILPHYGABY	LIGRISTCAQCE RECOGLIGATION 31 ACCURACION OF THE CONTROL OF THE C	THITDISPICS ARROYSCHUS	CERGYVLAGE PYELGIP SOR S1 CCOGCAGCA CCAGCAA CCAGCAAAAAC COGCAAAAAC COCCAGCAC CCCCGCGCC CCCCGCGCCC CCCCCGCCCC CCCCCC	420 480 540 600 120 180 240 360 360 420 480 480 480 900 900 900 1020 1080
50 55 60 65 70 75 80	TROUGRECOM DOTOCOMONIO DOTOCOMONIO DOTOCOMONIO DOTOCOMONIO SOME SERVICE SERVICE SERVICE SERVICE COCINE SERVICE	VOTEROGREE VOTEROGREE	GACGIVIDECA SILERITGIBE SI PROGRADETS PROGRA	LIGRISPCAQUE LIGRI	THITDISPIGS ARROYSCHIS	CERGYVIA-GE PYELGIP-SE S1 CCCGCAGGA COCGAAAAA COCGAAAAAC GOCCCAGGCA GOCCCAGGCA GOCCCAGGCA GATCAGCAGCA GATCAGCAGCA GATCAGCAGCAC GATCAGCAGCAC GATCAGCACCAC GATCAGCACCAC GATCAGCACCAC GATCAGCACCAC GATCAGCACCAC GATCAGCACCAC GATCAGCACCAC GATCAGCACCAC CATCAGCACCAC S1 APMVISROUE APMVISROUE S1 APMVISROUE APMVISROUE APMVISROUE S1 APMVISROUE AP	420 480 540 600 120 180 240 340 340 340 540 660 6720 780 990 1020 1080
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5	Seq ID NO: Nucleotide Coding sequ	348 DNA sec Accession i sence:	uence : NM_0026 120-473	38			
•	1	11	21	31	41	51	
10	GCTGGACTGC TGAGGGCCAG AGGCAGCTGT TCAATGGACA	AAGGAATTAT ATAAAGATTG CAGCTTCTTG CACGGGAGTT AGATCCCGTT AGTCAAAGGT	GTATGGCCTT ATCGTGGTGG CCTGTTAAAG AAAGGACAAG	AGCTCTTAGC TGTTCCTCAT GTCAAGACAC TTTCAGTTAA	CAAACACCTT CGCTGGGACG TGTCAAAGGC AGGTCAAGAT	CTGACACCA CTGGTTCTAG CGTGTTCCAT AAAGTCAAAG	60 120 180 240 300 360
15	TCCGGTGCGC TCAAGAAGTG CGGTCCTTGC TGCTGCCCTT	CATGTTGAAT CTGTGAAGGC TGCACCTGTG CCCCTTCCCA TCTCATCCAC	CCCCTAACC TCTTGCGGGA CCGTCCCCAG CACTGTCCAT	GCTGCTTGAA TGGCCTGTTT AGCTACAGGC TCTTCCTCCC	AGATACTGAC CGTTCCCCAG CCCATCTGGT	TGCCCAGGAA TGAAGGGAGC CCTAAGTCCC	420 480 540 600
20	Seq ID NO: Protein Ac	349 Protein cession #:	sequence: NP_0026	29			
	1	11	21	31	41	51	
25	1	 VFLIAGTLVL	1	1		NORTH CODE IN	60
23	AQEPVKGPVS	TKPGSCPIIL	IRCAMLNPPN	RCLKDTDCPG	IKKCCEGSCG	MACEVEQ	60
30	Nucleic Ac	350 DNA sec id Accession uence: 75-2	#: NM_0071	.83			•
	1	11	21	31	41	51	
35	GAATTCCGGA	CAGGACGTGA	AGATAGTTGG	GTTTGGAGGC	GGCCGCCAGG	CCCAGGCCCG	60
	GTGGACCTGC	CGCCATGCAG	GACGGTAACT	TCCTGCTGTC	GGCCCTGCAG	CCTGAGGCCG	120 180
	CGGAGGCCGA	GCGGCTGCGG	GCAGCCCGCG	TCCAGGAGCA	GGTCCGCGCC	CGCCTCTTGC	240
40	ACCTOCCACA	acaeccecee.	CACAACGGGG	CCCCTGAGCC	CORCOTTORG	GCCGAGACTG	300 360
40	CCAGAGGCAC	ATCCAGGGGG TGGGGACAAG	CAGTACCACA	TOGGGGGGAT	COCCAAGCCG	CCTACAGCC	420
	CAGCCTCCTG	GTCCTCCCGC	TCCGCCGTGG	ATCTGAGCTG	CAGTCGGAGG	CTGAGTTCAG	480
	CCCACAATGG	GGGCAGCGCC	TTTGGGGCCCG	CTGGGTACGG	GGGTGCCCAG	CCCACCCCTC	540 600
45	ATGREACACT	CTCCCTGCGC	TCGCTGCGGC	TGGGGCCCGG	GGGCCTGGAC	GACCGCTACA	660
	GCCTGGTGTC	CTCCCTGCGC TGAGCAGCTG	GAGCCCGCGG	CCACCTCCAC	CTACAGGGCC	TTTGCGTACG	720
	AGCGCCAGGC	CAGCTCCAGC	TCCAGCCGGG	CAGGGGGGCT	GGACTGGCCC	GAUGUCCACIG	780 840
	CONCOUNTER	CACCOCCCCCC	CTT ACCCCCCC	CAGTGCCGGG	CCCCCTCCTC	GAGCCAGTGG	900
50	CTCGAGCGCC	ATCTGTGCGC	AGCCTCAGCC	TCAGCCTGGC	TGACTCGGGC	CACCTGCCGG	960
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23	AGGTGCAGCG	CCATGCCACA GGTGGAGGAG	AACGGGATCT	TOGRECITECT	GOGGACACTG	CGGGAGCAGG	1320
	ATGATGAGCT	TCGCAAAAAT	GTCACAGGGA	TCCTGTGGAA	CCTTTCATCC	AGCGACCACC	1380
	TGAAGGACCG	CCTGGCCAGA TGGGGGTCCC	GACACGCTGG	AGCAGCTCAC	GGACCTGGTG	TTGAGCCCCC	1440 1500
60	ACAACGCCAC	CGGCTTCCTC	AGGAACCTCA	GCTCAGCCTC	TCAGGCCACT	CGCCAGAAGA	1560
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	GGGACCTGGC	GGGGGGGGCG	CCGGGAGAGG	TCGTGGGCTG	CTTCACGCCG	CAGAGCCGGC	1800
65	GGCTGCGCGA	GCTGCCCCTC	GCCGCCGATG	CGCTCACCTT	CGCGGAGGTG	TCCAAGGACC	1860 1920
	AGCCCTCCCA	CGAGTGGCTG GCTCAACCGG	CACACGACGC	AGGCGGCCGC	CGGGGGGGCTG	CAGAACATCA	1920
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70	TTCTGAACCC	CCTGCTAGAC CCGAAACCTG	CGTGTCAGGA	CCGCCGACCA	CCACCAGCTG	CGCTCACTGA	2100
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	TCGCTGGCGC	GCTGCTTGGC	AGCCCAGCCT	GTCCTGGGCC	ACCAGGAGGG	GCAGGGTCTT	2640
00	ATAGCTGGGG	ACTTGGCTTC	CGCAGGGCAG	GGGGTGGGGC	AGGGCTCAAG	GCTGCTCTGG	2700
80	TOTATOGGGT	GGTGACCCAG	TCACATTGGC	AGAGGTGGGG	GTTGGCTGTG	GCCTGGCAGT	2760 2820
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85	Seq ID NO: Protein Ac	351 Protein	NP_0091	14.1			
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	1	1	1.	1	1	1	60
	MQDGNPLLSA	LOPEAGVCSL PEAETARGTS	ALPSDLQLDR	RGAEGPEAER	DEMOCREDITA	KAKILIQUGQQ WILL VERN CHE	120
	PRHNGAAEPE	RRLSSAHNGG	PARCANOVOC	ACDUDATED	DELIGEREDICA	CCDANVITTLE	180
5	SKSAVDLSCS	LDDRYSLVSE	OFFINANCIA	MUPIPPMPIA	eccepacar.	WDEATEUEDE	240
,	DESTRUCTOR	PDDKISDASE	DUCKUCANDUS GREENWITSII	VIEDVARARA	VESTSLELAD	SCHLPDVHGF	300
	MOVOCUDTIO	LORFOSSHRS RLSSGFDDID	LOCAUKYT.MA	SDENTOVICA	AYTORKCYSD	AAAKKOARSL	360
							420
	KNYTGILWNL	SSSDHLKDRL ATROKMRECH	ARDTLEOLTD	LVLSPLSGAG	GPPLIQQNAS	EABIFYNATG	480
10	FLRNLSSASO	ATROKMRECH	GLVDALVTSI	NHALDAGKCE	DKSVENAVCV	LRNLSYRLYD	540
	EMPERALORI.	ECRERRETIAG	APPGEVVGCF	TPOSRRLREL	PLAADALTFA	EVSKDPKGLE	600
	WINCOUTURE.	AND L'UD CET	NEHTTERARG	ALONITAGOR	RWAGVLSRLA	LEGERILNPL	660
	LDRVRTADHH	QLRSLTGLIR ASPIAARDLL	NLSRNARNKD	EMSTKVVSHL	IEKLPGSVGE	KSPPAEVLVN	720
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15	HRDFRAKGYR	KEDPLGP					
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20	Nucleic Aci	d Accession	#: M31469				
20	Coding sequ	ience: 1-65	•				
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	ATGGCTGCGC	AGGGAGAGCC	CCAGGTCCAG	TICAAACTIG	TATTGGTTGG	TGATGGTGGT	60
25	ACTGGAAAAA	CGACCTTCGT GTGTTGAGGT	GAAACGTCAT	TTGACTGGTG	AATTTGAGAA	GAAGTATGTA	120
	GCCACCTTGG	GTGTTGAGGT	TCATCCCCTA	GTGTTCCACA	CCAACAGAGG	ACCTATTAAG	180
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	ATCCAAGCCC	AGTGTGCCAT	CATAATGTTT	GATGTAACAT	CGAGAGTTAC	TTACAAGAAT	300
20	GTGCCTAACT	GGCATAGAGA	TCTGGTACGA	GTGTGTGAAA	ACATCCCCAT	TGTGTTGTGT	360
30							420 480
	AAGAAGAATC	TTCAGTACTA TTGCTAGGAA	CGACATTTCT	GCCAAAAGTA	ACTACAACTT	TGAAAAGCCC	480 540
	TTCCTCTGGC	TTGCTAGGAA	GCTCATTGGA	GACCCTAACT	TGGAATTTGT	TGCCATGCCT	600
	GCTCTCGCCC	CACCAGAAGT CTCAGACAAC	TGTCATGGAC	CCAGCTTTGG	CAGCACAGTA	TGAGCACGAC	600
35	TTAGAGGTTG	CTCAGACAAC	TGCTCTCCCG	GATGAGGATG	ATGACCIGIG	^	
33		353 Protein					
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40	î	ī	ī -	ī	1	Ī	
	MAAOGEPOVO	FKLVLVGDGG	TGKTTFVKRH	LTGEFEKKYV	ATLGVEVHPL	VPHTNRGPIK	60
	ENVENTAGOE	KEGGLEDGYY	TOACCALIMF	DVTSRVTYKN	VPNWHRDLVR	VCENIPIVLC	120
	GNKVD1KDRK	VKAKSIVFHR	KKNLOYYDIS	AKSNYNFEKP	FLWLARKLIG	DPNLEFVAMP	180
	ALAPPEVVMD	PALAAQYEHD	LEVAOTTALP	DEDDDDL			
45	ALAPPEVVMD	PALAAQYEHD	LEVAOTTALP	DEDDDL			
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45	ALAPPEVVMD	PALAAQYEHD 354 DNA sec	LEVAQTTALP	DEDDDL			
45	Seq ID NO: Nucleic Ac:	PALAAQYEHD 354 DNA secid Accession	LEVAQTTALP quence 1 #: NM_0028	DEDDDL			
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45 50	Seq ID NO: Nucleic Ac:	PALAAQYEHD 354 DNA sec id Accession uence: 304-	LEVAQTTALP quence 1 #: NM_0028	DEDDDL		51	
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50	Seq ID NO: Nucleic Ac: Coding sequence 1 CCGGTTCGCA	PALAQYEHD 354 DNA secid Accession uence: 304-1 11 AAGAAGCTGA CGAACCTAGG	LEVAQTTALP Tuence 1 #: NM_0026 331 21 CTTCAGAGGG	DEDDDL 120 31 GGAAACTTTC GCCAGATTAA	41 TTCTTTTAGG	51 AGGCOGTTAG CTATGGGAGA	120
	Seq ID NO: Nucleic Ac: Coding sequents 1 CCGGTTCGCA CCTGTTCCA	PALAQYEHD 354 DNA secid Accession uence: 304-1 11 AAGAAGCTGA CCGAACCCAGG CACTACTTAT	TUENCE TUENCE TH: NM_0026	20 31 GGAACTTC GCCAGATTAA	41 TTCTTTTAGG TTAGACATTG CATTTTATTT	51 AGGCGGTTAG CTATGGGAGA TCGCTATTAT	120 180
50	Seq ID NO: Nucleic Ac: Coding sequence 1 	354 DNA secid Accession uence: 304-1 11 AAGAAGCTGA CGAACCCAGG CACTACTTAT	LEVAQTTALP Quence 1 #: NM_0026 331 21 CTTCAGAGGG AGAACTGCTG CATTGATGCA	31 GGAAACTITC GCCAGATTAA TATATAAAAC	41 TICTITTAGG TIAGACATTG CATTITATIT	51 AGGCGGTTAG CTATGGGAGA TCGCTATTAT	120 180 240
50	ALAPPEVVMD Seq ID NO: Nucleic Ac: Coding sequence COGOTTCGCA CCCTGTTCCA CCTGTAAACA TTCAGAGGAA GTTTCAGAGGAA	PALAAQYEHD 354 DNA set id Accession uence: 304-1 11 AAGAAGCTGA CGACCCAGG CACTACTTAT GCGCCTCTGA AGCACGTTG	LEVAQTTALP quence que que que que que que que que que qu	31 GGAAACTITC GCCAGATTAA TATATAAAAC TITTCCCTTT	41 TICTITIAGG TIAGACAITG CATTITATIT TIGCTCTTIC AGTCCCGAGC	51 AGGCOGTTAG CTATGGGAGA TCGCTATTAT TGGCTGTGTG GCGAGCOGAG	120 180 240 300
50	ALAPPEVVMD Seq ID NO: Nucleic Ac: Coding sequ COGGTTCGCA CCCTGTTCCA CCTGTTCCA CTTCAGAGGAA GTTTCAGAGGAA GTTTCAGAGGAA ACCASTGAGGAA ACCASTGAGAA ACCATGAGAA ACCATGAC	PALAAQYEHD 354 DNA secid Accession uence: 304-1 11 AAGAAGCTGA CGAACCCAGG CACTACTTAT AGGCCTCTGA AGCACAGTTG AGGACCTGTGA AGGACAGTTG	LEVAQTTALP Quence 1 #: NM_0028 331 21	31 	41 TTCTTTTAGG TTAGACATTG CATTTTATT TTGCTCTTC AGTCCCGAGC	51 AGGCGGTTAG CTATGGGAGA TCGCTATTAT TGGCTGTGTG GCGAGCGGAG	120 180 240 300 360
50	ALAPPEVVMD Seq ID NO: Nucleic Ac: Coding sequ COGGTTCGCA CCCTGTTCCA CCTGTTCCA CTTCAGAGGAA GTTTCAGAGGAA GTTTCAGAGGAA ACCASTGAGGAA ACCASTGAGAA ACCATGAGAA ACCATGAC	PALAAQYEHD 354 DNA secid Accession uence: 304-1 11 AAGAAGCTGA CGAACCCAGG CACTACTTAT AGGCCTCTGA AGCACAGTTG AGGACCTGTGA AGGACAGTTG	LEVAQTTALP Quence 1 #: NM_0028 331 21	31 	41 TTCTTTTAGG TTAGACATTG CATTTTATT TTGCTCTTC AGTCCCGAGC	51 AGGCGGTTAG CTATGGGAGA TCGCTATTAT TGGCTGTGTG GCGAGCGGAG	120 180 240 300 360 420
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50	ALAPPEVVMD Seq ID NO: Nucleic Ac: Coding sequ CCGGTTCGCA CCTGTTCCA TCTGCAGGAA ATTGGAGGAA ACGATGCAGC GTGCCTCCT GAACATCAGC CTTCACCATC CTTAACTCCA	PALAQVEHD 354 DNA secid Accession uence: 304-1 11 AAGAAGCTGA CGAACCCAGG CACTACTTAT GGCCTCTGA AGCACAGTTG GGAGACTGGT GCAGGCGCTC TCCTCCATGA TCCTCCATGA TGATCGCAGA AGCACTTGCATGA AGCACTCTGCATGA AGCACTCTGCATGA AGCACTCTGCA	LEVAQTTALP Quence 1 %: NM_0028 331 21 CTTCAGAGGG AGAACTGCTG CATTGATGCA TTTGTTCTT TGAGAGGGAGGAG TCAGCAGGGGAGGAG AATCCACAGA	DEDDL 31	41 TTCTTTTAGG TTAGGACTTG CATTTTATT TTGCTCTTC GCCTCANAGG GCTCCANAGG GAGGTACTG GAGGTACTTG TCCGATTTG	51 AGCOGTTAG CTATGGAGA TOGCTATTAT TGGCTGTGTG GAGGTAGGO AGCTGTGTTCT GGAGGTATCT GGAGGTATCT GGAGGTATCT GGAGGTATCA	120 180 240 300 360 420 480
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AC ATGCTTTGTG GCTATCCATC AACATAAGT Sea ID NO: 357 Protein sequence Protein Accession #: NP_059992 PRIVATEDED DILDISDEDD CHRICTORDS PTONGGICH EMRICOGESE CPOSSBERA TOTROPORTAL SECONDARY CONTROL YRKTTEEEDE DELHIGRTAQ IGHVYPARVA LSLEDDGLP Seg ID NO: 358 DNA sequence Nucleic Acid Accession #: M27826 Coding sequence: <1-503 AGCCCAAGAA ACATCTCACC AATTTCAAAT CTGATCTATT CGGCTTAGCG ACTGAAGATT GACGCTGCCC GATCGCCTCG GAAGTCCCCT GGACCATCAC AGAAGCCGAG CTTCGGGTAA CTCTCACAGT GGAGGGTAAG TCCATCCCCT GTTTAATCGA TACGGGGGCT ACCCACTCCA COTTOCCTTC TTTTCAAGGG CCTGTTTCCC TTGCCCCCAT AACTGTTGTG GGTATTGACG GCCAAGCTTC AAAACCCCTG AAAACTCCCC CACTCTGGTG CCAACTTGGA CAACACTCTT TTATGCACTC TITTITAGTT ATCCCCACCT GCCCACTICC CITATIAGGC CGAAATATIT
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CACTIGAAGC AGCCCTGAGA AACATCGCCC ATTCTCTCTC CATACCACCC CCCAAAAATT
TTCGCCGCTC CAACACTTCA ACACTATTTT GTTTTATTTG TCTTATTAAT ATCAGAAGGC

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	ACATCCAGAT	GGCCTGAAGT	AACTGAAGAT	CCACAAAAGA	AGTAAAAACA	GCCTTAACTG	780
	ATGACATTCC	ACCATTGTGA	TTTGTTCCTG	CCCCACCCTA	ACTGATCAAT	GTACTTTGTA	840 900
5	TGAGATCCAC	CCCTTAAGAA CCCTGCCCAC	CAGAGAACAA	CCCCTTTGA	ACCULTGAGA	TTATTACCTT	960
•	CCCAAATCCT	ATAAAACAGC	CCCACCCCTA	TCTTCCTTCA	CTGACTCTCT	TTTCGGACTC	1020
	AGCCACCGGC	ACCCAGGTGA	AATAAACAGC	TTTATTGCTC	AC		
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15	PKKHLTNFKS	DLFGLATEDW	RCPIASEVPW	TITEAELRVT	LTVEGKSIPC	LIDTGATHST	60
13	LPSPOGPVSL	APITVVGIDG GVQLHLIAAL	QASKPLKTPP LDNDVDDLCD	LWCQLGQHSF	ODLESA	PLPLLGRNIL	120
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0.5	CCAGAGGCTT	AGGTCCTAGA CCCTGGACCT	CCTGGTCCAA	TAGGTCTTCA	GGGTCTGCCA	GGCCCACCTG	3720
	GTGAAAAAGG	TGAAAATGGG	GATGTTGGTC	CATGGGGGCC	ACCTGGTCCT	CCAGGCCCAA	3840

	anacaaaaaa	AGGTCCCAAT	DEKOTOMOD	CACCACAACC	ACCCCCAGGT	TOTATICATI	3900
	and a constant	TGTTGGAGAA	PACCCECANC	CTCCACAACC	ACCIDANCCCA	CCCCCCCCC	3960
	0101100100	TGTAGGCGGT TGGACCTCCA TGTTGGTTTT	20001000	************	Charcecta	CCTCCTCCAC	4020
	GGGAAGGCAGG	IGIAGGCGGI	CCCOOMGGAG	aggaggggana.	man managed	COMPACCOURA	4080
5	CTGGAGCTGC	TGGACCTCCA	GGTGCCAAGG	GGCCGCCMGG	IGAIGAIGGC	CCIMAGGGIA	4140
3	ACCCGGGTCC	TGTTGGTTTT	CCTGGAGATC	CTGGTCCTCC	TGGGGGGGCTT	GGCCCTGCAG	4200
	GTCAAGATGG	TGTTGGTGGT	GACAAGGGTG	AAGATGGAGA	TCCTGGTCAA	CCGGGTCCTC	4260
	CTGGCCCATC	TGGTGAGGCT	GGCCCACCAG	GTCCTCCTGG	AAAACGAGGT	CCTCCTGGAG	
	CTGCAGGTGC	AGAGGGAAGA	CAAGGTGAAA	AAGGTGCTAA	GGGGGAAGCA	GGTGCAGAAG	4320
							4380
10	ANCOTOTO	CCCCATCCCT	COTCCTGTGG	GAGAACAAGG	TCTCCCTGGA	GCTGCAGGCC	4440
	AAGATGGACC	ACCTGGTCCT	ATGGGACCTC	CTGGCTTACC	TGGTCTCAAA	GGTGACCCTG	4500
							4560
	1100001111	AGGTGACCGA TCCTGGTCCT CCCAAAGGGT	COCCECCO	CAACTCAAGG	ATCTCCAGGA	GCAAAAGGGG	4620
	MUGGGAMM	MOGIGACCOA	GOOCICCCIO	MACCECCA CC	TOOTCOTCCA	GGCTTCACCAG	4680
15	ATGGGGGAAT	TCCTGGTCCT	GCIGGICCCI	TAGGICCACC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ANACCITCACA	4740
13	GTCCTCAAGG	CCCAAAGGGT	AACAMIGGCI	CIMCIGGACC	CGC1GGCCAG	ANAGOTONOM C	4800
	CTGGTCTTCC	AGGGCCTCCT	GGGCCTCCAG	GICCHCCIGG	TGANGICATI	CAGCCTTTAC	4860
	CAATCTTGTC	CTCCAAAAAA	ACGAGAAGAC	ATACTGAAGG	CATGCAAGCA	GATGCAGATG	
	ATAATATTCT	TGATTACTCG	GATGGAATGG	AAGAAATATT	TGGTTCCCTC	AATTCCCTGA	4920
	BACABOACAT	CCACCATATC	AATTTTCCAA	TYGGTACTCA	GACCAATCCA	GCCCGRACTT	4980
20	CTABAGACCT	GCAACTCAGC	CATCCTGACT	TCCCAGATGG	TGAATATTGG	ATTGATCCTA	5040
	ACCAAGGTTG	CTCAGGAGAT	TCCTTCAAAG	TTTACTGTAA	TTTCACATCT	GGTGGTGAGA	5100
							5160
	CITOCATITA	TCCTCTCTCTCT	CA A TOTAL A CA	CCCCAAAACT	CCTTTCATAC	TTAGATGTTG GCCTCTGCTC	5220
	AACCAGGAAG	TIGGITIAGI	GARTITANGA	GGGGRANACI	B CONTICTOR CT	COTOTOTO	5280
25	AAGGAAATTC	CATCAATATG	GIGCAMATGA	CATTCCTGAC	ACTICIONCI	MCD MCD CCD A	5340
25	GGCAAAATTT	CACCTACCAC	TGTCATCAGT	CAGCAGCCIG	GINIGAIGIG	ICAICAGGAA	
	GTTATGACAA	AGCACTTCGC	TTCCTGGGAT	CAAATGATGA	GGAGATGTCC	TCATCAGGAA TATGACAATA	5400
							5460
	TCATTGAAAT	CANTACACCA	AAAATTGATC	AAGTACCTAT	TGTTGATGTC	ATGATCAGTG	5520
	ACTITIGGTGA	TCAGAATCAG CAAAGAACAT CATGCAAGTT	AAGTTCGGAT	TTGAAGTTGG	TCCTGTTTGT	TTTCTTGGCT	5580
30	BACATTANCA	CARAGARCAT	BYCABATCAA	CAGAAAATGT	ACCTTGGTGC	CACCAACCCA	5640
50	MUNITARION	CATCCAACTT	TTGBBTABGG	ATVZTATCICAA	AACAACGCTG	CATATACAGG	5700
	IIIIGIGCCA	GAAATACCGA	TIGOTIANGO	CCCCCACAAT	CACAGACAAA	ACCTTTOAAA	5760
							5820
	ATCATAAAGA	TATAAGTTGG	TOTGGCTAAG	ATGUARACAG	COCTONITO	DARRAGORA	5880
25	TTCTCAACTC	TATAGETIGG TCCTTTTCCT CATAAAAAAT AAATTGTAAT CACGTGTCCC	ATTTGAATTT	CTTIGGIGCI	GIAGAAAACA	ACCUPATION AND COLOR	5940
35	AATATATATT	CATAAAAAAT	ATGGTGCTCA	TTCTCATCCA	TCCAGGATGT	ACTAAAACAG	5940
	TOTOTTTAAT	AAATTGTAAT	TATTTTGTGT	ACAGTTCTAT	ACTGTTATCT	GTGTCCATTT	6000
	CCAAAACTTG	CACGTGTCCC	TGAATTCCGC	TGACTCTAAT	TTATGAGGAT	GCCGAACTCT	6060
					TTCCGATGAC	CCTAAGTCCC	6120
	TTTCTTTGGT	TAATGATGAA	ATTCCTTTGT	GTGTGTTT			
40							
	Seq ID NO:	161 Protein	semience				
	Protein Ac	cession #:	NP 0018	345			
	Protein Ace	cession #:	NP_0016	145			
	Protein Acc	cession #:	NP_0018		41	51	
45	Protein Acc	cession #:	NP_0016	31 ·	41	51 1	
45	Protein Acc	cession #:	NP_0016	31 .	1	1	60
45	Protein Ace	cession #:	NP_0016	31 REVRGAAPVD	 VLKALDPHNS	PEGISKTTGF	60 120
45	Protein Acc	11 KRWLWDFTVT	NP_0018	31 REVRGAAPVD PGGTFPEDFS	VLKALDPHNS ILPTVKPKKG	PEGISKTTGF IQSFLLSIYN	120
45	Protein Act	11 KRWLWDFTVT	NP_0018	31 REVRGAAPVD PGGTPPEDPS	VLKALDFHNS ILPTVKPKKG	PEGISKTTGF IQSPLLSIYN VEKKTVTMIV	120 180
	Protein Act	11 KRWLWDFTVT	NP_0018	31 REVRGAAPVD PGGTPPEDPS	VLKALDFHNS ILPTVKPKKG	PEGISKTTGF IQSPLLSIYN VEKKTVTMIV	120 180 240
45 50	Protein Act	11 	NP_0018 21	31 REVEGAAPVD PGGTFPEDFS YPLFRTVNIA LDEEVFEGDI YEYGEAEYKB	VLKALDPHNS ILPTVKPKKG DGKNHRVAIS QQPLITGDPK AESVTEGPTV	PEGISKTTGF IQSPLLSIYN VEKKTVTMIV AAYDYCEHYS TEETIAQTEA	120 180 240 300
	Protein Act	11	NP_0018 21	31 REVRGAAPVD PGGTFPEDPS YPLFRTVNIA LDEEVFEGDI YEYGEAEYKE PNPVEEIFTE	VLKALDPHNS ILPTVKPKKG DGKWHRVAIS QQFLITGDPK AESVTEGPTV EYLTGEDYDS	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCEHYS TEETIAQTEA QRKNSEDTLY	120 180 240 300 360
	Protein Act	11	NP_0018 21 TLALTFLFQA QLSAPTKQLF DHTGKPAPED NGITVFGTRI YAPEDIIEYD APRHVSGTNB YDFYBYKEYB	31 	VLKALDPHNS ILPTVKPKKG DGKWHRVAIS QQFLITGDPK AESVTEGPTV EYLTGEDYDS FGPGVPAZTD	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCEHYS TEETIAQTEA QRKNSEDTLY ITETSINGHG	120 180 240 300 360 420
	Protein Act MEPWSSRWKT CTNRKNSKGS ENGIQQIGVE DCKKRTTKPL PDCDSSAPKA NIVDDFQEYN ENKEIDGRDS	11	NP_0018 21 TLALTFLFQA QUSAPTKQLF DHTGKPAPPED NGITVFGTRI YAPEDIIEYD APRHVSGTNE YDFYEYKEYE	31 REVRGAAPVD PGGTPPEDFS YPLFRTVNIA LDBEVPEGDI YEVGBABYKE PNPVERIFTE DKPTSPPNEE	VLKALDPHNS ILFTVKPKKG DGKNHRVAIS QQFLITGDPK AESVTEGPTV EYLTGEDYDS FGPGVPASTD	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCEHYS TEETIAQTEA QRKNSEDTLY ITETSINGHG PGDDGRPGLP	120 180 240 300 360 420 480
50	Protein Act MEPWSSRWKT CTNRKNSKGS ENGIQQIGVE DCKKRTTKPL PDCDSSAPKA NIVDDFQEYN ENKEIDGRDS	11	NP_0018 21 TLALTFLFQA QUSAPTKQLF DHTGKPAPPED NGITVFGTRI YAPEDIIEYD APRHVSGTNE YDFYEYKEYE	31 REVRGAAPVD PGGTPPEDFS YPLFRTVNIA LDBEVPEGDI YEVGBABYKE PNPVERIFTE DKPTSPPNEE	VLKALDPHNS ILFTVKPKKG DGKNHRVAIS QQFLITGDPK AESVTEGPTV EYLTGEDYDS FGPGVPASTD	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCEHYS TEETIAQTEA QRKNSEDTLY ITETSINGHG PGDDGRPGLP	120 180 240 300 360 420 480
50	Protein Act MEPWSSRWKT CTNRKNSKGS ENGIQQIGVE DCKKRTTKPL PDCDSSAPKA NIVDDFQEYN ENKEIDGRDS	11	NP_0018 21 TLALTFLFQA QUSAPTKQLF DHTGKPAPPED NGITVFGTRI YAPEDIIEYD APRHVSGTNE YDFYEYKEYE	31 REVRGAAPVD PGGTPPEDFS YPLFRTVNIA LDBEVPEGDI YEVGBABYKE PNPVERIFTE DKPTSPPNEE	VLKALDPHNS ILFTVKPKKG DGKNHRVAIS QQFLITGDPK AESVTEGPTV EYLTGEDYDS FGPGVPASTD	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCEHYS TEETIAQTEA QRKNSEDTLY ITETSINGHG PGDDGRPGLP	120 180 240 300 360 420 480
	Protein Act MEPWSSRWKT CTNRKNSKGS ENGIQQIGVE DCKKRTTKPL PDCDSSAPKA NIVDDFQEYN ENKEIDGRDS	11	NP_0018 21 TLALTFLFQA QUSAPTKQLF DHTGKPAPPED NGITVFGTRI YAPEDIIEYD APRHVSGTNE YDFYEYKEYE	31 REVRGAAPVD PGGTPPEDFS YPLFRTVNIA LDBEVPEGDI YEVGBABYKE PNPVERIFTE DKPTSPPNEE	VLKALDPHNS ILFTVKPKKG DGKNHRVAIS QQFLITGDPK AESVTEGPTV EYLTGEDYDS FGPGVPASTD	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCEHYS TEETIAQTEA QRKNSEDTLY ITETSINGHG PGDDGRPGLP	120 180 240 300 360 420 480
50	Protein Act MEPWSSRWKT CTNRKNSKGS ENGIQQIGVE DCKKRTTKPL PDCDSSAPKA NIVDDFQEYN ENKEIDGRDS	11	NP_0018 21 TLALTFLFQA QUSAPTKQLF DHTGKPAPPED NGITVFGTRI YAPEDIIEYD APRHVSGTNE YDFYEYKEYE	31 REVRGAAPVD PGGTPPEDFS YPLFRTVNIA LDBEVPEGDI YEVGBABYKE PNPVERIFTE DKPTSPPNEE	VLKALDPHNS ILFTVKPKKG DGKNHRVAIS QQFLITGDPK AESVTEGPTV EYLTGEDYDS FGPGVPASTD	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCEHYS TEETIAQTEA QRKNSEDTLY ITETSINGHG PGDDGRPGLP	120 180 240 300 360 420 480
50	Protein Act	11	NP_0018 21 TLALTFLFQA QLSAPTKQLF DHTGKPAPED HTGKPAPED AFRHVSTIFY APRDIIEY APRDIIEY APROJEGAFA GGSKGPTIS GGPRGVGGP GGPRGVGGP GGPRGPGPGDG	31 REVRGAAPVD PGGTFPEDFS YPLFRTWHIA LDBEVPEGDI YEYGEAEYKE DKPTSPPNEE GIMGFPGLOG AQEAQAQAIL GPTGKPGKRG GMCREDGEIG GOOGMPGPGS	VLKALDFHNS ILFTVKPKKG DGKNHRVAIS QQFLITGDPK AESVTEGPTV EYLTGEDYDS FGFGVPAETD PTGPPGDPGD QQARIALRGP RPGADGGRGM PRGLPGEAGP LPGPCGDIGP	PEGISKTTGF PEGISKTTGF PGSFLASIYN VEKKTVTMIV AAYDYCEHYS TEETIAOTEA QRKNSEDTLY ITETSINGHG RGPPGRPGLP PGPMGLTGRP PGEPGAKGDR RGLLGPRGTP PGEKGPQGKP	120 180 240 300 360 420 480 540 600 720
50	Protein Act	11	NP_0018 21 TLALTFLFQA QLSAPTKQLF DHTGKPAPED HGITVFGTRI YAPEDIIEYD APREVSGTNE EGPPGPAGPA GDGSKGPTIS GGPRGVQGPP GGPPGDD MGPQGEPGED MGPQGEPGED MGPQGEPGED MGPQGEPGED	31 REVRGAAPVD PGGTTPPEDFS YPLFRTVNIA LDBEVFECDI YEYGGAEYKE PNPVEEIFTE DKFTSPPNEE GIMGPFGLQG QCMGPGQG GHRGEDGEIG QQQMGEQG GPGGFIGGREG	VLKALDPHNS ILFTVKPKKG DGKHRVAIS QQPLITGDPK AESVTEGPTV EYLTGEDYDS FGFGVPAETD PTGPPGDPGD QQARIALRGP RPGADGGRGM PRGLPGEAGP LPGFQGPIGP PRGVRADGV	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCEHYS TEETIAQTEA QRKNSEDTLY ITETSINGHG RGPPGRPGLP PGEPGAKGDR RGLLGPRGTP PGEKGPQGKF RGLLGPRGTP RGLKGSKGGEK	120 180 240 300 360 420 480 540 600 720 780
50	Protein Act	11 KRWLWDFTVT DTAYXVSKQA VGRSPVFLAP URSEVFLAP URSEVFLAP URSEVFLAP URSEALVDT AQAGEPUDT AQAGEPUDT YOTHSYVTE DLLVDGDLGE YOTHSYVTE DLLVDGDLGE AKGESGDPOP DKGHRGERGP PDGPHFAKEGQ	NP_0016 21 TLALTFLPQA QLSAPTKQLF DHTCKPAPED HGITVFGTRI APRENISTINE APRENISTINE SUPPEPAGPA GDGSKGPTIS GGPRGVQGPP QGPRGVQGP QGPRGVQGP SGEKGALGPP SGEKGALGP	31 REVEGAAPVD PGGTPPEDPS YPLFRTWILL LDBEVPEGDI YEYGEAEYKE PNPVEEIFTE GIMGPGLQG AQEAQAQAI AQEAQAQAI AQEAQAQAI GQQGMEGDGEIG GQQGMEGDGEG GPGGPIGREG	VLKALDPHNS ILPTVKPKKG DGKHRVAIS QOPLITGDPK AESVTEGPTV EYLTGEDYDS FGPGVPAETD TGPPGDPDD QQARIALRGP RPGLADGGRGM PRGLPGEAGP LPGPCGPIGP PRGVKGADGV	PEGISKTTGF IQSFLLSI'N VEKKTVTMI'V ANYDYCEHYS TEETIAQTEA QRKNSEDTLY ITETSINGHG RGPPGRPGLP PGPMGLTGRP PGEFGAKGDR RGLLGPRGTP PGEKGPPQKP RGLKGSKGEK AGEKGKKEK	120 180 240 300 360 420 480 540 600 720 780 840
50	Protein Act	11	NP_0018 21 TLALTFLFQA QLSAPTKQLF DHTGKPAPED HGITVFGTRI YAPEDLIEYD GEPCPAGPA GDGSKGPTIS GGPKRVQGPP GQPPCPPCGD MGPQGPAGPA MGPQGPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPAGA	31 REVRGAAPVD PGGTTPEDFS YPLFRTWILA LDSEVPEGDI YEYGGAEYKE NHYUEIFTE GIMGPFGLQG AQEAQAQAL GPTGKPGKRG GMGEDGEIG QQCMGEQGG GPGGFGGRG GPGGFGGRG GPGGFGGRG GPGGFGGRG	ULKALDPENS ILPTVKPKKG DGKHRVAIS QOPLITGDPK AESVTEGPTV EYLAGENYOS PGGPGPAZTD PTGPPGDPGD PGGPGGRGRGRGRGRGRGRGRGRGRGRGPGFGPGPGPFGPGPGGPGPGPGP	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCENYS TEETIAQTEA QRKNSEDTLY ITETSINGHG RGPGRPGLP PGENGLIGRE PGENGANGDR RGLIGPRGTP PGENGANGDR RGLIGPRGTP PGENGRYGEN RGLIGPRGTP RGLIGSKUGW RGLIGRGKLIGVP RGABGPTOKE	120 180 240 300 360 420 480 540 600 720 780 840 900
50	Protein Act	11	NP_0018 21 TLALTFLFQA QLSAPTKQLF DHTGKPAPED HGITVFGTRI YAPEDLIEYD GEPCPAGPA GDGSKGPTIS GGPKRVQGPP GQPPCPPCGD MGPQGPAGPA MGPQGPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPQGEPAGPAGPA HGPQGEPAGPA HGPQGEPAGPA HGPAGA	31 REVRGAAPVD PGGTTPEDFS YPLFRTWILA LDSEVPEGDI YEYGGAEYKE NHYUEIFTE GIMGPFGLQG AQEAQAQAL GPTGKPGKRG GMGEDGEIG QQCMGEQGG GPGGFGGRG GPGGFGGRG GPGGFGGRG GPGGFGGRG	ULKALDPENS ILPTVKPKKG DGKHRVAIS QOPLITGDPK AESVTEGPTV EYLAGENYOS PGGPGPAZTD PTGPPGDPGD PGGPGGRGRGRGRGRGRGRGRGRGRGRGPGFGPGPGPFGPGPGGPGPGPGP	PEGISKTTGF IQSFLLSIYN VEKKTVTMIV AAYDYCENYS TEETIAQTEA QRKNSEDTLY ITETSINGHG RGPGRPGLP PGENGLIGRE PGENGANGDR RGLIGPRGTP PGENGANGDR RGLIGPRGTP PGENGRYGEN RGLIGPRGTP RGLIGSKUGW RGLIGRGKLIGVP RGABGPTOKE	120 180 240 300 420 480 540 660 720 780 840 960
50	Protein Act MEPMSSRWKT CTNRKNSKOS EMGIQQIGVE DCKKRTTKPL PDCDSSAPKA MIVUDFQEYM ENKEIDGRUS AYGERGQKGE GPOGLPGGPGG GPOGLPGGPGG GPOGLPGGPGG GAGGLPGGAGG GLAGLPGADG GLAGLPGADG GDGPFGFRG GPGTTSGGBG GPGTTSGGBG GPGTTSGGBG	cession 8: 11 KRWLMDFTVT DTAYXVSKQA VGRSDVFLPE DRSERAIVT AQAGEPQIDE YGTHESYGTE PAVVEEGHLV DLLVVSGUS DKGHRGEGDPGP DKGHRGEGG DVGDPGPKGHRGEGG DMGLKGDRGE PKGSTGPFGF PPGPPGERGP	NP_0018 21 TLALTFLFOA QLSAPTKQLP DHTGKPAPED HTGKPAPED HTGKPAPED GGTPFGTRI YAPEDILEYD APREVSGTNE GGPSGPGAGPA GGPSGPGAGPA GGPSGPGDD MGPQGPGDP MGPQGPGDP GGPGAGAGA GGPQGPGDD GGRGAGAG GGPQGPGDD GGRGAGAG GGPQGPGDD GGRGAGAG GGPQGPGDD GGRGAGAG GGPQGPGDD GGRGAGAG GGPQGPGDD GGRGAGAG GGPGGPGDD GGRGAGAG GGPGGPGDD GGRGAGAG GGPGGPGDD GGRGAGAG GGPGGPGDD GGRGAGAG GGPGGPGGPGD GGRGAGAG GGPGGPGGPGD GGRGAGAG GGPGGPGGPGD GGRGAGAG GGPGGPGGPGD GGRGAGAG GGPGGPGGPGD GGRGAGAG GGPGGPGGPG GGRGAGAG GGPGGGGG GGRGAGAG GGPGGGGG GGGGGGGGG GGGGGGGGGG	31 REVERGAAPVD PGGTPPEDFS YPLFRTVNIA LDSEVFECDI YEYGRAEYKE PINFVEZIFTE DKPTSPPEEEE GIMGPPGLQQ QCAMPGPQG GPGGPKGRAG GPGGPKGRAG GPGGPKGRAG GPKGPKGPKG GPKGPKGPKG GPKGPKGPKG GPKGPKGPKG GPKGPKGPKG GPKGPKGPKG GPKGPKGPKG GPKGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKGPKG GPKGPGPKG GPKGPGPKG GPKGPGPKG GPKGPGPKG GPKGPGPKG GPKGPGPKG GPKGPG GPKG GP	ULKALDPENS ILPTVKPKKG DGKHRVALS QPELITGDPK AESVTEGPTV EYLTGEDYDS FGPGVPAATD PTGPPGDPGD QQARTALRGP RPGADGGRGM PRGLPGEAGP PRGWKGADGV PTGDPGPGGQ QRGPTGPRGS RMGCGGHPGQ AAGKRGAKGB	PEGISKTTGF IQSPLLSIYN VEKKTVTMIV VEKKTVTMIV VEKKTVTMIV VEKTVTMIV TEGILAOTEA ANTOYCHYS TEGILAOTEA ROPPORTOIL PGPMGINTOR PGPEGAKDP RGELAPROTP PGERGAKDP RGLIAPROTP PGERGAKDP RGLIAPROTP RGLIA	120 180 240 300 420 480 540 660 720 780 840 900 960 1020
50	Protein Act	CEGRION #: 11 KRMLMDFTVT DTATRVSKQA VGRSPVFLFE DRSERAIVDT AQAGEPOIDE FAVVEFGHE PAVVEFGHE AKGESODEP DKGHRGERGP DDGFPGHE PGFPGKE DMGLKGBRGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE	NP_0018 21 TLALTFLFQA QLSAPTKQLF DHTKRAPED MGITVFGTRI XAPEDIIEYD APRRUSGTNE EGPFGPAGFA GDGSKGPIT QGFRGVQGPP QGPGPGPGDG GGRGALGPF VGQLGPRGKD GGAMGEKGALGPF GGMGEKGALGPF GMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GMGEKGALGPF GGMGEKGALGPF GGMGEKGA	31 REVERGAAPUD PEGTTPEDFS PLFETVNIA LDBEVPEGDI PEGTES PIESE PNIVES LFTE DKPTSPPRESE GIMGPFGLQG AQEAQAQAIL QQCMREGEGE GPGGPIGREG GPGGPIGREG GPGGPIGREG GPGGPKGRAG GVAKFGPRE GPKGPAGPG GPKGPAGPAGPG GPKGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG	ULKALDPENS ILPTVKPKKG GGNHERVALS QPELITGDFK AESVIEGETV EVILTGDFK EVILTGDFK EVILTGDFK EVILTGDFK EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFGSSG EVILTGDFGSSG EVILTGDFGSSG EVILTGDFGSSG EVILTGDFGSSG AAGKEGAKGA	PEGISKTTGF IQSPLLSIYN VEKKTVTMIV VEKKTVTMIV ANTYCEHYS TEETIAOTEA ORKNSEDTLY ITETSINGHG RGPPGRPGLP PGEMGLIGRP PGEMGLIGRE PGEMGLIGRE FGLIGPRGTP GEMGPQGKP RGLIGPRGTP GEMGPQGKP RGLIGPRGTP GEMGPGGKP GGMGGLIGVE GGMGGTGKP GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
50 55 60	Protein Act	CEGRION #: 11 KRMLMDFTVT DTATRVSKQA VGRSPVFLFE DRSERAIVDT AQAGEPOIDE FAVVEFGHE PAVVEFGHE AKGESODEP DKGHRGERGP DDGFPGHE PGFPGKE DMGLKGBRGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE PKGSTGPFGE	NP_0018 21 TLALTFLFQA QLSAPTKQLF DHTKRAPED MGITVFGTRI XAPEDIIEYD APRRUSGTNE EGPFGPAGFA GDGSKGPIT QGFRGVQGPP QGPGPGPGDG GGRGALGPF VGQLGPRGKD GGAMGEKGALGPF GGMGEKGALGPF GMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GGMGEKGALGPF GMGEKGALGPF GGMGEKGALGPF GGMGEKGA	31 REVERGAAPUD PEGTTPEDFS PLFETVNIA LDBEVPEGDI PEGTES PIESE PNIVES LFTE DKPTSPPRESE GIMGPFGLQG AQEAQAQAIL QQCMREGEGE GPGGPIGREG GPGGPIGREG GPGGPIGREG GPGGPKGRAG GVAKFGPRE GPKGPAGPG GPKGPAGPAGPG GPKGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG	ULKALDPENS ILPTVKPKKG GGNHERVALS QPELITGDFK AESVIEGETV EVILTGDFK EVILTGDFK EVILTGDFK EVILTGDFK EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFG EVILTGDFGSSG EVILTGDFGSSG EVILTGDFGSSG EVILTGDFGSSG EVILTGDFGSSG AAGKEGAKGA	PEGISKTTGF IQSPLLSIYN VEKKTVTMIV VEKKTVTMIV ANTYCEHYS TEETIAOTEA ORKNSEDTLY ITETSINGHG RGPPGRPGLP PGEMGLIGRP PGEMGLIGRE PGEMGLIGRE FGLIGPRGTP GEMGPQGKP RGLIGPRGTP GEMGPQGKP RGLIGPRGTP GEMGPGGKP GGMGGLIGVE GGMGGTGKP GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO GGMGGISCKO	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
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		/086443 cccacctccc	COCCERCOAL	CACTTORGE	CCACTTOO	concorraca	240
	CGTCTTCCCG	TTCGGCGTGT	GCTTGGCCCG	GGGAACCGGG	AGGGCCCGGC	GATCGCGCGG	300
	CGGCCGCCGC	GAGGGTGTGA	GOGOGOGTGG	GCGCCCGCCG	AGCCGAGGCC	ATGGTGCAGC	360
5	AAACCAACAA	TGCCGAGAAC GCTGGGAATC	ACGGAAGCGC	TGCTGGCCGG	CGAGAGCTCG	TOTACGGGGG	420 480
•	GCAAGGCCGA	CGACCCGAGC	TGGTGCAAGA	CCCCGAGTGG	GCACATCAAG	CGACCCATGA	540
	ACCCCTTCAT	GGTGTGGTCG	CAGATOGAGO	GGCGCAAGAT	CATGGAGCAG	TCGCCCGACA	600
		CGAGATCTCC TTTCATTCGA		GCAAACGCTG			660 720
10	COGACTACAA	GTACCGGCCC	AGGAAGAAGG	TGAAGTCCGG	CAACGCCAAC	TCCAGCTCCT	780
	CGGCCGCCGC	CTCCTCCAAG	CCGGGGGAGA	AGGGAGACAA	GGTCGGTGGC	AGTGGCGGGG	840
	GCGGCCATGG CGAGTGGCGG	GGGCGGCGGC	GGCGGGGGA TCCAAACCGG	GCAGCAACGC CGCAGAAAAA	GGGGGGAGGA	GGCGGCGGTG	900 960
	CGGGCGGCGC	GGGCGCCAAC	GTTAGCAAAC	CGCACGCCAA	GCTCATCCTG	GCAGGCGGCG	1020
15	GCGGCGGCGG	GAAAGCAGCG	GCTGCCGCCG	CCGCCTCCTT	CGCCGCCGAA	CAGGCGGGGG	1080
	CCGCCGCCCT	GCTGCCCCTG	GGCGCCGCCG	COGACCACCA	CTCGCTGTAC	AAGGCGCGGA	1140
	CGGGCAAGCA	CCTGGCGGAG	AAGAAGGTGA	AGCGCGTCTA	CCTGTTCGGC	GGCCTGGGCA	1260
	CGTCGTCGTC	GCCCGTGGGC	GGCGTGGGCG	CGGGAGCCGA	CCCCAGCGAC	CCCCTGGGCC	1320
20	TGTACGAGGA	GGAGGGCGCG	GGCTGCTCGC	CCGACGCGCC			1380
	GOGCCGCCTC	GTCCCCCGCC CTCGCCCGCC	COGRECCECT	CGCCCGCCGA	CCACCGCGGG	TACGCCAGCC	1440 1500
	CCCACTCCTC	CTCTTCCTCC	TCCTCGGGCT	CCTCGTCCTC	CGACGACGAG	TTCGAAGACG	1560
0.5	ACCTGCTCGA	CCTGAACCCC	AGCTCAAACT		GTCCCTGGGC		1620
25	CGTCGTCGGC	GCTCGACCGG	GACCTGGATT	TTAACTTCGA TGAGCGAGAT	GCCCGGCTCC	GGCTCGCACT	1680
	AGTCCAGCAT	CTCCAACCTG	GTTTTCACCT	ACTGAAGGGC	GCGCAGGCAG	GGAGAAGGGC	1800
	CGGGGGGGGT	AGGAGAGGAG	AAAAAAAAAG	TGAAAAAAAG	AAACGAAAAG	GACAGACGAA	1860
30	GAGTTTAAAG	AGAAAAGGGA	AAAAAGAAAG	AAAAAGTAAG	CAGGGCTCGT	TCGCCCGCGT	1920
30	TCTCGTCGTC	GGATCAAGGA GGGACCCACT	GCGCGGCGGC	GTTTTGGACC	COCCCCCA	GAGGGTAGAC	1980 2040
	AGGGGGGGCCG	TGTGATTGTT	GTTATTGATG	TIGITGITGA	TGGCAAAAAA	AAAAAGCGAC	2100
	TTCGAGTTTG	CTCCCCTTTG	CTTGAAGAGA	CCCCCTCCCC	CTTCCAACGA	GCTTCCGGAC	2160
35		CCCCAGCAAG			AGACTTGAAG		2220
33	CTTCCTGCAT	CACCOCTOCC	CCCCTTTTT	TANACTOCTTC	TTGGTCAAGA	AAGGCTCCGG	2280 2340
	GGTGACGAAT	TTGGCCGATG	GCAGATGTTT	TGGGGGAACG	CCGGGACTGA	GAGACTCCAC	2400
	GCAGGCGAAT	TCCCGTTTGG	GGCCTTTTTT	TOCTCCCTCT	TTTCCCCTTG	CCCCCTCTGC	2460
40	AGCCGGAGGA	GGAGATGTTG	AGGGGAGGAG	GCCAGCCAGT	GTGACCGGCG	CTAGGAAATG	2520 2580
70		GGGGGTTCAC					2640
	CCCCCCCCCC	TGGGCCTCCG	CCTTCTTTTC	TACGTGAAAT	CAGTGAGGTG	AGACTTCCCA	2700
					TACAGGGGCA	GTCAGTGGAG	2760
45		GCGTGGAGGA TTCGGAAAAA			TACAGGGGCA	GTCAGTGGAG	2760
45	GGCGAGTGGT	TTCGGAAAAA	AAAAAAGAAA		TACAGGGGCA	GTCAGTGGAG	2760
45	GGCGAGTGGT	TTCGGAAAAA 363 Protein	AAAAAAGAAA	AAAAGGG	TACAGGGGCA	GTCAGTGGAG	2760
	GGCGAGTGGT Seq ID NO:	TTCGGAAAAA 363 Protein	AAAAAAGAAA sequence	AAAAGGG	TACAGGGGCA	GTCAGTGGAG \$1	2760
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50	GGCGAGTGGT Seq ID NO: Protein Acc MVQQTNNAEN RPMNAFMVWS ADYPDYKYRP GGGAGGGAN QAGAAALIPL GLGTSSSPVG	TTCGGAAAAA 363 Protein cession #: 11	AAAAAGAAA sequence NP_0030 21	AAAAGGG 98 31 ASSPTPGSTA KRLGKRNKLL PGEKGDKVGG VSKPHAKLIL ASSAASASA GCSPDAPSLS	41 STGGKADDPS KDSDKIPPIR SGGGGGGGA AGGGGGGKAA LAAPGKHLAB GRSSAASSPA	51 WCKTPSGHIK BEAERLRLKHM GOGSSNAGGG AAAASPAAE KKVKRYYLPG AGRSPADERG	60 120 180 240 300 360
50	GGCGAGTGGT Seq ID NO: Protein Act MYQQTNNAEN RPMMAFMYWS ADYPDYKYRP GGGASGGGAN QAGAAALLPL GLGTSSSPVG GVASSBASSPASSPVG GVASSBASSPASSPASSPASSPASSPASSPASSPASSPASSP	TTCGGAAAAA 363 Protein cession #: 11 TEALLAGESS QIERRKIMEQ RKKYKSGNAN KKYAQKKSCG GAAADHHSLY	AAAAAGAAA a sequence NP_0030 21 DSGAGLELGI SPIMENAEIS SSSSAAASSK SKVAGGAGGG KARTFSASAS PLGLYESEGA ARSSKSSSS	98 31 ASSPTPGSTA KRLGKRNKLL PGERGDKVGG VSKPHAKLIL ASSAASASAA GCSPDAFSLS SSGSSSSDB	41 STGGKADDPS KDSDKIPFIR SGGGGGGGGAA AGGGGGGKAA LAAPGKHLAE GRSSAASSPA FEDDILDINP	51 WCKTPSGHIK EAERLRIKHM GOOSSNAGGG AAAASFAAE KKVKRVYLPG AGRSFADHRIG SEMPESMIG	60 120 180 240 300
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50 55 60	GGGGAGTGGT Seq ID NO: Protein Act NO: Protein Act MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN MYOCTRUMEN SPESSSALDR SPESSSALDR SPESSSALDR SPESSSALDR SPESSSALDR MOLEIC ACCODING SEQUENTIAL	TTCGGAAAAA 363 Protein cession #: 11	AAAAAAGAAA a sequence NP_0036 21	AAAAGGG 98 31	41 STGRADDPS KDSDKIPPIR SGGGGGGGAA AGGGGGGGAA GRSAASSPA PEDDLLDLDP DWLESSISNL	51 WCKTPSGHIK EAERLRIKEM GOGSSWAGGG AAAAASPAA KKWKWYLPG AGRSFADERG SSWPESNSLG VFTY	60 120 180 240 300 360
50	GGCGAGTGGT Seq ID NO: Protein Act	TTCGGAAAAA 363 Protein cession #: 11 TEALLAGESS QIERKIMEQ RKEVKSGNAN SKPAQKRSCG GAAADHHSLY GVGAGADPSD DLDPNPEPGS 364 DNA see Ld Accession	AAAAAAGAAA a sequence NP_0036 21	AAAAGGG 98 31	41 STGGKADDPS KDSDKIPFIR SGGGGGGGGAA AGGGGGGKAA LAAPGKHLAE GRSSAASSPA FEDDLLDLNP	51 WCKTPSGHIK EAERLRIKHM GOOSSNAGGG AAAASFAAE KKVKRVYLPG AGRSFADHRIG SEMPESMIG	60 120 180 240 300 360
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50 55 60	GGGGAGTGGT Seq ID NO: Protein Act WOOTNNAEN RPMENAFMWER GGGASGGGAN QAGANALLPL GLGTSSEVG GASSGALDR Seq ID NO: Nucleic Act Coding sequ TGCGGGCGCGTGC GGGACCCTCC	TTCGGAAAAA 363 Proteir cession %: 11 i TEALLAGESS QIERRKIMEQ GRAADHHSLY GVGAGAPESD DLDINPERGS 364 DNA set dd Accession sence: 11 i TCCTGGACCA CGCCCGGTCT	ARAAAAGAAA a sequence pm_0030 21 1 DegodoleLoi SPDMERAE19 SSSSAAASEK SKYKOGOAGGO KARTPANAS PMOVENER 4 # U10860 123-220 21 21 21 26 GGGCTCCTTC CGTACTOTCC	ARANGG 98 31 ASSPTPGSTA KELGKENKILL PGEKGENKELL ROSKPHAKILL ASSAASANSA CGSYDASPIS SSGSSSSDB TPEVSEMISG 44 31 TCAACCTCAG COGTCACCGC	41 FORGKADDPS KOSDKIPPIR SOCOGIOGOKAA LAPCKILAS GRESPASSES PEDDLIDLAP DMLBSSISKL	S1 WCKTPSGHIK EAERLELKHM GOGSSINAGG AAAASFAAE KYWRWYLPG AGRSTADERG SSHFESNSLG VPTY	60 120 180 240 300 360 420
50 55 60 65	GGGGAGTGGT Seq ID NO: Protein Acc. 1	TTCGGAAAAA 363 Protein 263 Protein 264 Protein 274 Protein 275 Pro	AAAAAAAAA a sequence NP_0030 21	ARANGGG 98 31 ARSPIPOSTA KOLGKRNILLI POEKKORNOGO VSKPIRALILI ASSASANSAN SSGSSSDSD TPEVSENISG 4 31 TCAACCTCAG COGTCACCCC	41 STOCKADDPS KOSDKIPPIR SOGOGOGOGO AGGGGGGKAA LAAPGKILAB GRSSAASSFA FEDOLLOLDIP DWILESSISKI 1 CCCGGGGGGCCCCCGCGGCTCCC TGGGAGGGCTCCC	S1 VETT PORHIX AREALALKIM GOOSSINAGG AAAAASFA KKVKRVYLFG AGRSFADHRG SSIFESNSLG VFTY S1 GGACCCTTCC GCCCTGGCCC CTTAAGGATG	60 120 180 240 360 420
50 55 60	GCCGAGTGGT Seq ID NO: Protein Aci	TTCGGAAAAA 363 Proteiression 8: 11 TEALLAGESS QIERREIMEQ RIKKYKSGNA GAAADHEISI; GYGAADHEISI; GYGAADHEISI; GYGAADHEISI; LIDINFERGS 164 DRA gedd Accessionence: 11 TCCTGGACCA CGCCCCCTCT GTGCAACGAA	AAAAAAAAAA a sequence NP_003t 21 SEMENTALELUI SEMENTALEU SEMENTALELUI SEMENTALELUI SEMENTALELUI SEMENTALELUI SEMENTALELUI SEMENTALELUI SEMENTALELUI SEMENTALELUI SEMENTALELUI SEMENTALEUI SEMENTALELUI SEMENTALELUI SEMENTALELUI SEMENTALELUI SEMENTALE	AAAAGGG 31 31 ASEPTRESTA ASEPTRESTA ASEPTRESTA ASEA ASEA ASEA ASEA ASEA ASEA ASEA	41 STOSPADDES	S1 WCTFBSHIK W	60 120 180 240 300 360 420
50 55 60 65	GCCGAGTGGT Seq ID No. Protein Ac. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TTCGGAAAAA 363 Proteiression 8: 11 11 TEALLAGESS (CIERKING) RIKKYKSGNAN SKYAQKKSGO RIKKYKSGNAN SKYAQKKSGO RIKKYKSGNAN SKYAQKKSGO RIKKYKSGNAN SKYAQKKSGO RIKKYKSGNAN SKYAQKKSGO RICHARD SKYAQKKSGO RICHARD SKYAQKKSGO RICHARD SKYAQKKSGO RICHARD SKYAQKKSGO RICHARD SKYAQKKSGO RICHARD	AAAAAAAAAA sequence NP_003t 21 11 DSGAALELOI SSSSAAASEK SSSSAAASEK SSSSSAASEK SSKVAGGAAGA KARTPSASAS PHOUVEEEC 2 # 110860 123-22t 1 GOCTICCTIC COTACTOTOG GAACTOTTOG GAACTOTTOG GAACTOTTOG GAACTOTTOG GAACTOTTOG GAACTOTTOG GAACTOTTOG GAACTOTTOG GAACTOTTOG	ARAAGGG 98 31 ASSPTPGSTA ASSPT	41 FOGKADDPS F	S1 WICKTPSGHIK W	60 120 180 240 300 360 420
50 55 60 65	GCCGAGTGGT Seq ID No: Protein Ac. NO: NO: NO: NO: NO: NO: NO: NO: NO: NO	TTCGGAAAAA 363 Froteir session 8: 11	AAAAAAAAA a sequence NP_003/ 21 21 31 32 32 32 32 32 32 32 32 32 32 32 32 32	ARANGGG 198 31 ASSPIPAGETA RELEGEMENT ASSANSIAN GESTERMENT ASSANSIA	41 TOTAL PER PROPERTY OF THE	S1 WICKTPSGHIK EARCHLEIGH GOGSSKAGG ANAMASFAGE KRIEGE KR	60 120 180 240 300 420 60 120 180 240 360 420
50 55 60 65	GCCGAGTGGT Seq ID No. Protein Ac. 1 1 1 NYONTHANN RPMATATVIX RPMATATVIX ROGASGGGAN GGAAALLEL GCGTSSSPU YASILAASPA SPSSSALDS Seq ID NO. Nucleic Ac. CGCAGCTGC GCCACCTCC GCCACCTCC CGCACCTCC CCACATTGCC CCACATTCC CCACATTGCC CCACATTGCC CCACATTGCC CCACATTCC CCACA	TTCGGAAAAA 363 Proteiression 8: 11 11 17 17 17 17 17 17 17 17 17 17 17	ANAMAGAA sequence NP_0031 1 1 1 1 1 1 1 1 1 1 1 1	ANAAGGG 98 31 1 ASSPTPGSTA RELGERNELL PERKEDIVGG VSKPHALLI ASSAANSAA GCSPDASDIS TPEVSENISG 11 TCAACCTCAG TCGAGCACTCAG TCGAGCACTCAGCACTCAGCACTCAGCACTCAGCACTCAGCACTCAGACTCAGACTCAGAATCATTCAGGTTAGATAAGGT TCAACTTAGAGTTAGATAAGGT TCAACTTAGAGTTAGATAAGGT TCAACTTAGATAAGGT TCAACTTAGAGTTAGATAAGGT TCAACTTAGATAAGGT TCAACTTAGATTAAGGT TCAACTTAGATAAGGT TCAACTTAGATAAGGT TCAACTTAGATAAAGGT TCAACTTAGATAAGGT TCAACTTAGATAAGGT TCAACTTAGATAAGGT TCAACTTAGATAAGGT TCAACTTAGATAAAGGT TCAACTTAGATAAAGGT TCAACTTAGATAAAGGT TCAACTTAGATAAAAAAAAAA	41 STOCKADDPS STOCKADDPS SOCIOGICO ANGOGGICAC ANGOGGICAC ANGOGGICAC ANGOGGICAC COCCACC C	S1 WONTFESSHIK WONTESSHIKE WONTESSHIKE WONTESSHIKE WONTSHIKE WONTSHIKE WONTSHIKE SINGWIYE \$1 WONTSHIKE WONTSHIKE WONTSHIKE SINGWIYE WONTSHIKE SINGWIYE SINGW	60 120 180 240 300 360 420
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	TTGCAAGTGG	CARAGCTGAA	CTCATCAAAA	CCCATCACAA	TGACACAGAG	CTCATCAGAA	1320
	AGTTGAGAGA	GGAGGGAAAA	GTAATAGAAC	CTCTGAAAGA	TTTTCATAAA	GATGAAGTGA	1380
	GAATTTTGGG	CAGAGAACTT GGCAATCAGA	GGACTTCCAG	AAGAGTTAGT	TTCCAGGCAT	CCATTTCCAG	1440 1500
5	GTCCTGGCCT	CAATATTTTG	GTAATATGTG	CIGARGARCC	TIMIMITIUI	ANGGACTITC	1560
,	CTGAMACCAA	ACACACACTC	ADACCCTCCA	CARCAGAAGA	GGATCAGGAG	AAGCTGATGC	1620
	ABATTACCAG	ACAGAGAGTC TCTGCATTCA	CTGAATGCCT	TCTTGCTGCC	AATTAAAACT	GTAGGTGTGC	1680
	AGGGTGACTG	TCGTTCCTAC	AGTTACGTGT	GTGGAATCTC	CAGTAAAGAT	GAACCTGACT	1740
	GGGAATCACT	TATTTTTCTG	GCTAGGCTTA	TACCTCGCAT	GTGTCACAAC	GTTAACAGAG	1800
10	TTGTTTATAT	ATTTGGCCCA	CCAGTTAAAG	AACCTCCTAC	AGATGTTACT	CCCACTTTCT	1860
	TGACAACAGG	GGTGCTCAGT	ACTITACGCC	AAGCTGATTT	TGAGGCCCAT	AACATTCTCA	1920
	GGGAGTCTGG	GTATGCTGGG CCCACTTCAA	AAAATCAGCC	AGATGCCGGT	GATTTTGACA	CCATTACATT	2040
							2100
15	ACCTOCTATT	AAAGATGGTC	ACTGAGATTA	AGAAGATTCC	TGGTATTTCT	CGAATTATGT	2160
	ATGACTTAAC	AAAGATGGTC ATCAAAGCCC	CCAGGAACTA	CTGAGTGGGA	GTAATAAACT	TC	
	Seq ID NO:	365 Protein	sequence				
20	Protein Acc	cession #:	AAA6033	1			
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	MALCNGDSKL	ENAGGDLKDG	HIHYEGAVVI	LDAGAQYGKV	IDRRVRBLFV	OSEIPPLETP	60
	APATKEOGER	ATTTSGGPNS	VYARDAPWED	PAIFTICKPY	LGICYGMOMM	NKVPGGTVHK	120
25	KSVREDGVFN	I SVDNTCSLF PEVGLTENGK	RGLQKEEVVL	LTHGDSVDKV	ADGFKVVARS	GNIVAGIANE	180
	SKKLYGAQPH	PEVGLTENGK	VILKNFLYDI	AGCSGTFTVQ	NRELECTREI	KERVGTSKVL	240 300
	VLLSGGVDST	VCTALLNRAL	MORGATANHI	TODEPURE	COLEARY	GIQVKVIMUK GIQVKVIMUK BE	360
	BURLACCTI.B	PISDEDRTPR PDLIESASLV	ASCKARLIKT	HHNDTRLIRK	LREEGKVIEP	LKDPHKDEVR	420
30							480
	TLLQRVKACT	TEEDQEKLMQ PRMCHNVNRV	ITSLHSLNAP	LLPIKTVGVQ	GDCRSYSYVC	GISSKDEPDW	540
	ESLIFLARLI	PRMCHNVNRV	VYIPGPPVKB	PPTDVTPTFL	TTGVLSTLRQ	ADPEAHNILR	600
	RSGYAGKISO	MPVILTPLRF	DRDPLOKOPS	CORSVVIRTE	ITSDFMTGIP	ATPGNEIPVE	660
35	VVLKMVTEIK	KIPGISRIMY	DLTSKPPGTT	EMB			
33							
	Sea ID NO:	366 DNA see	nuence				
	Nucleic Ac	id Accession	#: NM 0042	19			
	Coding seq	uence:	46-654				
40							
	1	11	21	31	41	51	
	COCCOORCE	A TOTAL TOTAL	CTCTTTANGAC	CTCCAATAAT	CCAGAATGGC	TACTCTGATC	60
	TATGETGATA	ATGAATGCGG AGGAAAATGG	AGAACCAGGC	ACCORDIGATE	TTGCTAAGGA	TOGGCTGAAG	120
45	CTGGGGTCTG	GACCTTCAAT	CAAAGCCTTA	GATGGGAGAT	CTCAAGTTTC	AACACCACGT	180
45	CTGGGGTCTG	GACCTTCAAT	CAAAGCCTTA	GATGGGAGAT	CTCAAGTTTC	AACACCACGT GGCTTTGGGA	180 240
45	CTGGGGTCTG TTTGGCAAAA ACTGTCAACA	GACCTTCAAT CGTTCGATGC GAGCTACAGA	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA	GATGGGAGAT TTACCTAAAG AAGACCAAGG	CTCAAGTTTC CTACTAGAAA GACCCCTCAA	GGCTTTGGGA ACAAAAACAG	180 240 300
45	CTGGGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT	GACCTTCAAT CGTTCGATGC GAGCTACAGA CTGCCAAAAA	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGAG	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT	180 240 300 360
	CTGGGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT	GACCTTCAAT CGTTCGATGC GAGCTACAGA CTGCCAAAAA	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGAG	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT	180 240 300 360 420
50	CTGGGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG	GACCTTCAAT CGTTCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTGCCTGA	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGAG AGAAATAGAA AGAGCACCAG	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA AAATTCTTTC ATTGGGCACC	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG CCTTCAATCC TCCCCTTGAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT TCTAGACTTT TGGAGTGCCT	180 240 300 360 420 480
	CTGGGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG	GACCTTCAAT CGTTCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTGCCTGA	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGAG AGAAATAGAA AGAGCACCAG	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA AAATTCTTTC ATTGGGCACC	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG CCTTCAATCC TCCCCTTGAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT TCTAGACTTT TGGAGTGCCT	180 240 300 360 420 480 540
	CTGGGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG	GACCTTCAAT CGTTCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTGCCTGA	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGAG AGAAATAGAA AGAGCACCAG	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA AAATTCTTTC ATTGGGCACC	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG CCTTCAATCC TCCCCTTGAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT TCTAGACTTT TGGAGTGCCT	180 240 300 360 420 480 540 600
50	CTGGGGTCTG TTTGGCABAA ACTGTCABCA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG CTCATGATCC CCTGTGAAGA CTGTCGACCC TAGTGCTCA	GACCTTCAAT CGTTCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTGCCTGA	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGAG AGAAATAGAA AGAGCACCAG	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA AAATTCTTTC ATTGGGCACC	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG CCTTCAATCC TCCCCTTGAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT TCTAGACTTT TGGAGTGCCT	180 240 300 360 420 480 540
	CTGGGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG	GACCTTCAAT CGTTCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTGCCTGA	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGAG AGAAATAGAA AGAGCACCAG	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA AAATTCTTTC ATTGGGCACC	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG CCTTCAATCC TCCCCTTGAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT TCTAGACTTT TGGAGTGCCT	180 240 300 360 420 480 540 600
50	CTGGGGTCTG TTTGGCARAAA ACTGTCARCA CCAAGCTTTT GCCTCARATG GAGAGTTTTG CTCATGATCC CCTGTGAAGA CTGTGGACC TAGTGCTCA AAAAAAAA	GACCITCAAT CGITCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTGCCTGA TTGACGAGGA TTGCCTCCC TGGATGTTGA GAGTITGTGT	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATCACTGAG AGAAATAGAA AGAGCACCAG GAGAGAGCTT ACCATGGGAA ATTGCCACCT GTATTTGTAT	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA AAATTCTTTC ATTGGGCACC	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG CCTTCAATCC TCCCCTTGAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT TCTAGACTTT TGGAGTGCCT	180 240 300 360 420 480 540 600
50	CTGGGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG CTCATGATCC CCTGTGAAGA CTGTCGACCC TAGTGCTCCA AAAAAAAA Seq ID NO:	GACCITCAAT CGITCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTGCCTGA TTGACGAGGA TTGACGAGGA TGGCCTCTCC TGGATGTTGA GAGTTTGTGT 367 Protei:	CAAAGCCTTA CCCACCAGC AAAGTCTGTA GATGACTGAG AGAAATAGAA AGAGCACCAG GAGAGAGCTT ACCATGGGAA ATTGCCACCT GTATTTGTAT	GATGGSAGAT TTACCTANAG AAGACCAAGG AAGACTGTTA AAATTCTTTC GATGGGCACC GAAAAGCTGT TCCAATCTGT GTTTGCTGT TAATAAAGCA	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG CCTTCAATCC TCCCCTTGAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT TCTAGACTTT TGGAGTGCCT	180 240 300 360 420 480 540 600
50 55	CTGGGGTCTG TTTGGCARAAA ACTGTCARCA CCAAGCTTTT GCCTCARATG GAGAGTTTTG CTCATGATCC CCTGTGAAGA CTGTGGACC TAGTGCTCA AAAAAAAA	GACTICAAT CGITCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTCCTCA TGGACGAGGA TGGCCTCTCC TGGATGTTGA GAGTTTGTGT 367 Protei: CCESion #:	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGGA AGAAATAGAA AGAGCACCAG GAGAGAGCTA ACCATGGGACA ATTGGCACCT GTATTTGTAT n sequence NP_0042	GATGGGAGAT TTACCTANAG AAGACCAAGG AAGACTGTTA AAATTCTTTC GAAAAGCTGT TCCAATCTGT TCCAATCTGT TCTTTGCTGTG TAATAAAGCA	CTCAAGTTTC CTACTAGANA GACCCTTCAA AGCAAAAG CCITCAATCC TCCCCTTGAG TTCAGCTGGG TGCAGTCTCC ACATTGATATC TTCTTCAACA	AACACCACOT GGCTTTGGA ACAAAACAG CTCTGTTCCT TCTAGACTT TCAGACTT TCOCCCCTTCA TTCAAGCATT TTAAATTTCT GAAAAAAAAA	180 240 300 360 420 480 540 600
50	CTGGGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG CTCATGATCC CCTGTGAAGA CTGTCGACCC TAGTGCTCCA AAAAAAAA Seq ID NO:	GACCITCAAT CGITCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTGCCTGA TTGACGAGGA TTGACGAGGA TGGCCTCTCC TGGATGTTGA GAGTTTGTGT 367 Protei:	CAAAGCCTTA CCCACCAGC AAAGTCTGTA GATGACTGAG AGAAATAGAA AGAGCACCAG GAGAGAGCTT ACCATGGGAA ATTGCCACCT GTATTTGTAT	GATGGGAGAT TTACCTANG AAGACCTANG AAGACCTATA AAATTCTTC ATTGGGCACC GARAAGCTGT TCCAATCTGT GTTTGCTGTG TATTANAGCA	CTCAAGTTTC CTACTAGAAA GACCCCTCAA AAGCAAAAAG CCTTCAATCC TCCCCTTGAG	AACACCACGT GGCTTTGGGA ACAAAAACAG CTCTGTTCCT TCTAGACTTT TGGAGTGCCT	180 240 300 360 420 480 540 600
50 55	CTOGGGTCTG TTTGGCAAA ACTGTCAACA CCAAGGTTTT GCCTCAGATG GAGAGTTTG GCTCAGATG CTCATGAAGA CTGTGAACC CTGTGAAGA CTGTGACCC AAAAAAAA Seq ID NO: Protein Act	GACTICAAT CGTTCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACCTGCCTGA TTGACGAGGA TGCCTCTCC TGGATGTTGA GAGTTTTGTG 367 Prote1: cession #:	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGGG AGAAATAGAA AGAGCACCAG GAGGAGAGCTT ACCATGGGAA ATTGCCACCT GTATTTGTAT sequence NP_0042 21 i	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA ATTGGGCACC GAAAAGCATT TCCAATCTGT TCCAATCTGT TATTACCTGT TATTACCTGT TAATAAAGCA	CTCAAGTTTC CTACTAGAAA GACCCTCAA AAGCAARAGG CCTTCAATCC TCCCCTTGAG TTCAGCTGG TGCAGTCTCC ACATAGATAT TTCTTCAACA	ARCACCAGT GGCTTTGGA ACANAACAG CTCTGTTCCT TCTAGACTTT TGGAGTGCCT TCAAGCATT TTAAATTTCT GAAAAAAAAA	180 240 300 360 420 480 540 660 720
50 55	CHOGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG GAGAGTTTTG CTCATGAACC TAGTGCTTCA AAAAAAAA Seq ID NO: Protein Ac. 1	GACTICAAT CGITCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACTGCCTGA TTGACGAGGA TGGCCTCTCC TGGATGTTGA GAGTTTGTGT 167 Protei: cession #: 11	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGGA AGAAATAGAA AGAAGTACGA AGAAGCACCAG GAGAGGACTT ACCATGGGAA ATTGCCACCT GTATTTGTAT sequence NP_0042 21 RDGLKLGSGP	GATGGGAGAT TTACCTANG AAGACCAAGG AAGACTGTTA AAATTCTTC ATTGGGCACC GAAAAGCTGTT TCCAATCTGT TTTGCTGTG TTTGCTGTG TAATAAAGCA	CTCAAGTTTC CTCAAGAAA GACCCTCAA AAGCAAAAAG CCTTCAATCC TCCCCTTGAG TTCAGCTGGG TGCAGTCTCC ACATAGATAT TTCTTCAACA	AACACCAGT GGCTTTGGGA ACAAAACAG CTCTGTTCCT TCTAGACTTT TGAGGTTCT TTCAAGCATT TTCAAGCATT TTAAAATATTCT GAAAAAAAAA	180 240 300 360 420 480 540 600
50 55 60	CTOGGGTCTG TTTGGCAAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG GCTCAGATG CTCTTGAACA CTGTTGAACA CTGTTGAACA AAAAAAAA Seq ID NO: Protein Acc 1 MATLIYUDER REALCTUNEA	GACTICANT CGTTCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATACC ACCTGCCTGA TGACCACCTCC TGGATGTTGA GAGTTTGTGT 167 Protei: CCBSion #: 11	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA GATGACTGAG AGAAATAGAA AGAAGCACCAG GAGAGAGCTT ACCATGGGAA ATTGCCACCT GTATTTGTAT sequence np_0042 21	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA ATTGGGCACG GAAAAGCTTTT TCCAATCTGT TCCAATCTGT TAATTAAAGCA 10 31	CTCAAGTTTC CTACTAGAAA GACCCTCAA AAGCAAAAG CCTTCAATC CCCCTTCAG TTCAGCTGG TGCAGTCTCC ACATAGATAT TTCTTCAACA 41 VSTPRFGKTF VSTVPASDDA	AACACCAGT GGCTTTGGGA ACAAAACAG CTCTGTTCCT TCTAGACTTT TGAAGTCTT TTGAAGTTCT CCCCCTTCA TTCAACATT TTAAATTTCT GAAAAAAAAA 51 DAPPALPKAT PREIKEFPP	180 240 300 360 420 480 540 600 660 720
50 55	CTOGGTCTO TTTGGCTAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG CTCATGAATC CCTGTGAAGA CTGTGGACC TAGTGCTTCA AAAAAAAA Seq ID NOI Protein AC 1 MATLIYVDEE REALGTVNEA REALGTVNEA REPLDFESFDL	GACTICAAT CGITCGATGC GAGCTACAGA CTGCCAAAAA ATGCCTATCC ACTGCCTGA TTGACGAGGA TGGCCTCTCC TGGATGTTGA GAGTTTGTGT 167 Protei: cession #: 11	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA CATGACTGAG AGAAATAGAA AGAGCACCAG GGAGAGACTA ACCATGGGAA ATTGCCACT GTATTTGTAT sequence NP_0042 21 KGGLKLGSGP LKGKQPFFSA LKGKQPFFSA LKGVCPFFSA LKGVCPFFSA LKGVCPFFSA	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA ATTGGGCACG GAAAAGCTTTT TCCAATCTGT TCCAATCTGT TAATTAAAGCA 10 31	CTCAAGTTTC CTACTAGAAA GACCCTCAA AAGCAAAAG CCTTCAATC CCCCTTCAG TTCAGCTGG TGCAGTCTCC ACATAGATAT TTCTTCAACA 41 VSTPRFGKTF VSTVPASDDA	AACACCAGT GGCTTTGGGA ACAAAACAG CTCTGTTCCT TCTAGACTTT TGAAGTCTT TTGAAGTTCT CCCCCTTCA TTCAACATT TTAAATTTCT GAAAAAAAAA 51 DAPPALPKAT PREIKEFPP	180 240 300 360 420 480 540 600 650 720
50 55 60	CTOGGTCTO TTTGGCTAAA ACTGTCAACA CCAAGCTTTT GCCTCAGATG GAGAGTTTTG CTCATGAATC CCTGTGAAGA CTGTGGACC TAGTGCTTCA AAAAAAAA Seq ID NOI Protein AC 1 MATLIYVDEE REALGTVNEA REALGTVNEA REPLDFESFDL	GACCITCAAT CSITCGATGC GAGCTACAGA ATGCCTATCC ACCTGCCTGA TTGACGAGGA TGCCCTCTCC TGGATOTTGA GAGTTTGTT 167 Protei: CBSSion #: 11 MGEPGTRVVA TEKSVKTMGP FESSGIANLP	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA CATGACTGAG AGAAATAGAA AGAGCACCAG GGAGAGACTA ACCATGGGAA ATTGCCACT GTATTTGTAT sequence NP_0042 21 KGGLKLGSGP LKGKQPFFSA LKGKQPFFSA LKGVCPFFSA LKGVCPFFSA LKGVCPFFSA	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA ATTGGGCACG GAAAAGCTTTT TCCAATCTGT TCCAATCTGT TAATTAAAGCA 10 31	CTCAAGTTTC CTACTAGAAA GACCCTCAA AAGCAAAAG CCTTCAATC CCCCTTCAG TTCAGCTGG TGCAGTCTCC ACATAGATAT TTCTTCAACA 41 VSTPRFGKTF VSTVPASDDA	AACACCAGT GGCTTTGGGA ACAAAACAG CTCTGTTCCT TCTAGACTTT TGAAGTCTT TTGAAGTTCT CCCCCTTCA TTCAACATT TTAAATTTCT GAAAAAAAAA 51 DAPPALPKAT PREIKEFPP	180 240 300 360 420 480 540 600 650 720
50 55 60	CNGGGTCTO TITGGGCAAAA ACTGTCAACA CCAAGTTTT GCCTCAGATG GAGAGTTTTG CCCTGTGAAGA CTGTGGACCC TAGTGCTTCA AAAAAAAA Seq ID NO: Protein AC: 1 MATLIYVDKE RRALGTVNRA NPLDFESFDL SPSSILSTLD	GACCTICANT CGITCGATGC GAGCTACAGA CTGCCTACAGA ATGCCTATCC AGCTGCTAC TGGATGTTGA TGGACGTATGC TGGATGTTGA GAGTTTTGT 367 Protei: cession #: 1 1 1 MGBPGTRVVA TERSVKTKGP PERGGIAILP VELPPVCCDI	CARAGECTTA CCCACCAGCC ARAGECTGGA GAGAATACGAA AGACCACCAGC GAGAGAGAGCT ACCATGGGAA ATTGCCACCT GTATTTGTAT sequence NP_0042 21 ptcccccccccccccccccccccccccccccccccccc	GATGGGAGAT TTACCTAAAG AAGACCAAGG AAGACTGTTA ATTGGGCACG GAAAAGCTTTT TCCAATCTGT TCCAATCTGT TAATTAAAGCA 10 31	CTCAAGTTTC CTACTAGAAA GACCCTCAA AAGCAAAAG CCTTCAATC CCCCTTCAG TTCAGCTGG TGCAGTCTCC ACATAGATAT TTCTTCAACA 41 VSTPRFGKTF VSTVPASDDA	AACACCAGT GGCTTTGGGA ACAAAACAG CTCTGTTCCT TCTAGACTTT TGAAGTCTT TTGAAGTTCT CCCCCTTCA TTCAACATT TTAAATTTCT GAAAAAAAAA 51 DAPPALPKAT PREIKEFPP	180 240 300 360 420 480 540 600 650 720
50 55 60	CNGGGTCTO TTTGGCGAAAA ACTGTCAACA CCAAGGTTTT GCCTCAGATO GAGAGTTTTG CCCATGATCC CCTGTGAAGA CCTGGACGA AAAAAAAA Seq ID NO: Protein Act	GACCTICAAT GGTGGATGC GAGGTACAAA ATGCCTATCC TGGATGCTGA ATGCCTTCA TGCCCTCTCC TGGATGTTGA GAGTTGTGA 367 Protes: cension #. 11 NGEPGTRVVA TEKSVKTKGP PEBEGGIATH VELPPVCCDI 368 DNA sc.	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA CATCACTGAG AGAAATAGAA AGAGCACCTG GAAATTGGAA ACCATGGGAA ATTGCACCT GTATTTGTAT sequence NP_0042 21 RUGGLKLGSGP LKOKQPSFSA LSGVPLMILD DI	GATGGGAGAT TTACCTANAG AAGACCANGG AAGACCATGT AAAATCTTTA AAAATCTTTA CAATGGGACC GAAAAGCTGT TCCAAICTGT GTTTGCTGTG TAATAAAGCA 10 31 SIKALDGRSQ KOMTEKTVKA EBRELEKLFQ	CTCAAGTTTC CTACTAGAAA GACCCTCAA AAGCAAAAG CCTTCAATC CCCCTTCAG TTCAGCTGG TGCAGTCTCC ACATAGATAT TTCTTCAACA 41 VSTPRFGKTF VSTVPASDDA	AACACCAGT GGCTTTGGGA ACAAAACAG CTCTGTTCCT TCTAGACTTT TGAAGTCTT TTGAAGTTCT CCCCCTTCA TTCAACATT TTAAATTTCT GAAAAAAAAA 51 DAPPALPKAT PREIKEFPP	180 240 300 360 420 480 540 600 650 720
50 55 60 65	CHOGGITCHO TITGGCAAAA ACTGTCAACAC CCAAGGTTTT GCCTCAGATO GAGAGTTTTG CCCATGATCC CCTGTGAAGA CCTTGACCT AAAAAAAA Seq ID NO: Protein Ac MATLIYVDRE RRALGTVNRA NPLDFESFDL SPSILSTLD Seq ID NO: NSSILSTLD Seq ID NO: Nucleic Ac	GACTICANT COTTCGATC GAGCTACAGA ACTICCTAGA ATGCCTATC TGGATGTTAGA TTGACGAGGA TTGACGAGGA TGCCCTCT TGGATGTTTGA 367 Protei: cession #: 11 NGEPGTRVVA TEKSYKTKGP PEBG[AHLP VELPPVCC] 368 DNA sci d Accession	CARAGOCTTA CCCACCAGCC ARAGTCTGTA CATGACTGAG AGAAATAGGA AGAGCACCAG GAGAGAGCTT ACCATGGGA ATTGCACCT GTATTTGTAT SEQUENCE NP_0042 21 LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKC/GFFAA LSGVPLMILD DI QUENCE THE THE TOTAL TOTAL THE TOTAL TH	GATGGGGAGT TTACCTAAAG AAGACCATGTA AAGACCTATA AAATCTTTC ATTGGGCACC GAAAAGCTGT TCCAATCTGT TTACTGTG TTAATAAAGCA 10 31 81KALDGRSQ SCMTERTVKA EERELEKLFQ	CTCAAGTTTC CTACTAGAAA GACCCTCAA AAGCAAAAG CCTTCAATC CCCCTTCAG TTCAGCTGG TGCAGTCTCC ACATAGATAT TTCTTCAACA 41 VSTPRFGKTF VSTVPASDDA	AACACCAGT GGCTTTGGGA ACAAAACAG CTCTGTTCCT TCTAGACTTT TGAAGTCTT TTGAAGTTCT CCCCCTTCA TTCAACATT TTAAATTTCT GAAAAAAAAA 51 DAPPALPKAT PREIKEFPP	180 240 300 360 420 480 540 600 650 720
50 55 60	CNGGGTCTO TTTGGCGAAAA ACTGTCAACA CCAAGGTTTT GCCTCAGATO GAGAGTTTTG CCCATGATCC CCTGTGAAGA CCTGGACGA AAAAAAAA Seq ID NO: Protein Act	GACTICANT COTTCGATC GAGCTACAGA ACTICCTAGA ATGCCTATC TGGATGTTAGA TTGACGAGGA TTGACGAGGA TGCCCTCT TGGATGTTTGA 367 Protei: cession #: 11 NGEPGTRVVA TEKSYKTKGP PEBG[AHLP VELPPVCC] 368 DNA sci d Accession	CAAAGCCTTA CCCACCAGCC AAAGTCTGTA CATCACTGAG AGAAATAGAA AGAGCACCTG GAAATTGGAA ACCATGGGAA ATTGCACCT GTATTTGTAT sequence NP_0042 21 RUGGLKLGSGP LKOKQPSFSA LSGVPLMILD DI	GATGGGGAGT TTACCTAAAG AAGACCATGTA AAGACCTATA AAATCTTTC ATTGGGCACC GAAAAGCTGT TCCAATCTGT TTACTGTG TTAATAAAGCA 10 31 81KALDGRSQ SCMTERTVKA EERELEKLFQ	CTCAAGTTTC CTACTAGAAA GACCCTCAA AAGCAAAAG CCTTCAATC CCCCTTCAG TTCAGCTGG TGCAGTCTCC ACATAGATAT TTCTTCAACA 41 VSTPRFGKTF VSTVPASDDA	AACACCAGT GGCTTTGGGA ACAAAACAG CTCTGTTCCT TCTAGACTTT TGAAGTCTT TTGAAGTTCT CCCCCTTCA TTCAACATT TTAAATTTCT GAAAAAAAAA 51 DAPPALPKAT PREIKEFPP	180 240 300 360 420 480 540 600 650 720
50 55 60 65	CHOGGITCHO TITGGCAAAA ACTGTCAACAC CCAAGGTTTT GCCTCAGATO GAGAGTTTTG CCCATGATCC CCTGTGAAGA CCTTGACCT AAAAAAAA Seq ID NO: Protein Ac MATLIYVDRE RRALGTVNRA NPLDFESFDL SPSILSTLD Seq ID NO: NSSILSTLD Seq ID NO: Nucleic Ac	GACTICANT COTTCGATC GAGCTACAGA ACTICCTAGA ATGCCTATC TGGATGTTAGA TTGACGAGGA TTGACGAGGA TGCCCTCT TGGATGTTTGA 367 Protei: cession #: 11 NGEPGTRVVA TEKSYKTKGP PEBG[AHLP VELPPVCC] 368 DNA sci d Accession	CARAGOCTTA CCCACCAGCC ARAGTCTGTA CATGACTGAG AGAAATAGGA AGAGCACCAG GAGAGAGCTT ACCATGGGA ATTGCACCT GTATTTGTAT SEQUENCE NP_0042 21 LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKL/GSGP LNGKC/GFFAA LSGVPLMILD DI QUENCE THE THE TOTAL TOTAL THE TOTAL TH	GATGGGGAGT TTACCTAAAG AAGACCATGTA AAGACCTATA AAATCTTTC ATTGGGCACC GAAAAGCTGT TCCAATCTGT TTACTGTG TTAATAAAGCA 10 31 81KALDGRSQ SCMTERTVKA EERELEKLFQ	CTCAAGTTTC CTACTAGAAA GACCCTCAA AAGCAAAAG CCTTCAATC CCCCTTCAG TTCAGCTGG TGCAGTCTCC ACATAGATAT TTCTTCAACA 41 VSTPRFGKTF VSTVPASDDA	AACACCAGT GGCTTTGGGA ACAAAACAG CTCTGTTCCT TCTAGACTTT TGAAGTCTT TTGAAGTTCT CCCCCTTCA TTCAACATT TTAAATTTCT GAAAAAAAAA 51 DAPPALPKAT PREIKEFPP	180 240 300 360 420 480 540 600 650 720
50 55 60 65	CTGGGGTCT TTTGGCABAA ACTGTCABCA CCMAGCTTT GCCTCABATG GCCTCABATG GCCTCABATG GCTCTGBACAG CTGTGGACC TAGTGGTCTC TAGTGTTABAA Seq ID NO Protein Ac H AMAMANAA SAMAMANA SEQ ID NO PROTEIN AC H COMMINISTRA SEQ ID NO PROTEIN AC L SPSSILSTLD Seq ID NO Nucleic Ac COding seq 1	GACTITCANT GRITCHATE GRITCHATCH G	CARAGECTTA CCCACCAGGC ANASTECTOTA ACTIVATED ACTIVATA CATAGGAA ACTIVATA ACCATGGAA ACTIVATA ACCATGGAA ACTIVATA ACCATGGAA ACTIVATA ACCATGGAA ACCATGAA ACCATGAA ACCATGAA ACCATGAA ACCATGAA ACCATGAA ACCATGAA ACCAT	GATGGGAGAT TTACCTANAG AAGACCTAG AAGACCTAG AAGACCTAG AAGACCTAG AAGACCTAG CAGAAAACCAG CAGAAACCAG CAGAAAACCAG CAGAAACCAG AACCAG CAGAAACCAG AACCAG CAGAAAACCAGAAACCAG CAGAAACCAGAAACCAGAACAACAACAACAACAACAACAA	CTCAGGTTC CTCAGGTTC CTCAGGTTC CTCAGGTTC CCTCAGGTTC CCTC	AACACCAOT GOCTTIOGRA ACMAAAAAA ACMACCACTCAGTICCT TOTAGACTCT TOTAGACTCT TOTAGACTCT TITAAATTCT GAAAAAAAA 51 DAPPALPKAT TYPELEKFFFP SPPWESHLLQ	180 240 300 360 420 480 540 660 720
50 55 60 65 70	CTGGGGTCTT TTTGGCABAA ACTGTCABCA CCAMCCTTTT TTGGCABAA ACTGTCABCAC CCAMCCTTTT TGGCABAA CTGTCAGCC CTGTGGACC CTGTGGACC CTGTGGACC CTGTGGACC TAGTGCTCC AAAAAAAAA Eeg ID NO Protein Ac 1 1 NATLIYUDER RKALGTURA SP85ILSTID Seq ID NO Seq ID NO Seq ID NO Seq ID NO Seq ID NO Seq ID NO TTGGGGGCG TTGGGGGGGCG	GACCITCANT GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	CANAGCCTTA CCCACCAGCC ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTACCAG ANAGTCTGTA ANAGTACCAG ANAGTCTGTA	GATGGGGGT TTACCTANAS ANGACCAAGG ANGACCAAGG ANGACCTAT COMACCTAG TCOMACCTAG TCOMACCTAG TACTAGAGCG TTACTAGAGCG TACTAGAGCG TA	CTCAGTTTC CTCAGTTTC CTCAGTTCAG AGCCCCTCAA AGCCCACAG CCTCCAATCC TCCCCTTGAG CTTCAACC TTCTCCACTCAG 41 VSTPRPGKTP VSTPRPGKTP 41 CCCCCCTCGCACAC 41	AACACCAOTT GOCTTTUGGA ACCAAAACAC ACCAAAACAC TCTAGACTT TGGAGTACCT TCTAGACTT TTCAAGCATT TTCAACGATT TTCAACGATT TTCAACGATT TTCAACGATT TTCAACTACT GAAAAAAAAAA	180 240 300 360 420 480 540 660 720
50 55 60 65	CTGGGGTCTT TTTGGCAMAA ACTGTCAACA CCAACCTTT GRAAAA ACTGTCAACAC CCAACCTTC GRACAGTTTTG GRAGAGTTTTG GRAGAGTTTTG GRAGAGTTTTG GRAGAGTTTTG GRACAGTTTTG GRACAGTTTTG AAAAAAAAA Seq ID No. Protein Ac. 1 ACALLYUMER FRALGTTRTA NPLDFESFOL SPSSILSTLU SPSSILSTLU SPSSILSTLU SPSSILSTLU LI ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC TRACAGTGGAGC	GACTITCANT GRIPCITCANT GRIPCITACRA CTROCCANAA ATROCTACTOR TOURANAA ATROCTACTOR TOURANT GRIPCITAVA 367 Protei cession #; 11 11 12 13 168 DNA sci 1d Accession 11 26 DNA sci 1d Accession 11 1 1 1 1 1 1 1 1 1	CANAGCCTTA CCCACCAGC ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCCCAC ANAGTCTGTA ANAGTCCCAC ANAGTCGTA ANAGTCCCAC ANAGTCGTA ANAGTCCCAC ANAGTCGTA ANAGTCCAC ANA	GATGGGGGT TAGCTANG ANGACCANGG ANGACCANGG ANGACCANGG ANGACCANGG ANGACCANGG ANGACCANGG ANGACCANGG TAGCANGGCGGC TAGCANGGCGGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGA	CTCAGTTTC CTCAGTTTC CTCAGTTGAG GACCCTCAA GACCCCTCAA GACCCAAAG CCTTCAATCC TTCAGCTGG TGCAGTCTCC ACATGGATT TTCTTCAACA 41 VSTPSPGKTP KSSVSAGDAA LGPPSPVKMP 41 CCGCCTGCCAGC CCGCTGCCAGC CCGCTGCCGCAGC CCGCTGCCGAGC CCGCTGCCGAGC	AACACCAOTT GCGCTTUGGA ACCAAAACAC ACCAAAACAC ACCAAACAC TCTAGACTTT TGGAGTUCT CCCCCCTCTCA TCTAGACTTT TCTAGATTTT TGAAATACAT TTCAAACATT TTCAAACATT TTCAAACATT TTCAAATACAT TTCAAATACAT S1 DAPPALPKAT YPEIKKFFF SPPWESKLLQ 51 GGCCGTGCA	180 240 300 360 420 480 540 560 720
50 55 60 65 70	CTGGGGTCTT TTTGGCAMAA ACTGTCAACA CCAACCTTT GRAAAA ACTGTCAACAC CCAACCTTC GRACAGTTTTG GRAGAGTTTTG GRAGAGTTTTG GRAGAGTTTTG GRAGAGTTTTG GRACAGTTTTG GRACAGTTTTG AAAAAAAAA Seq ID No. Protein Ac. 1 ACALLYUMER FRALGTTRTA NPLDFESFOL SPSSILSTLU SPSSILSTLU SPSSILSTLU SPSSILSTLU LI ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC 1 ACALLYUMER TRACAGTGGAGC TRACAGTGGAGC	GACTITCANT GRIPCITCANT GRIPCITACRA CTROCCANAA ATROCTACTOR TOURANAA ATROCTACTOR TOURANT GRIPCITAVA 367 Protei cession #; 11 11 12 13 168 DNA sci 1d Accession 11 26 DNA sci 1d Accession 11 1 1 1 1 1 1 1 1 1	CANAGCCTTA CCCACCAGC ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCTGTA ANAGTCCCAC ANAGTCTGTA ANAGTCCCAC ANAGTCGTA ANAGTCCCAC ANAGTCGTA ANAGTCCCAC ANAGTCGTA ANAGTCCAC ANA	GATGGGGGT TAGCTANG ANGACCANGG ANGACCANGG ANGACCANGG ANGACCANGG ANGACCANGG ANGACCANGG ANGACCANGG TAGCANGGCGGC TAGCANGGCGGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGA	CTCAGTTTC CTCAGTTTC CTCAGTTGAG GACCCTCAA GACCCCTCAA GACCCAAAG CCTTCAATCC TTCAGCTGG TGCAGTCTCC ACATGGATT TTCTTCAACA 41 VSTPSPGKTP KSSVSAGDAA LGPPSPVKMP 41 CCGCCTGCCAGC CCGCTGCCAGC CCGCTGCCGCAGC CCGCTGCCGAGC CCGCTGCCGAGC	AACACCAOTT GCGCTTUGGA ACCAAAACAC ACCAAAACAC ACCAAACAC TCTAGACTTT TGGAGTUCT CCCCCCTCTCA TCTAGACTTT TCTAGATTTT TGAAATACAT TTCAAACATT TTCAAACATT TTCAAACATT TTCAAATACAT TTCAAATACAT S1 DAPPALPKAT YPEIKKFFF SPPWESKLLQ 51 GGCCGTGCA	180 240 300 360 420 480 540 660 720
50 55 60 65 70	CTGGGGGTCTTTTTGGCABAA ACTOTCAACAA ACTOTCAACAA ACTOTCAACAAA AAAAAAAAA AAAAAAAAA AAAAAAAAAA	GACTITCANT GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	CANAGCCTTA CCCACCAGGC AAGATCTATA AAGATCACTATA AGNATAGAA AGNAGCACAG GGGGGGGCTT ACCATGGGAA AATTGCCACCT GTATTTGTAT CACTGGGAA ACACGGGAA CCCACGCGCGCCCCCCGGGCCCCCCCC	GATGGGAGAT TTACCTANAS AMGRICTAGGGAC AMATICTITE ATTAGGCAC GANAAGCTT TCCAATCTG TCCAATCTG TCTACTAGT TACTANAGCA SILALDGRSQ SILALDGRSQ SILALDGRSQ GAGGGGCGCGCCC TGCCGCCCCCCCCCCCCCCCCCCCC	CTCAGGTTC CTCAGGTTC CTCAGGTTC CTCAGGTTC CCCCTTGAG TTCAGCTGG TCCAGTTCAGCT TCCCCTTGAG TTCAGCTGG TCCAGTTGAGT TCGTTCAACA 41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AACACCAOT GCCTTUGGA ACCAANACCA ACCAANACCA ACCAANACCA TCHAGACTT TGGGGTGCT TGAGGTT TTCAGGTT GAAAAAAA 51 1 0 DAPPALPKAT FYPP SPPWSSELQ 51 1 GGGCGGTGCA GGGCGTGCA GCGCAGGAT GCGCGGCAGCAT GCCGCAGGTT CCCGGAGGTT CCCGAGGT CCCGGAGGT CCCGGAGGT CCCGGAGGT CCCGGAGGT CCCGAGGT CCCCGAGGT CCCGAGGT CCCGAGGT CCCGAGGT CCCGAGGT CCCCGAGGT CCCGAGGT CCCCGAGGT CCCCGAGGT CCCCCCCCCC	180 240 300 350 420 480 540 660 720 120 180
50 55 60 65 70 75	CTGGGGGTCTTTTTGGCABAA ACTOTCAACAA ACTOTCAACAA ACTOTCAACAAA AAAAAAAAA AAAAAAAAA AAAAAAAAAA	GACTITCANT GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	CANAGCCTTA CCCACCAGGC AAGATCTATA AAGATCACTATA AGNATAGAA AGNAGCACAG GGGGGGGCTT ACCATGGGAA AATTGCCACCT GTATTTGTAT CACTGGGAA ACACGGGAA CCCACGCGCGCCCCCCGGGCCCCCCCC	GATGGGAGAT TTACCTANAS AMGRICTAGGGAC AMATICTITE ATTAGGCAC GANAAGCTT TCCAATCTG TCCAATCTG TCTACTAGGCAC GANAAGCTT TCCAATCTG TATAAAGCA SILALDGRSQ SILALDGRS SILALDGRS SILALDGRS SILALDGRS SILALDGRS SILALDGRS SILALDGRS SILALDGRS SILALDGRS SILALDGRS SILALDGRS SILALDGRS SI	CTCAGGTTC CTCAGGTTC CTCAGGTTC CTCAGGTTC CCCCTTGAG TTCAGCTGG TCCAGTTCAGCT TCCCCTTGAG TTCAGCTGG TCCAGTTGAGT TCGTTCAACA 41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AACACCAOT GCCTTUGGA ACCAANACCA ACCAANACCA ACCAANACCA TCHAGACTT TGGGGTGCT TGAGGTT TTCAGGTT GAAAAAAA 51 1 0 DAPPALPKAT FYPP SPPWSSELQ 51 1 GGGCGGTGCA GGGCGTGCA GCGCAGGAT GCGCGGCAGCAT GCCGCAGGTT CCCGGAGGTT CCCGAGGT CCCGGAGGT CCCGGAGGT CCCGGAGGT CCCGGAGGT CCCGAGGT CCCCGAGGT CCCGAGGT CCCGAGGT CCCGAGGT CCCGAGGT CCCCGAGGT CCCGAGGT CCCCGAGGT CCCCGAGGT CCCCCCCCCC	180 240 360 420 420 480 660 720 660 720 180
50 55 60 65 70	CTGGGGTCTG TTGGCABAA ACRECAMAA ACREC	GACTITCANT GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	CANAGCCTTA CCCACCAGGC AAGETCATTA AAGATCACACA AAGATCACACACACACACACACACACACACACACACACAC	GATGGGAGAT TTAGCTAMAG AMGRICTAMGG AMGRICTAMGG AMAGTGTTTA ATTGGGACC GAMAAGCTT TCCAATCTG TTAGCTAMG TATAMAGCA SI ALLDGRS SIKALDGRS SIKALDGRS GAMAGCTGT TATAMAGCA 110 31 11 GAMGGGGGCT GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CTCAGGTTC CTCAGGTTC CTCAGGTTC CTCAGGTTC CCCCTTGAG TTCAGCTCG TCAGCTCG TCAGCTTGAG TTCAGCTCG TCAGCTTGAG TTCAGCTCG TCAGCTTGAG TTCAGCTCG TCAGCTGGAG TCAGCTGC TCAGCTGGAG TCAGCTGC TCAGCTGGAG TCAGCTGC TCAGCTGGAG TCAGCTGAG TCAGCTGGAG TCAGCTGAG TCA	AMARCACONT GOCTTTORAGE TOTAGACTTT TOGAGTATT 180 240 360 420 480 540 660 720 60 120 180 240 360 360 360 360 360 360 360 360 360 36	
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	ACCATCCGGG	GGGACCCCGA	GTGTCATCTC	TTCTACAATG	AGCAGCAGGA	CCCTTCCCCC	1080
5	GTGCACACCC	AGCGGATGCA	GTAGACCGCA	GCCAGCCGGT	GCCTGGCGCC	CCTGCCCCCC	1140
	TTOCACTTCT	CACACACCGGC	TTTATATTT	GARAGAGACC	AGCACCGAGC	TOGGCACCTC	1260
	CCCGGCCTCT	CTCTTCCCAG	CTGCAGATGC	CACACCTGCT	CCTTCTTGCT	TTCCCCGGGG	1320
10	CCCGGCCTCT	GTTGTGGTCG	GGGAGCTGGG	GTACAGGTTT	GGGGAGGGG	AAGAGAAATT	1380
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20	RKPLKSOMKE	LAUPREKUTE	OHROMOKOOK	HHLGLEBPKK	LRPPPARTPC	OCELDOVLER	240
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	CAGCACTGAT	TGCACGAACA	CAGCCAGCIA	TTGATGTTTT	GATAGATTCC	TTACCCAGTG	240
	AAGAATCTAC	AGCTGCTTTA	CAGGCTGCTA	GCTTGTATAA	GCTAGAAGAA CATGCTTCTG	GAAAACCATG	300
35	AAGCTGCTAC	ATGTGTGGAG	GATGTTGTTT	ATCGAGGAGA	CATGCTTCTG	GAGAAGATAC	360
	AAAGCGCACT	TGCTGATATT	GCACAGTCAC	AGCTGAAGAC	AAGAAGTGGT	ACCCATAGCC	420 480
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	TTAAACACTA	TGACACATTA	CCTTTTTAGC	TATTTTTAAT	AGTCTTCTAT	TTTCACTCTT	600
40	GATAAGCTTA	TAAATCATGA	TTGAATCAGC	TTTAAAGCAT	CATACCATCA	TTTTTTAACT	660
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60	ALADIAGSQL Seq ID NO: Nucleic Ac: Coding seq I I ATGGAGAATC CTGCGGTGG CATTCTAAAG TTCTTAGAC ACAGTCAAG ACTGTTTTTGA AGAGCTAAGG ACTGTTTTCGAA TTCTTCCTGGA TTCTCCTGGA TATGGACAT GAAACTATCA	ETESGTHSQS 372 INA set td Accession Hence: 1-11 11 11 12 AGGTGTTGAC AGCTGAGTGA CTCAAGGACA CTCAGGACA CTCAGGACA CTCAGGACA CTCCTGACTT AAGAAGAGCA ACTTAAGGAA TCTTTGTCAA TCCATACTGT ATGCAGCAT TCCATACTGT ATGCAGCAT TCCATACTGT ATGCAGCATT	LPDS quence a #: AJ27105 13 21 GCCGCATGTC CGTACAGAAC TGGTGCCAAA AGAGCCTGTG TGATCGTTGG TGATCGTTGG TGATCGTTGG TGATCGTTGG TGATCGTTGG TGATCACTGT TGGAGACATG TGGAGTCACTTG TGGAGTCACTTT TGGAGTCACTTT	31 TACTGGGCTC CCTGCATCA GGAGACANTG TACAAACTNA CTCGGATGGAT TTTANGTATA CGATTCTGTA ACGTTCTCTA ACGTCACCOG	41 AGGGACACCG GCATCACTGA TCTATGAATT CCAAGAGGCA CAAGACGAGG AAAGCAAGG ATCTTGTGCA TCTTGGGAAA GCCAGATGCT TGCTGCCTTC CCATGGAAGA	51 CGAGCTATAT AAAGCGTCCTG TCACCTGGAG GGTAAACATT AAAGCGACCA AATGGAGCTC CTCTCCTGAA AGAGTCCTTT GGCAGTTOTG TCTGATCCAG AATGCAGAAC	120 180 240 300 360 420 480 540 600 660 720
60	ALADIAGSQL Seq ID NO: Nucleic Ac: Coding seq I I ATGGAGAATC CTGCCOTIGG CATTCTAAAG TTCTTAGAC ACAGTCAAG ACTGTTTTTGA AGAGCTAAGG ACTGTTTTCACA TTCTTCCTGGA TTCTCCTGGA TATGGACAT GAAACTATCA	ETESGTHSQS 372 INA set td Accession Hence: 1-11 11 11 12 AGGTGTTGAC AGCTGAGTGA CTCAAGGACA CTCAGGACA CTCAGGACA CTCAGGACA CTCCTGACTT AAGAAGAGCA ACTTAAGGAA TCTTTGTCAA TCCATACTGT ATGCAGCAT TCCATACTGT ATGCAGCAT TCCATACTGT ATGCAGCATT	LPDS quence a #: AJ27105 13 21 GCCGCATGTC CGTACAGAAC TGGTGCCAAA AGAGCCTGTG TGATCGTTGG TGATCGTTGG TGATCGTTGG TGATCGTTGG TGATCGTTGG TGATCACTGT TGGAGACATG TGGAGTCACTTG TGGAGTCACTTT TGGAGTCACTTT	31 TACTGGGCTC CCTGCATCA GGAGACANTG TACAAACTNA CTCGGATGGAT TTTANGTATA CGATTCTGTA ACGTTCTCTA ACGTCACCOG	41 AGGGACACCG GCATCACTGA TCTATGAATT CCAAGAGGCA CAAGACGAGG AAAGCAAGG ATCTTGTGCA TCTTGGGAAA GCCAGATGCT TGCTGCCTTC CCATGGAAGA	51 CGAGCTATAT AAAGCGTCCTG TCACCTGGAG GGTAAACATT AAAGCGACCA AATGGAGCTC CTCTCCTGAA AGAGTCCTTT GGCAGTTOTG TCTGATCCAG AATGCAGAAC	120 180 240 300 360 420 480 540 600 660 720 780
60 65 70	ALADIAGSQL Seq ID MO: Nucleic Ac: Coding sequ I ATGGGGAAATC CTGCGGGTGG CATTTCAAAG TTCTTTAGAC AGAGTAAGG AGAGTAAGG AGTCTTACAGA ATCTTTAGAC ATCTTAGAA ATCTTTAGAC CTCTTAGAA AAAGCTGTAA	XTESGTHSQS 372 INA set Id Accession Dence: 1-11 11	LPDS quence a #: AJ27105 13 21	31.	41 	51 CGAGCTATAT AAACGTGCTG GGTAAACATT AAACGGCCA AATGGAGCTC CTCTCCTGAA AGAGTCCTTT GGCAGTTTGG TCTGATCAG AGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG TCTGAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCT	120 180 240 360 420 480 540 660 720 780 840 900
60	ALADIAGSQL Seq ID MO: Nucleic Ac: Coding sequ I ATGGGGAAATC CTGCGGGTGG CATTTCAAAG TTCTTTAGAC AGAGTAAGG AGAGTAAGG AGTCTTACAGA ATCTTTAGAC ATCTTAGAA ATCTTTAGAC CTCTTAGAA AAAGCTGTAA	XTESGTHSQS 372 INA set Id Accession Dence: 1-11 11	LPDS quence a #: AJ27105 13 21	31.	41 	51 CGAGCTATAT AAACGTGCTG GGTAAACATT AAACGGCCA AATGGAGCTC CTCTCCTGAA AGAGTCCTTT GGCAGTTTGG TCTGATCAG AGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG TCTGAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCT	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
60 65 70	ALADIAGSQL Seq ID MO: Nucleic Ac: Coding sequ I ATGGGGAAATC CTGCGGGTGG CATTTCAAAG TTCTTTAGAC AGAGTAAGG AGAGTAAGG AGTCTTACAGA ATCTTTAGAC ATCTTAGAA ATCTTTAGAC CTCTTAGAA AAAGCTGTAA	XTESGTHSQS 372 INA set Id Accession Dence: 1-11 11	LPDS quence a #: AJ27105 13 21	31.	41 	51 CGAGCTATAT AAACGTGCTG GGTAAACATT AAACGGCCA AATGGAGCTC CTCTCCTGAA AGAGTCCTTT GGCAGTTTGG TCTGATCAG AGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG TCTGAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
60 65 70	ALADIAGSQL Seq ID MO: Nucleic Ac: Coding sequ I I ATGGAGAATC CTGCOGTING CATTICAAAG TICTITAGAG ACTCTITAGAG AAAGTAGAT AAAGTAGAT AAAGTAGAT AAAGTAGAT ATAAATTTT	XTRSOTHISOS 372 DNA eedd Accession Lence: 1-31 11 30 ASGINITIGAC ACCURATION ACCURACY	LPDS quence a #: AZZ7105 13 21	31 TACTGGGCTC CCTGCCATCA GGGGACAATO TACAAACTTA GAGGACTC TTTACTGTATC ACTTCACTC ACTTCACCA TGGATGTAT TGGATGTC TGGATGTAT TGGATGTC TGGATGTAT TGGATGTC TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TACTTTATAA	41 AGOGACACOG GCATCACTGA TCTATGAATT CCCAGGAGCA CAAGCAGGA AAACCAAGA ACTTGTGCA TCTTGGGAAA GCCAGATGCT TGCTGCCTTC CCATGGAAGA TGAAATTTT TCACATGGTT TCACATGGTT	51 CGAGCTATAT AAACGTGCTG GGTAAACATT AAACGGCCA AATGGAGCTC CTCTCCTGAA AGAGTCCTTT GGCAGTTTGG TCTGATCAG AGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG TCTGAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCT	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
60 65 70 75	ALADIAGSQL Seq ID MO: Nucleic Ac: Coding sequ I I ATGGAGAATC CTGCOGTING CATTICAAAG TICTITAGAG ACTCTITAGAG AAAGTAGAT AAAGTAGAT AAAGTAGAT AAAGTAGAT ATAAATTTT	XTESGTHSQS 372 INA set Id Accession Dence: 1-11 11	LPDS quence a #: AZZ7105 13 21	31 TACTGGGCTC CCTGCCATCA GGGGACAATO TACAAACTTA GAGGACTC TTTACTGTATC ACTTCACTC ACTTCACCA TGGATGTAT TGGATGTC TGGATGTAT TGGATGTC TGGATGTAT TGGATGTC TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TACTTTATAA	41 	51 CGAGCTATAT AAACGTGCTG GGTAAACATT AAACGGCCA AATGGAGCTC CTCTCCTGAA AGAGTCCTTT GGCAGTTTGG TCTGATCAG AGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG TCTGAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
60 65 70	RADITAGSOL Seq ID NO. Nucleic Ac. Coding sequil	XTRESTHISOS 372 DNA see dd Accessio Ac	LPDS Junea 1 1: AJ27101 21 GCCGCATGTC COTACAGAAC TOGTGCCAA AGAGCTGTT TOGTGCCAA AGAGCTGTT TOGTGCCAA AGAGCTGTT TOGTGCCAA GCGTGACAAT TTGGTTATAG TTGGTTATAG TTGGTTATAG TTGGTTATAG TTGGTTATATAG TTGATATTAG TTTGATATTAG TTTAGATAGA	31 TACTGGGCTC CCTGCCATCA GGGGACAATO TACAAACTTA GAGGACTC TTTACTGTATC ACTTCACTC ACTTCACCA TGGATGTAT TGGATGTC TGGATGTAT TGGATGTC TGGATGTAT TGGATGTC TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TACTTTATAA	41 	51 CGAGCTATAT AAACGTGCTG GGTAAACATT AAACGGCCA AATGGAGCTC CTCTCCTGAA AGAGTCCTTT GGCAGTTTGG TCTGATCAG AGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG TCTGAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
60 65 70 75	RADITAGSOL Seq ID NO. Nucleic Ac. Coding sequil	XTRSOTHISOS 372 DNA sed da Accessión lennes 1-21 11 AGGINATIGAC ACCESSIÓN ACCESSI	LPDS Junea 1 1: AJ27101 21 GCCGCATGTC COTACAGAAC TOGTGCCAA AGAGCTGTT TOGTGCCAA AGAGCTGTT TOGTGCCAA AGAGCTGTT TOGTGCCAA GCGTGACAAT TTGGTTATAG TTGGTTATAG TTGGTTATAG TTGGTTATAG TTGGTTATATAG TTGATATTAG TTTGATATTAG TTTAGATAGA	31 TACTGGGCTC CCTGCCATCA GGGGACAATO TACAAACTTA GAGGACTC TTTACTGTATC ACTTCACTC ACTTCACCA TGGATGTAT TGGATGTC TGGATGTAT TGGATGTC TGGATGTAT TGGATGTC TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TGGATGCA TACTTTATAA	41 	51 CGAGCTATAT AAACGTGCTG GGTAAACATT AAACGGCCA AATGGAGCTC CTCTCCTGAA AGAGTCCTTT GGCAGTTTGG TCTGATCAG AGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG CAGGAGTCCTT TCTGATCAG TCTGAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCTGATCAG TCT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
60 65 70 75	RADITAGSOL Seq ID NO. Nucleic Ac. Coding sequil	XTRSOTHISOS 372 DNA serid Accession 1-11 11 11 13 NASTRITURAL TO ACCOUNT ACCOU	LPDS JUNEAGE SELECTION LICENTIFICATION CONTROL OF THE SELECTION LICENTIFICATION LICEN	31 TACTGGGCTC CCTGCCATCA GGGGGCATG GGGGGCATG TACAAACTGA GGGGGGCATG TACAAACTGA GGGGGGCATGAAT TACAACTGA ACTGGAA ACTGGAA ACTGGAA ACTGGAA ACTGGAA ACTGGAA ACTGGAA TGGAAGTGCA TGGAAGTGCA TGGAAGTGCA TGGAAGTGCA TACTTTATATA TACTTATATA	A1 AGGGACACCG GCATCACTAR TCTATGAST CCCAMAGCAC ACAMCACGA ACATCATAR TCTATGAST AT TCTATGAST TCTATGATGAT TCTATATGATT TCTATATGAT TCTATATATGAT TCTATATGAT TCTATATATGAT TCTATATGAT T	51 CSACCTATAT AAAGGTGCTG TCACCTGGMG GGTAAACAT AATGGGGCTA AATGGAGTTGG ATGGAGTTGG TCTGATCGG AATGCAGTGG AATGCAGTGG CGGTTGGG CGGTTGGG CGGTTGGG ATGCAGGAG AATGC	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
60 65 70 75	ALBITAGSOL Seq ID NO. Nucleic Acc Coding seq. 1 1 INGURANA TCTCACCO ACGGTACGA ACGGTACGA ACGGTACGA ACGGTACGA ACGGTACGA TCTCACCACA TCTCACCACA TCTCACCACA TCTCACCACA TCTCACACAC TCTCTGGAA AAAGCTTACGA AAAGCTTACGA AAAGCTTACGA AAAGCTTACGA AAAGCTTACGA AAAGCTTACGA TCTCACACC TCTCTGGAA AAAGCTTACGA AAAGCTTACGA TCTCACACC TCTCTGGAA AAAGCTTACGA TCTCACACC TCTCTGGAA AAAGCTTACGA TCTCACACC TCTCTGGAA AAAGCTTACGA TCTCACACC TCTCTGGAA ACTACACTAC	372 EMA SE the Accession of the Accessi	LPDS Number 1	11 INTERSECTION OF THE PROPERTY OF THE PROPER	41 ACCEPTANTS	S1 S1 SAACTAPAT ANACOTOCTR TOXOCTIGANG GGTBALCATT ANACGACCA ANTOGRACIC ANTOGRACIC TOTTCOTTR ANTOGRACIC TOTTCATACAG ANTOGRACIC TOTTLACACT TOTTLACACT ANTOGRACIC ANTOGRACIC ANTOGRACIC ANTOGRACIC ANTOGRACIC ANTOGRACIC COCAG	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
60 65 70 75	ALBITAGSOL Seq ID NO. Nucleic Acc Coding seq. 1 1 INGURANA TCTCACCO ACGGTACGA ACGGTACGA ACGGTACGA ACGGTACGA ACGGTACGA TCTCACCACA TCTCACCACA TCTCACCACA TCTCACCACA TCTCACACAC TCTCTGGAA AAAGCTTACGA AAAGCTTACGA AAAGCTTACGA AAAGCTTACGA AAAGCTTACGA AAAGCTTACGA TCTCACACC TCTCTGGAA AAAGCTTACGA AAAGCTTACGA TCTCACACC TCTCTGGAA AAAGCTTACGA TCTCACACC TCTCTGGAA AAAGCTTACGA TCTCACACC TCTCTGGAA AAAGCTTACGA TCTCACACC TCTCTGGAA ACTACACTAC	372 EMA SE the Accession of the Accessi	LPDS Number 1	11 INTERSECTION OF THE PROPERTY OF THE PROPER	41 ACCEPTANTS	S1 S1 SAACTAPAT ANACOTOCTR TOXOCTIGANG GGTBALCATT ANACGACCA ANTOGRACIC ANTOGRACIC TOTTCOTTR ANTOGRACIC TOTTCATACAG ANTOGRACIC TOTTLACACT TOTTLACACT ANTOGRACIC ANTOGRACIC ANTOGRACIC ANTOGRACIC ANTOGRACIC ANTOGRACIC COCAG	120 180 360 360 420 480 540 660 720 780 840 900 960 1020
60 65 70 75	Seq ID NO. NUCLEIC ACCOUNTS SEQ ID NO. NUCLEIC ACCOUNTS COUNTS ATTORNAME ATTORNAME TACTIONAME TACTI	J72 EMA SE EMA ACCESSAGE 1-11 11 13 14 15 16 17 17 18 18 17 17 17 18 18 18 18 18 18 18 18 18 18	LPDS Numbers 1 8: AJ27105 2 1 COCCANGER COCCANGE	11 ACTUACION CONTROL	41 I AGGRACACCG GCATCACTGA TCTATGATT CCCMMAGGG CCCMMAGGG ACTTGATGGGA ANAGGGAAGA TCTATGGGA ANAGGGAAGA TCTATGGGA TCTATGGAA TCTATGAA TCT	S1 CARGCTATAT A AAAGGTCCTG GOTALGATATAT AAAAGTCCTGGAG GGTAAAGATC CTCTCCTGGAA AATGGAGACCT TCTCATCCGA AATGGAGACCT TCTCATCCGA AATGGAGACCT TCTCATCCGA AATGGAGACCT TCTCATCCAC CAGGTACTCT CTCATCCAC CAGGTCCTT CCTCATCCGC CAGGTCCTT CCTCATCCCC CAGGTCCT CCTCATCCCC CAGGTCCT CCTCATCCCC CAGGTCCT CCTCATCCCC CAGGTCCT CCTCATCCC CAGGTCCT CCTCATCCC CAGGTCTATCC CCCAGTTGCT CCTCATCCC CCCAGTCCC CCCAGTCCC CCCAGTCCC CCCAGTCCC CCCACCC CCACCC CCACCCC CCACCC CCACCCC CCACCCACCC CCACCCCACCC CCACCCACCCA	120 180 360 360 420 480 540 660 720 840 900 900 1020 1080
60 65 70 75	Seq ID NO. NUCLEIC ACCOUNTS SEQ ID NO. NUCLEIC ACCOUNTS COUNTS ATTORNAME ATTORNAME TACTIONAME TACTI	J72 EMA SE EMA ACCESSAGE 1-11 11 13 14 15 16 17 17 18 18 17 17 17 18 18 18 18 18 18 18 18 18 18	LPDS Numbers 1 8: AJ27105 2 1 COCCANGER COCCANGE	11 ACTUACION CONTROL	41 ACCEPTANTS	S1 CARGCTATAT A AAAGGTCCTG GOTALGATATAT AAAAGTCCTGGAG GGTAAAGATC CTCTCCTGGAA AATGGAGACCT TCTCATCCGA AATGGAGACCT TCTCATCCGA AATGGAGACCT TCTCATCCGA AATGGAGACCT TCTCATCCAC CAGGTACTCT CTCATCCAC CAGGTCCTT CCTCATCCGC CAGGTCCTT CCTCATCCCC CAGGTCCT CCTCATCCCC CAGGTCCT CCTCATCCCC CAGGTCCT CCTCATCCCC CAGGTCCT CCTCATCCC CAGGTCCT CCTCATCCC CAGGTCTATCC CCCAGTTGCT CCTCATCCC CCCAGTCCC CCCAGTCCC CCCAGTCCC CCCAGTCCC CCCACCC CCACCC CCACCCC CCACCC CCACCCC CCACCCACCC CCACCCCACCC CCACCCACCCA	120 180 360 360 420 480 540 660 720 780 840 900 960 1020

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5	KAVVPFVPYL	MYFCOMLAVV WSAIBIFRYS SFTLPYPVKI	PYMLTCIDMD	WKVLTWLRYT	LWIPLYPLGC	LAEAVSVIQS	240 300 360
	Nucleic Aci	374 DNA seq d Accession lence: 1-111	#: NM_0163	95			
10	couring sequ						
	1	11	21	31	41	51	
15	CTGCGCGTGG CATTTCAAAG TTCTTAGACC	AGGTGTTGAC AGCTGAGTGA CTCAAGGACA TTGTGAAACC	CGTACAGAAC TGGTGCCAAA AGAGCCTGTT	CCTGCCATCA GGAGACAATG TACAAACTGA	GCATCACTGA TCTATGAATT CCCAGAGGCA	TCACCTGGAG GGTAAACATT	60 120 180 240
20	ACAGTACAGA CTGTTTTTGG AGAGCTAAGG	AGAAAGTGAG CTCCTGACTT AAGAAGAGCG	TCAGTGGTGG TGATCGTTGG CCTAAATAAA AGGATACCTG	GAGAGACTCA CTGGATGAAT CTCCGACTGG TTTATGTATA	CAAAGCAGGA CTGATGCGGA AAAGCGAAGG ATCTTGTGCA	AAAGCGACCA AATGGAGCTC CTCTCCTGAA ATTCTTGGGA	300 360 420 480
25	TATGACACAT GAAACTATCA CTTCTTGGAA	TCTTTGTCAA TCCATACTGT ATGCAGCAAT GAAATTTTAT	TGGAGTCACT TTTGTTTATC	ACGTCACCGG ACCTCTTGGCA	TGCTGCCTTC CCATGGAAGA	TCTGATCCAG AATGCAGAAC	540 600 660 720 780
25	TTCTACATGC CTGTGGATTC ATTCCAATAT	TTTTCTTTGT TGACGTGCAT CCTTATATCC TCAATGAGAC TTTCCTTTTT	TGACATGGAT ACTGGGATGT CGGACGATTC	TGGAAGGTGC TTGGCGGAAG AGTTTCACAT	TCACATGGCT CTGTCTCAGT TGCCATATCC	GATTCAGTCC AGTGAAAATC	900 960 1020
30	ATANATTTTC CATGCCTGTG	GTCACCTTTA ATCCCAGCGC	TAAACAGCGC TTTGGGAGGC	AGACTGAAAA TGA	TGAGGGCAGG	CGCAGTGGCT	1080
35	Seq ID NO: Protein Acc	375 Protein cession #:	NP_0574	.79			
	1	11	21	31	41	51	
40	FLDLVKPEPV	YWAQRHRELY YKLTQRQVNI LRLESEGSPE MYPCQMLAVV WSAIEIPRYS	TVQKKVSQWW	ERLTKQEKRP	LPLAPDFORM	DESDARMEL	60 120 180 240 300
45	IPIPNETGRF STKKKDLDGP	PBA SEAPPABAKI	KVRPSPPLQI	YLIMIPLGLY	INFRHLYKQR	RRRYGKKRKR	360
50	Seq ID NO: Nucleic Ac: Coding sequ		Tuence 1 #: NM_0059 1-270	31	41	51	
	1	11	i	ī	1	1	
55	GTGAAACAAC TGCCAACCCA ATTCCAGAGC	AGCAGCAGAA CTTGCCAGCC AGGTGCCTGA CCTGCCAGCC AGAAGACCAA	TCCACCCCAG GCCCTGCCAC CAAGGTGCCT	GAACCATGCA	TCCCCAAAAC	CAAGGAGCCC	60 120 180 240
60	Seq ID NO: Protein Acc	377 Protein cession #:	n sequence NP_005				
65	1 MNSQQQKQPC IPEPCQPKVP	11 TPPPQPQQQQ EPCPSTVTPA	PAQQKTKQK	31 EPCIPKTKEP	41 CQPKVPEPCH	51 PKVPEPCQPK	60
70	Seq ID NO: Nucleic Ac: Coding seq	378 DNA sed id Accession wence:	quence 1 #: NM_002: 74-505	ıos			
	1	11	21	31	41	51	
75	CTACCTCCCT	CACTGOGGCG AGCATGTCGG	CCCCCCCAA	GACTGGCGGC	AAGGCCCGCG	CTTCACCGGT CCAAGGCCAA GGCTGCTGCG	60 120 180
	GAAGGGCCAC	TACGCCGAGC	GCGTTGGCGC	CGGCGCGCAAT	GTGTACCTGG	CGGCAGTGCT ACAACAAGAA AGCTCAACAA AGGCCGTGCT	240 300 360
80						AGGCCGTGCT GCAAGAAGGC CCCAGCTCCC AGCTGAGCCG	420 480 540 600
85	TOGCOGCOG	GCCTCGAGTC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCTCCCG	TCCCGCACCG	TCGCCCGCCT CCTGCCGCGT CTTCCGGATG CCGGGGGGAG	660 720 780 840

85	CAATGAAAGA	CCTTCTGCTT	ACATGAGGGA	GCACAATCAA	CGGGGAGACA	ATGTGCTGGG GGTCTTCTGA TGAGGTGGAA CAGCCCTCGT	180 240 300 360
80	CCTTGAGTGC	CTGCGTCCGT	GAGAATTCAG	CATGGAATGT	CTCTACTATT	51 CAGAGTTAAA TCCTGGGATT	60 120
	Seq ID NO: Nucleic Ac Coding seq	382 DNA sec id Accession uence:	quence n #: NM_002: 92-177	510 4			
75	GGDFEFMDDA TVLIYPNSIQ RYINGRNSSD	NMCIAIAISL EYIRQLPPNF VLVYVTSNDT	LMILICAMAT PYRDDVMSVN TVLLPPYDDA	YGAYKQRAAW PTCLVLIILL TVNGAAKEPP	PISIILTFKG	DFALNMLVAI YLISCVWNCY	120 180
70	1	11	21	31 WYLIINAVVL	41 -	51 DOYNESSEL	60
65		381 Protein		76			
60	TAAAATGTAA GACTACCTGA TGTTGGTTCA	ACATTTTCAG	AAAAATGAGG ATTTTTATAT TGCTGTAAAT	TTGAACTTCC ATTGCCTTCC ATTCATATGT TAAGTCGTTT	TACAAAGTCA	GCAACTCTCC	1860 1860 1920 1980
	GATCTTGTGT GTGTTTGGCG GGCCCGCTTT TATCAAGTGG	CCAGGGACAT CTGCATGGGA TACTAAGTGT AATTGGGATA	GGGGTGACAT TCTGGTGCCC TCTGCCCTAG TATTTGATAT	GCCTCGTATG CTCTTCTCCT ATTGGTTCAA ACTTCTGCCT	TGTTAGAGGG GGATTCACAT GGAGGTCATC AACAACATGG	TGGAATGGAT CCCCACCCAG CAACTGACTT AAAAGGGTTT	1560 1620 1680 1740 1800
55	CCAGCATAGA ATTAGGTAAA	GAACAAAACC TAGAAGTCCT	TTATGGAAAC TATGTATGTG	AGGAATGTCA TTACAAGAAT GTGGTAAAGG AGCAGTGACC	TTCCCCCACA ATTTCTCCA	ACATCCTTTA TGGCCTGAAT	1320 1380 1440 1500
50	TCAACATATG TGGGGATATA	CTTTGCTAGA ACGGGCTTCA	ACACTGTGAT CTACCTTCC GTACCTGCTG	ATTTAGATGT AGATTAACTG CTAGGCATTG GGCCCCAAAG CAAAAATAGA	TAGAATTCTT AAACTTCCCC TTGGGCATTT	CCTGTACGAT CAAATCTGAT TTCTCTCTGT	1020 1080 1140 1200 1260
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40	TGGATCATCC ATCACTGTGC TTTCCCTACA	TCCTGATATG CATTCTTCTG TTATTTATCC GAGATGATGT GCATTATCTT	TGCTATGGCT TTACCAGATC AAACTCCATT CATGTCAGTG GACTTTTAAG	ACTTACGGAG TTTGACTTTG CAGGAATACA AATCCTACCT GGTTACTTGA	CGTACAAGCA CCCTGAACAT TACGGCAACT GTTTGGTCCT TTAGCTGTGT	ACGCGCAGCC GTTGGTTGCA GCCTCCTAAT TATTATTCTT TTGGAACTGC	480 540 600 660 720
35	CAGGCGAGGC GCGATGAAGA CATGTCCGCA CTGTTGATTT CTGGGAGGTG	GGTCGACGCT TGGTCGCGCC CCGGCACCAT TATTGAGTGC ACTTTGAGTT	CCTGAAAACT CTGGACGCGG CCTGCTCGGC CCTGGCTGAT CATGGATGAT	TGCGCGCGCG TTCTACTCCA GTCTGGTATC CCGGATCAGT GCCAACATGT	CTCGCGCCAC ACAGCTGCTG TGATCATCAA ATAACTTTTC GCATTGCCAT	TGCGCCCGGA CTTGTGCTGC TGCTGTGGTA AAGTTCTGAA TGCGATTTCT	180 240 300 360 420
30	1 J ACGCGTCCGG	11) CAGAAGCTCG	21 GAGCTCTCGG GGAGCGGCGG	31 GGTATCGAGG AGGAGCCGGC	AGCAGCGGCG	CGGCGGGCTC	60 120
25		380 DNA seq d Accession	пепсе	2			
20	AEILELAGNA	ARAKAKSRSS	PRHLQLAIRN	31 VHRLLRKGHY DEBLNKLLGG	41 AERVGAGAPV VTIAQGGVLP	51 YLAAVLBYLT NIQAVLLPKK	60 120
15		379 Protein		96			
10	CTGCCTCCTA CTATGTGGAC CCGACGCCGC CAGCACAGT CTGCAGCTAA TTTATTAAAG	CCCATTTCCC	TTCCAGCAAA CTGTCTGGAC ACTAGAACCT	CTCAACTCGG	CAATCCAAGC	ACCTAGATAC	1380 1440 1500 1560
5	GCCGGCGGCG GCTAAGGGGC CAGGGCCGAG CGGCAGCTGC AGACGGCCGC GCCCCTTCTG AGGTCTGCGC	TGCGGGGAGG GTGGGCAGTC AGCCGGGGTG TGGCCGGGAG CGGCCGGGAC	COGCAGCACC CAGGCCGAGA TCTGGTACCC GCTTTGGTGG CCAGGCCTTT	TTCTGGAAGA GCCGGCGCC CCCCGGCGTG GAGAGACGCG CACATCAGCT TXXTTAACAGG	CTTGGCCTTC CTGAAGGTGA GTGCTTAGCC ATCGCCGATT CTCCCTCCAT CACATCTTCC	GCTCTGACG GTGAGGCCCT CAGGACTTTC TCGGTCTGGC CTTCATTCAT TCCCGAGTGA	900 960 1020 1080 1140 1200 1260
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	GGGCTCAAAT	ATAACATTTG	CGGTGAACCT	GATATTCCCT	AGATGCCAAA	AGGAAGATGC	420
	CAATGGCAAC	ATAGTCTATG	AGAAGAACTG	CAGAAATGAG	GCTGGTTTAT	CTGCTGATCC	480
	ATATGTTTAC	AACGTCTTCC	CATGGTCAGA CTGATGGGAA	GGACAGTGAC	GGGGAAAATG	GCACCGGCCA	540 600
5	ATGGAATTTC	ATCTACGTCT	TCCACACACT	TGGTCAGTAT	TTCCAGAAAT	TGGGACGATG	660
	TTCAGTGAGA	GTTTCTGTGA	ACACAGCCAA	TGTGACACTT	GGGCCTCAAC	TCATGGAAGT	720
	GACTGTCTAC	AGAAGACATG	GACGGGCATA CTGTGTTTGT	TGTTCCCATC	GCACAAGTGA CAGAAGAACG		780 840
	ATCCGACGAA	ACCTTCCTCA	AAGATCTCCC	CATTATGTTT	GATGTCCTGA	TTCATGATCC	900
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	CCTGTTTGTT	TCCACCAATC	ATACTGTGAA CTGCAGCACC	TCACACGTAT	GTGCTCAATG CCGCCACCGC	CACCACCACCAC	1020
	CAGACCTTCA	AAACCCACCC	CTTCTTTAGG	ACCIGCIGGT	GACAACCCCC	TGGAGCTGAG	1140
15	TAGGATTCCT	GATGAAAACT	GCCAGATTAA	CAGATATGGC	CACTTTCAAG		1200
15	AATTGTAGAG	GAAAGCTCCC	AGGTTAACAT TAATAGACTT	TGTCGTGACC	ACAGACGTCC TGCCAAGGGA	TGATGCCGGT	1260
		ACCATCATTT	CTGACCCCAC	CTGCGAGATC	ACCCAGAACA		1380
	CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
20	GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCCT	1500 1560
20	GATTTCTGTT	TOTTTOTTO	ACCCAGCCTC TATTTGTCAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAAAACA	1620
	CRAGGARTAC	AACCCAATAG	AAAATAGTCC	TGGGAATGTG	GTCAGAAGCA	AAGGCCTGAG	1680
	TGTCTTTCTC	AACCGTGCAA	AAGCCGTGTT	CTTCCCGGGA	AACCAGGAAA	AGGATCCGCT	1740 1800
25	ACTCAAAAAC	CARGAATITA	AAGGAGTTTC AGATGTGCTG	GAGTGGCTAT	TAACCTTTTT	TTCCTAAAGA	1860
	TTATTOTTAA	ATAGATATTG	TGGTTTGGGG	AAGTTGAATT	TTTTATAGGT	TAAATGTCAT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCITCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	AGAGTAAGGA	TTCACTTATA	TATTGATTAG	2100
30	AGCCTAACCC	AGGTTAACTG	CAAGAAGAGG	CGGGATACTT	TCAGCTTTCC	ATGTAACTGT	2160
	ATGCATAAAG	CCAATGTAGT	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220 2280
	GTGCACACTT	CCTAGACTCA	TCCTGATGGA GAAAAAATAC	TACTOTOATA	AATGGGTGGG	AGTATTTTGG	2340
	TGACAACCTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCCAT	2400
35	GGACATTTAG	TTAGTGCTTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCTTGTGTAT	2460 2520
	ATTTCCAAAT	COTGOTTTTT	TCGCTGCACA CATGGCAACT	TGATCAGTAA	GGATTTCACC	TCTGTTTGTA	2580
	ACTAAAACCA	TCTACTATAT	GTTAGACATG	ACATTCTTTT	TCTCTCCTTC	CTGAAAAATA	2640
40	AAGTGTGGGA	AGAGACAAAA	AAAAAAAA				
40	Sea ID NO:	383 Protein	n sequence				
	Protein Ac	ession #:	NP_0025	01			
4.5	1	11	21	31	41	51	
45	ī	11	ī	31	í .	1	
45	MECLYYPLAP	11 	AAKRFHDVLG	31 NERPSAYMRE	HNQLNGWSSD IFPRCQKEDA	ENDWNEKLYP NGNIVYERNC	60 120
45	MECLYYPLGP VWKRGDMRWK RNEAGLSADP	11 LLLAARLPLD NSWKGGRVQA YVYNWTAWSE	AAKRFHDVLG VLTSDSPALV DSDGENGTGO	31 NERPSAYMRE GSNITFAVNL SHHNVFPDGK	HNQLNGWSSD IFPRCQXEDA PFPHHPGWRR	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL	120 180
	MECLYYPLGP VWKRGDMRWK RNEAGLSADP GOYPOKLGRC	11 LLLAARLPLD NSWKGGRVQA YVYNWTAWSE SVRVSVNTAN	AAKRFHDVLG VLTSDSPALV DSDGENGTGQ VTLGPOLMEV	31 NERPSAYMRE GSNITFAVNL SHENVFPDGK TVYRRHGRAY	HNQLNGWSSD IFPRCQXEDA PFPHHPGWRR VPIAQVKDVY	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL VVTDQIPVFV	120 180 240
45 50	MECLYYFLGF VWKRGDMRWK RNEAGLSADP GQYFQKLGRC TMFQKNDRNS	11 LLLAARLPLD NSWKGGRVQA YVYNWTAWSE SVRVSVNTAN SURTFLKDLP LNLIVKAAAP	AAKRFHDVLG VLTSDSPALV DSDGENGTGQ VTLGPQLMEV IMFDVLIHDP GPCPPPPPPP	31 NERPSAYMRE GSNITFAVNL SHENVFPDGK TVYRRHGRAY SHFLNYSTIN RPSKPTPSLG	HINQLINGWSSD IFPRCQKEDA PFPHHPGWRR VPIAQVKDVY YKWSFGDNTG PAGDNPLELS	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL VVTDQIPVFV LFVSTNETVN RIPDENCQIN	120 180 240 300 360
	MECLYYPLGP VWKRGDHRWK RNEAGLSADP GQYFQKLGRC TMFQKNDRNS HTYVLNGTPS RYGHFOATIT	11 LLLAARLPLD NSWKGGRVQA YVYNWTAWSE SVRVSVNTAN SDETFLKDLP LNLTVKAAAP LNLTVKAAAP	AAKRFHDVLG VLTSDSPALV DSDGENGTGQ VTLGPQLMEV IMFDVLIHDP GPCPPPPPP IOMTDVLMPV	31 - NERPSAYMRE GSNITFAVNL SHENVFPDGK TVYRRHGRAY SHPLNYSTIN RPSKPTPSLG FWPESSLIDF	HNQLNGWSSD IFPROQXEDA PFPHHPGWRR VPIAQVKDVY YKWSFGDNTG PAGDNPLELS VVTCOGSIPT	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL VVTDQIPVFV LFVSTNHTVN RIPDENCQIN EVCTIISDPT	120 180 240 300 360 420
50	MECLYYPLGP VWKRGDMWK RNEAGLSADP GQYFQKLGRC TMFQKNDRNS HTYVLNGTFS RYGHFQATIT CEITONTVCS	11 	AAKRFHDVLG VLTSDSPALV DSDGENGTGQ VTLGPQLMEV IMFDVLIHDP GPCPPPPPP IQMTDVLMPV TVRRTFNGSG	31 NERPSAYMRE GSMITFAVNL SHENVFPDGK TYYRHGRAY SHPLNYSTIN RPSKPTPSLG PWPESSLIDF TYCVNLTLGD	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR VPIAQVKDVY YKWSFGDNTG PAGDNPLELS VVTCQGSIPT DTSLALTSTL	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL VVTDQIPVFV LFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360
	MECLYYPLGF VWKRGDMRWK RNEAGLSADP GQYFQKLGRC TMFQKNDRNS HTYVLNGTFS RYGHFQATIT CEITQNTVCS PLRMANSALI	11 	AAKRFHDVLG VLTSDSPALV DSDGENGTGQ VTLGPQLMEV IMFDVLIHDP GPCPPPPPP IOMTDVLMPV	31 NERPSAYMRE GSMITFAVNL SHENVFPDGK TYYRHGRAY SHPLNYSTIN RPSKPTPSLG PWPESSLIDF TYCVNLTLGD	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR VPIAQVKDVY YKWSFGDNTG PAGDNPLELS VVTCQGSIPT DTSLALTSTL	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL VVTDQIPVFV LFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	MECLYYPLGF VWKRGDMRWK KNEAGLSADP GQYFQKLGRC TMFOKNDRNS HTYVLMGTFS RYGHFQATIT CEITQNTVCS PLRMANSALI FPGNQEKDPL	11	AAKRFHDVLG VLTSDSPALV VSDSGENGTGQ VTLGPQLMEV IMPDVI.HDP GPCPPPPPPP IQMTDVLMPV TVRRTFNGSG VISLLVYKKR	31 NERPSAYMRE GSMITFAVNL SHENVFPDGK TYYRHGRAY SHPLNYSTIN RPSKPTPSLG PWPESSLIDF TYCVNLTLGD	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR VPIAQVKDVY YKWSFGDNTG PAGDNPLELS VVTCQGSIPT DTSLALTSTL	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL VVTDQIPVFV LFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	MECLYYFLGF VWKRGDMWK RNEAGLSADP GQYFQKLGRC TMFQNNDRNS ETYVLMGTFS RYGHFQATIT CEITQNTVCS PLRMANSALI FGROEKDPL Seq ID NO: Nucleic Ac:	11 LLLARRLPLD NSWEGGRVQA YVYNTANSE SUTVEVENTAN SUETFLKOLP LINITYKAARP IVEGILENI PVDVDEMCLL SVGCLAIPVT LKNQEFKGVS 184 DNA sei id Accessio:	AAKRFHDVLG VITSDSPALV DSDGENGTGQ VTLGPQLMEV IMPDVLIHDP GPCPPPPPPP IQMTDVLMPV TVRRTFNGSG VISLLVYKKH	31 NER PSAYMRE GSNITFAVNL SHENVFPDGK TVYRHGRAY SHPLNYSTIN RPSKFTPSLG PWPESSLIDF TYCVNILIGD KEYNP LENSP	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR VPIAQVKDVY YKWSFGDNTG PAGDNPLELS VVTCQGSIPT DTSLALTSTL	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL VVTDQIPVFV LFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	MECLYYPLGF VWKRGDMRWK RNEAGLSADP GOYFOKLGRC TMFQKNDRNS HTYVLMGTFS RYGHFQATIT CEITQNTVCS PLRMANSALI FPGNQEKDPL Seg ID NO:	11 LLLARRLPLD NSWEGGRVQA YVYNTANSE SUTVEVENTAN SUETFLKOLP LINITYKAARP IVEGILENI PVDVDEMCLL SVGCLAIPVT LKNQEFKGVS 184 DNA sei id Accessio:	AAKRFHDVLG VLTSDSPALV DSDGENGTGQ VTLGPQLMEV IMPDVLIHDP GPCPPPPPPP IQMTDVLMPV TVRRTFNGSQ VISLLVYKKH	31 NER PSAYMRE GSNITFAVNL SHENVFPDGK TVYRHGRAY SHPLNYSTIN RPSKFTPSLG PWPESSLIDF TYCVNILIGD KEYNP LENSP	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR VPIAQVKDVY YKWSFGDNTG PAGDNPLELS VVTCQGSIPT DTSLALTSTL	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL VVTDQIPVFV LFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	MECLYYFLGF VWKRGDMWK RNEAGLSADP GQYFQKLGRC TMFQNNDRNS ETYVLMGTFS RYGHFQATIT CEITQNTVCS PLRMANSALI FPGNQEKDPL Seq ID NO: Nucleic Ac:	11 LLLARLPLD LLLARREDAN LLLARREDAN LLLARRENAN L	AAKRFHDVLG VLTSDSPALV VSDSGENGTQQ VTLGPOLMEV IMFDVLHED GPCPPPPPPP IQMTDVLMEV TVRRTFNGSG VISLLVYKKR Quence n #: NM_0011 48-187	31 NER PSAYMRE GSNITFAVNL SHENVFPDGK TVYRHGRAY SHPLNYSTIN RPSKFTPSLG PWPESSLIDF TYCVNILIGD KEYNP LENSP	HNQLNGWSSD IFPRCQKEDA PFPHHPGWRR VPIAQVKDVY YKWSFGDNTG PAGDNPLELS VVTCQGSIPT DTSLALTSTL	ENDWNEKLYP NGNIVYEKNC WNFIYVFHTL VVTDQIPVFV LFVSTNHTVN RIPDENCQIN EVCTIISDPT ISVPDRDPAS	120 180 240 300 360 420 480
50	MECLYYPLOP MECCHYPLOP	11 LLLARLPLD NSWKGGRVQA YVYNWTANS SETFLKOLP INLTVKAAAP IVEGILEVNI FVDUDEMCLL SVGCLAIPVT LKNQEPKGVS 384 DNA sei d Accessionence:	AAKRFHDVLG VLTSDSPALV VLTSDSPALV DSDGSNGTNG VTLGPDLMEV IMFDVLIHDP GPCPPPPPPP IQMTDVLMEV TVRRTFNGSG VISLLVYKKH Quence n #: NM_0011 48-1877	31 NER PEAYMRE GENITFAVAL SHEMVIPOGK SHPLIMYSTIM RPSKETPSLG PWPESSLIDF TYCVMILIGA KEYNPIENSP	HNQLNGWSSD HFPRCQKEDA FFPHHPGMRE VPLAQVEOVY YKWSFGDNTO PAGDNPLELS VVTCQGSIPT DTSLALTSTL GNVVRSKGLS	ENDMNEKLYP NGHIYYEKOC NNFIYYEKIC NNFIYYEKIC NNFIYYEKIT LFYSTHITVN RIPDENCQIN EVCTIISDPT SYPERDPAS VFLNRAKAVF	120 180 240 300 360 420 480 540
50	MECLYYFLGP WKKRGDMRWK RNEAGLSADP GQYFGKLGRC THFOKNDENS RTYVLNGTS RTYVLNGTS RYGHFQATIT CBITQNTCS RYGHFQATIT CBITQNTCS RYGHFQATIT CBITQNTCS RYGHFQATIT Seq ID NO: Nucleic Ac: Coding seq 1	11	AAKRFHDVLG VITSDSPALV VITSDSPALV DSDGENGTOG VITLGPGLMEV IMFDVLIHDP IQMTDVLMPV TVRRTFNGSG VISLLVYKKH QUENCG #; NM_0011 48-1877	31 NER PSAYMRE GSN ITPAVNL SHENVEPDGK TVYRREGRAY SHPLIN'ST SHPLIN'ST PMPESSLIDP TYCVILIGE KEYNPIENSP	HNQLNGWSSD IFPRCQKEDA FFPHHPGWRE VPIAQVKOVY YKWSFGDNTG PAGDNPLELS VVICQGSIPT DTSLALTSTL GNVVRSKGLS	ENDMNEKLYP NGNIVYEKNC MNIYYEKNC MNIYYEKNC MNIYYEKNT LFVSTNHTVN RIPDENCQIN EVCTISDPT ISVPDRDPAS VPLNRAKAVF	120 180 240 300 360 420 480 540
50	MECLYPILIP VMKREDMENK RNEAGLSADP QYFQXLGRC TMFQXNDENS RTGHIGATIF RTGHIGATIF RTGHIGATIF Seq ID NO: Nucleic Ac: Coding sequ TCCATATIGT AATACAATITI AATACAGATT AATACAGATT	11	AKKRPHDVLG VLTSDSPALV DSDGENGTNO VTLOPOLMEV IMPOVLIMDP IQMIDVLMEV TVRRTFNGSG VISLLVYKKH Quence n #: NM_0011 48-187: 21	31 NER PSAYMRE GSN ITPAVNL SHENVEPDGK TVYRREGRAY SHPLIN'ST ITPAVNL PSPESSLIDP TYCVILIGE KEYNPIENSP .34 31 CANANTAACT TTACTGAATC	HNQLINGWSSD IFPROXISDA PPPHHENGEN PPPHHENGEN VPLAQVIGOVY YEAGOVY YEAGOVY VYTOGSIPT DYSALISTL GNVVRSKGLS 41 	ENDMNEKLYP NGRIVYEKNC MNFIYVERIC WNFIYVERIC VTOQIEVEV LEVSTHEITU VTOQIEVEV LEVSTHEITU VTOQIEVEV LEVSTHEITU VTOQIEVEV LEVSTHEITU VTOQIEVEV LEVSTHEITU LEVETISE S1 AGTTGGGTGG CATAGAATG	120 180 240 300 360 420 540
50 55 60	MECLYYPLAP WHITEMANN MECLYPLAP WHITEMANN MECLYPLAP WHITEMANN MECLYPLAP GOTO MECLYPLAP	11 LLLARREPLD NSWEGGRVQA VYYNKTANSE SVRVSVNTAN SDETFIKDI LNLTVKAAAP IVEGILEN VEGILAIP LVEGILEN SVGCLAIP LKNQEFKGVS 384 DNA sei dd Accession tence: 11 GCTTCCACCA TTTTATTTTC AGCTTCCATCA AGCTTCATTTTT	AKREHDULG AKREHDULG VITSDSPALV DSDGENGTIGG GPCPPPPPP IQMTDVLHED TVRRIFINGS VISLLVYKKR QUENCE 18: NM 0011 48-1877 21 CTGCCAATAA CTACTAAATT TTGGATTCTT TTGGATTCTT GCCCAGTTTG GCCCAGTTTG	31 NER PSAYMRE GSNITFAVNL SHENVFPDGK TVYRRIGRAY SHPLNYSTI PWPESSLIDF TYCVNLTLGD KEYNPLENSP 31 CANAATAACT TTACTGAATC ACCAATGTAC TTCAAGGAACC	HMQLNGWSSD IFPRCOKEDA PFPHHFOGRR PFPHHFOGRR VPLACYKOVY YKWSFGINTG DYSLALTSTL GNVVRSKGLS 41 AGCAACCATG CAGRACACTG TGCAGAGACATA	ENDMNEKLYP NGRIVYEKOL WNFIYVEHTL WYTUQIEVFV LFVSTHITL VYTUQIEVFV RIPDENQIN RIPDENQIN SVPLNRAKAVF 51 AAGTGGGTGG CATAGAAATG AGTTTAGCTG	120 180 240 360 420 480 540
50 55 60	MECLYPILAP WHITEGOMENK RIMEAGLSADP GOYFORIGHE METAVLINGTES RYGHROATHS RYGHROATHS RYGHROATHS RYGHROATHS PERMANSALI Seq ID NO: Nucleic Ac: Coding sequ 1 { TCCATATTGT AATCAATTTT AATCAGGTTAA ACCTGGCTAC AAATGGTTGAA	11 LLLAARLPLD NSWKGGRVQA VYYNKIANSE SVRVSWTAN SDETFLKOLP LINLYKAAAP VYDUDECLL LINLYKAAAP VYDUDECLL LINLYKAAAP VYGLAAITVT LINNGFRGVS 384 DNA se- id Accessio- Lenco 1 GGTTCCACCA TTTAATTTTCA AGGTTCCATA CATATTTTTA CATATTTTTA CATATTTTTA AGATCATTG	AKKRPHDVLG VLTSDSPALV DSDGSRATOQ VTLGDQLMSV MFDVLLIEDP GPCPPPPPP IQMIDVAMPV TVRRTFNOSG VISLLVYKKH QUENCe n 8: NM_001) 48-187: CTGCCAATAA CTACTAAATT GCCCAGTTIG ACTGCAATTG	31 NER PSAYMRE GSNITFAVNI SHENVFPOCK TVYRRIGAN SHPINYSIIN RPSKETPSIG FWP ESSILDF TYCVNILLGD KEYNPIENSP	HNQLINGWSSD IFPROXISDA PPPHHENGREN PPHHENGREN VELOVICOVIC YKNGSEGDAY YKNGSEGDAY VYTCQGSIPT GNVVRSKGLS UVTCQGSIPT GNVVRSKGLS UVTCSKGLS UV	ENDMNEKLYP NGRIVYEKNC MNFIYVERIC WNFIYVERIC VTOQIEVEV LEVSTHEITU VTOQIEVEV LEVSTHEITU VTOQIEVEV LEVSTHEITU VTOQIEVEV LEVSTHEITU VTOQIEVEV LEVSTHEITU VTOQIEVEV LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU VTOQIEVE LEVSTHEITU LEVSTH	120 180 240 300 360 420 540
50 55 60 65	MECLYPELGE WHERGERENE RIMEAGLSADE GOYFELGRE THEONIDENS HTYLINGTES RYGHPOATI CEITONTYCES PLEMANSALI FFORDEKOPL Seq ID NO: COding sequ TCCATATIOT AATCAALITAT AATCAALITAT AATCAALITAT AATCAGGATA CCTGGCTAC GOTTTHAGA GOTTHAGA GOTTTHAGA GOTTHAGA GOTTTHAGA GOTTHAGA GOTTTHAGA GOTTHAGA GOTTTHAGA GOTTHAGA GOTTHA	11 LLIARREPLD NSWKOGRVOA VYVINNTANSE SVEUVINTAN SEETILADLE LIMITYRAAAP INVESILEEVIN LIMITYRAAAP INVESILEEVIN LENGEFROVS 384 DNA seed Accessionence: 11 GCTICCACCA TITAATITIC AGCTICCATCA AGCTICCATCA AGGTICCATCA AGAGCATCATA AGAGCATTCATA AGAGCATTCATA AGAGCATTCATA AGAGCATTCATA AGAGCATTCATA AGAGCATTCATA AGAGCATTCATA AGAGCATTCATA CATAATITTATA AGAGCATTCATA CATAATTTATA AGAGCACATTCA AGAGCACATTCA AGGGCACATTCA CGGGACATTCA	AKREHDVIG VITSDEPALV DSDGENGTGG VITLGPOLMEN GPCPEPPPPP GPCPPPPPPP VISLLVYKCH USLLVYKCH 48-187: 21 CTGCCAATAA CTACTAAATTT GCCCAGTTTG CCTGCCTTCC GCCCAGTTGC GACTGCTGCA	31 NERPEAYMRE GENTIFAVALL SHENVEPOK TYTRHIGHAY SHENVEPOK TYTRHIGHAY SHENVEPOK SHENVEPOK SHENVEPOK SHENVER SH	HNQLINGWSSD IFPROCKEDA IFPROCKEDA PPPHHEFGER VPIAQVKOVY YKNBFGDIT PAGDITE AUTOMOST DISLALTSTL GNVVRSKGLS 41 I AGCAACCATG CAGAACCATG CAGAACCATG TGCAGAGATA CACTTACAAG TGGAGATGAA TTGCCATGAG	ENDMNEKLYP NGBILYERGE MNFIYVEHTL WYTUQIEVFY LFYSTHETW RIPDENQIN RIPDENQIN FUCCIISDPT ISVPENCAM STORMAN AGTOGGTGG GAAGTAAGGA AAGAAATT CATAACTGT CATAACTGT CATAACTGT CATAACTGT CATAACTGT CATAACTGT CATAACTGT CATAACTGT CATAACTGT	120 180 240 300 420 480 540 60 120 180 240 300 360 420
50 55 60	MECLYPLOF VWKRCDMBWK KNEAGLSADP GOYFGELGR GOYFGELGR BTYVLNGTPS BTYVLNGTPS BTYVLNGTPS BTYGHOATIT CEITINTYCS Seq ID NO: Nucleic Ac: Coding sequ 1 { TCCATATIGT AATAGGAT AATAGGAT AATAGGAT AATAGGAT AGGAGAGTA TGGAGAGAGTA TGGAGAGTA TGGAGAGAGTA TGGAGAGAGTA TGGAGAGTA TGGAGAGAGTA TGGAGAGAGA	11	AARRPHOVLG VLTSDSPALV DSDSDSNTON VLTSDSPALV VLTSDSPALV VLTSDSDALV VLTSDSDLMSP VLTSDSDLMSP VLTSDSDLMSP VLTSDSDLMSP VLTSLDVKSR VLTSLLVYKSR V	31 NER PER YMER ES AVER PER YMER PER PER YMER PER PER YMER PER PER PER PER PER PER PER PER PER P	I INGLINGWSSD I PPROCNEDA PPRHINGWRING PPRHINGWRING VP LAQVIDVY VITAGOS IPP CONTROL OF C	ENDWINEKLYP NGBILVYERCE WHE I YVERT WIT LOUIS POP LIFYSTHET WAT TO LEVE VELOUIS TO LEVE STATEMENT TO L	120 180 300 360 420 480 540 60 120 180 240 360 420
50 55 60 65	MECLYYFLOP VMYRCDHWK RENGALSAND GYFGKLGHC THEYWGROBEN EYGHOALTH EYGHOALTH EYGHOALTH EYGHOALTH FYCHOALTH FYCHOALTH TOCHAATH TATATGAAT TCCAAATHTT AATATGAAT AATCAAGTTAA AATCGAATTAT TCCAAATHTT AATATGAAT TCCAAATHTT AATCAAGTTAA	11 AMERICAN PARTICIPATION OF THE PROPERTY OF	AKRRHUVLG VLTSDSPALV DSDSSMNTOS VLTSDSMNTOS VTLGSDLMSV VTLGSDLMSV VTLGSDLMSV VTLGSDLMSV VTLGSDLMSV VTLGSDLMSV VTLGSDLMSV VTLGSDLMSV VTLGSDLMSV VTLGSTLMSS	31	HINGLINGWSSD IPPROCNEDA PPPHHEORING PPPHHEORING PPHHEORING PPHHEORING PPHHEORING PPHHEORING PHHEORING	ERDINIEKCLYP NORITVERGC NORITVERG	120 180 240 300 420 480 540 60 120 240 306 420 480
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50 55 60 65 70	MECLYYFLOP WHERODHEWE REPACLAND GUYFYGUN GUYFYGU	11 ILLAMRIPLO ILLAMRIP	ARREHUVLG VLTSDSPALV DSDSSALV DSDSSALV DSDSSALV DSDSSALV DSDSSALV DSDSSALV TLGSDLESV VTLGSDLESV VTLGSDLESV VTLGSDLESV VTLGSDLESV VTLGSLESV LOVER	31 I I I I I I I I I	HINGLINGWISD I PPROCNEDA PPHHENORIKE VI PPROCNEDA PPHHENORIKE VI PPHHENORIKE VI PHHENORIKE VI	ERDMINEKLYP NORITVERNC NORITVERNC NORITVERNC NORITVERNC NORITVERNC EVCTITADET LEVERNETVN EVCTITADET LEVERNETVN EVCTITADET LEVERNETVN EVCTITADET CATAGORIC CATAGORIC GANGTINAGCA CATTINAGCA TITUNATINAGCA CATTINAGCA TITUNATINAGCA TITUNATINAGCA CATTINAGCA TITUNATINAGCA CATTINAGCA CATTINAGCA TITUNATINAGCA CATTINAGCA CATTINAGCA TITUNATINAGCA CATTINAGCA CATT	120 180 240 300 420 480 540 120 120 120 240 300 360 480 540 660 6720
50 55 60 65	MECLYYFLOF VMERCEDSWEK RENEALSADE VMERCEDSWEK NEW MECHANISM NEW MECHANISM NEW MECHANISM CETTORIVES	11 ILLAMRIPLD ILLAMRIPLD ILLAMRIPLD ILLAMRIPLD ILLAMRIPLD INSTRUCTOR YVYNNTANSE SVENSYNTAN SERTIFLOLIP LINGUERNI I VEGILERNI I VEGILERNI I VEGILERNI I VEGILERNI I I GENCALATE G	AMARPHOVLG VLTSDSPALV DESIGNATOR VLTSDSPALV DESIGNATOR VLTSDSMALV DESIGNATOR VLTSDSMALV VLTSDSMALV VLTSDSMALV VLTSDSMALV VLTSDSMALV VLTSDSMALV VLTSDSMALV VLTSLTVKKR VLTSLT VLTSLTVKKR VLTSLT VL	11 INTERPRETATION OF THE PROPERTY OF THE PROPE	I I I I I I I I I I I I I I I I I I I	ERIDMINEKLYP MORITYMENCE WITDLIFF MORITYMENCE WITDLIFF MORITYMENCE LEVESTMITYM REVETITSPPT ISVYDDEDYS VELESTMITYM REVETITSPPT ISVYDDEDYS VELESTMITYM RACTOGGTGG CATAGAAATO AAGTAAATT CATAACTGTT CATAAC	120 180 240 300 420 480 540 120 180 240 360 420 420 540 660 720
50 55 60 65 70	MECLYYFLOF VHERODHWK RENEALDADO GYFGOLDE GYFGOLD	11 ILLAMRIPLD ILLAMRIPL ILLAMRIPLD ILLAMRIPL ILLAMRIPLD ILLAMRIPL ILLAMRIPLD ILLAMRIPL ILLAMRIPL ILLAMRIPL ILLAMRIPL ILLAMRIPL ILLAMRIPL ILLAMRIPL ILLAMRIPL ILLAMRIPL ILLAMRIPL	AKRRPHUVLG VLTSDSPALV BODGENTGO VLTSDSPALV BODGENTGO VLTSUDGENG VL	31 IEE PBAYNRE GENITPAVINI SHENIPPOK TYREHGRAY SHETAIYSTIN RESKIPTSI PRESSILDF TYCHNICAG AGA 31 I CANAATAACT TTAATGAATC AGAACCAAC TTCAAGAACC AGAACCAAC GGAACCAAC CCAACAAACC GGAACCAAC TCCAAGAACC AGAACCAAC TCCAAGAACC AGAACCAAC TCCAAGAACC AGAACCAAC TCCAAGAACC AGAACCAAC TCCAAGAACC AAAACCAACT TCCAAGAACC TCCAAAATC AAAACCAACT TCCAAGAACC TCCAAAATC TCCAAGAACC TCCAAAATC TCCAAGAACC TCCAAAATC TCCAAGAACCA TCCAACAACCAC TCCAAAATC TCCAAGAACCAC TCCAAAATC TCCAAACCAC TCCAAAATC TCCAAGACCAC TCCAAAATC TCCAAGACCAC TCCAAAATC TCCAAGACCAC TCCAAACCAC TCCAAACCAC TCCAAACCAC TCCAACACCAC TCCAACCAC TCCACCAC TCCAACCAC TCCA	ENQLINGWESD IPPROXEDA PEPRINGWES ENQLINGWESD IPPROXEDA PEPRINGWES EN ENQLINGWEST ENQUIPMENT ENGLINGWEST ENGLING ENGLINGWEST ENGLINGWEST ENGLINGWEST ENGLINGWEST ENGLINGWEST EN	ENDMINEKLYP NORIVYERNC WHOTOVERNC WHOTOVERNC WHOTOVERNC WHOTOVERNC LEVESTHITVE REVEITLEDET LEVESTHITVE SEVERITES ANGTOGOTOC CHIGARANTO ANTITIAGCO CANGENCTIO CHARANATO CONGCIONATO CHARANATO CONGCIONATO CHARANATO CONGCIONATO CHARANATO CONGCIONATO CHARANATO CONGCIONATO CON	120 180 240 300 420 480 540 120 120 120 240 300 360 480 540 660 6720
50 55 60 65 70	MECLYYFLOF WHERODEWE MEROLICANO MEROLICANO MEROLICANO MEROLICANO MECLYFICAT METOLICANO MECLYFICAT MECHANICA MECLYFICAT MECHANICA MECHANI	11 ILLIAMRI PLD IL	AKRRFHUVLG VLTSDSBALV BODGENTOG ULTSDSBALV BODGENTOG GCCPPPPPPP IQMTDVLHV IMPOVLHDD IQMTDVLHV IMPOVLHDD IQMTDVLHV IMPOVLHDD IQMTDVLHV IMPOVLHV MPOVLHV IMPOVLH IMPOV	11 NEW PEAYMER SHENIFFAVNI SHE	ENQLINGWESD IPPROVIED A PROGRESS OF PROGRE	ENDMISKLYP MORITYPENIC MORITYP	120 120 240 360 420 420 540 540 600 120 180 240 360 480 660 6720 780 900
50 55 60 65 70	MECLITYFICAP WHEREDSHIKE MECLITYFICAP WHEREDSHIKE MECLITYFICAP MECLITYFICAP HITTOPHYSICAP HITTOPHYSI	11 LILAMRIPLO ILLIAMRIPLO INSTRUCTIVO INST	AKRRPHDVLG VLTSDSPALV BOSDSBALV BOSDSBALV BOSDSBALV BOSDSBALV BOSDSBALV BOSDSBALV BOSDSBALV VLTGDDLGB GCPP PPPPP IQMTDVLMPV TVRFTFMSSS VLSLLVYRGR VLSLLVYRGR VLSLLVYRGR VLSLLVYRGR LGCCATAGA CTACTAGATT CCCCATAGAT TTGGATCCT GCCCAGTTG ACTGCCTTC GCCAGTTG ACTGCCTGC GAAGAAGACAT TCCCTGCAAGA ACCGCAATG AACTGCAATG GAAGAAGACAT TCCTCCAGAAG ACCGCAATG CAAGACATTC CAAGACACT CAAGACT 11 NEE PEAYINE GESTITAVANI SHENNYPDOK TYVERHIGAN TYVERHIGAN TYVERH	ENQLINGWESD IF PROCNEDA PEPRINGWES AND IF PROCNEDA PEPRINGWES AND IF PROCNEDA PERINGWES AND IF PROCNEDA PERINGWES AND IF PROCNEDA PERINGWES AND IF PROCNEDA PERINGWES AND IF PROCNEDA PERINGWEST AND IT PROCNEDA PERINGWEST AND IT PROCNEDA P	ENDMISKLYF MORT VYENGE SERVING STATE OF SERVING SERVIN	120 180 240 300 420 420 120 120 120 120 300 420 420 420 660 720 660 720 840 900 960	
50 55 60 65 70	MECLYYFLOF WIREDSHIK MECLYYFLOF WIREDSHIK MENDCLADUR SHENDELDH MENDCLADUR SHENDELDH MENDCH MENDCH SHENDELDH	11 LILAREPED INSTRUCTION INSTR	AKRRPHUVLG VLTSDSBALV ULTSDSBALV	III NERIPEAYNEE SERVITYPOOL SE	INCLUDENCE OF THE PROCESS OF THE PRO	STATEMENT OF THE STATEM	120 240 300 300 300 420 480 540 60 120 180 300 420 420 420 480 480 490 660 780 780 780 780 780 780 780 780 780 78
50 55 60 65 70	MECLITYFLOP WRENDSHAW WRENDSHAW WRENDSHAW GOTFOTGLIBE THOTOGRAP HOTOGRAP HOTOGRAP HOTOGRAP I TOLOGRAP I TOLOGRAP HOTOGRAP I TOLOGRAP HOTOGRAP HO	11 LILAREPED ILLIAREPED INSTRUCTION INSTRU	AKRPHUVLG VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV IMPOVLHDB GGCPPPPPPP IMPOVLHDB IMPOVLHD	11 NEN PEAYINE GESTIFFAVIL SHEINTPPOK TYPERHEATS SHEINTP TYPERHEATS SHEINTP TY	INCLINING STATE OF THE STATE OF	STATEMENT OF THE STATEM	120 240 360 360 420 420 480 540 120 360 480 540 480 540 1020 900 900 900 900 1020
50 55 60 65 70	MECLYYFLOP WRENDSHAF WRENDSHAF WRENDSHAF GOFFEKLING THOUSESH HITVILIATES CONFECUNT PERMANEAL PERMANEAL TCACHAFTOT TCACHAFT TCACHAFTOT TCACHAFTOT TCACHAFT TCACHAFT TCACHAFT TCACHAFT TCACHA	11 LILARREPLD INSMIGHENO INSMIGHE	AKRPHUVLG VLTSDBBALV VLTSDBBALV VLTSDBBALV VLTSDBBALV VLTSDBBALV VLTSDBBALV VLTSDBBALV VLTSDBBALV MEDICA IMPOULTBB GCPP PPPPP TVERTFYBGS TVERTF	11 NENPEATMRE GESTIFFANT SHENTPPOK TYPERIGIAN SHENTPPOK TYPERIGIAN SHENTPPOK TYPERIGIAN SHENTPPOK TYPERIGIAN 3.34 3.3 3.1 3.1 3.1 3.1 3.1 3.1 3.1 3.1 3.1	INGLINGUESDA IPPRODUESDA IPPRO	SI SI SI SI SI SI SI SI SI SI SI SI SI S	120 240 360 420 480 540 540 60 120 120 120 120 780 860 720 780 860 900 900 900 900 910 120 120 120 120
50 55 60 65 70 75	MECLITYFLOP WIRELDSHAM MECLITYFLOP WIRELDSHAM MODIFICATION MODIFICATIO	11 LILIAREPED INSTRUCTION INST	AKRRPHUVLG VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV VLTSDSBALV IMFOVLTSBALV	11 NENDEATHRE GESTIFFANT SERNIFPOCK SERNIFFANT SERNIFPOCK SERNIFPOCK SERVING S	INGLINGWISD I PPRODUEDA POPLACIONO POPLACIONO POPLACIONO POPLACIONO PAGNINE PRODUEDA PAGNINE P	ENDMISKLYF MORITY TERM WITHOUT STATE OF THE PROPERTY OF THE PR	120 180 240 360 360 420 420 480 540 120 160 170 180 180 180 180 180 180 180 180 180 18
50 55 60 65 70	MECLYYFLOP WHENDRINK WHENDRINK GOYFPELINE GOYFPELINE THOUGHDES HTVLINGUES ELITINIVES FLEMMARIL PROMIEDE I TOM MUCHAL ANTOGEN ANTAGEN	11 LILAREPED INSTRUCTIVE INSTRUCTIVE SUPPLIES SU	AKREPHOVLG VLTSDERALV VLTSDERALV VLTSDERALV VLTSDERALV VLTSDERALV VLTSDERALV IMPOVLEDE GCC1P PPPPP TVLSTLTV TVLSTLT TVL	11 INENPRAYME GRAITFANT SERVICE SERVIC	INGLININS DI PPRODUZIONI DI PPRODUZIONI DI PPRODUZIONI DI PPRODUZIONI DI PPRODUZIONI DI PPRODUZIONI DI PRODUZIONI	I UNIVERSITY AND A CONTROL OF THE ACT OF THE	120 240 360 360 420 420 480 540 120 360 240 360 480 540 720 840 900 1020 1020 1020 1020 1020 1020 1020
50 55 60 65 70 75	MECLYYFLOP WHENDRINK WHENDRINK GOYFPELINE GOYFPELINE THOUGHDES HTVLINGUES ELITINIVES FLEMMARIL PROMIEDE I TOM MUCHAL ANTOGEN ANTAGEN	11 LILAREPED INSTRUCTIVE INSTRUCTIVE SUPPLIES SU	AKREPHOVLG VLTSDESALV VLTSDESALV VLTSDESALV VLTSDESALV VLTSDESALV VLTSDESALV IMPOVLHDS GEOPPPPPPP VLTSDESALV IMPOVLHDS GEOPPPPPPP VLTSDESALV IMPOVLHDS GEOPPPPPPP VLTSDESALV IMPOVLHDS GEOPPPPPPP VLTSDESALV IMPOVLHDS GEOPPPPPPP VLTSDESALV IMPOVLHDS GEOPPPPPP VLTSDESALV IMPOVLHDS GEOPPPPP VLTSDESALV IMPOVLHDS GEOPPPP CANCELL TOCKITAT GEOPPPP CANCELL TOCKITAT GEOPPP C	11 INENPRAYME GRAITFANT SERVICE SERVIC	INGLININS DI PPRODUZIONI DI PPRODUZIONI DI PPRODUZIONI DI PPRODUZIONI DI PPRODUZIONI DI PPRODUZIONI DI PRODUZIONI	I UNIVERSITY AND A CONTROL OF THE ACT OF THE	120 240 360 360 420 480 540 120 180 220 180 200 360 360 660 660 660 660 660 660 660 6

		TGAAATGACT					1560
		GAGGCCATGC					1620
		TGACAAGTTC					1680
_		GAAGCAAGAG					1740
5		TGAGGCTGTC					1800
		GGAAGTCTGC					1860
	CTGCTTTGGG	AGTTTAAATT	ACTTCAGGGG	AAGAGAAGAC	AAAACGAGTC	TTTCATTCGG	1920
	TGTGAACTTT	TCTCTTTAAT	TTTAACTGAT	TTAACACTTT	TTGTGAATTA	ATGAAATGAT	1980
• •	AAAGACTTTT	ATGTGAGATT	TCCTTATCAC	AGAAATAAAA	TATCTCCAAA	TG	

AAAGACITTI ATGTGAGATT TECTTATCAC AG Seq ID NO: 385 Protein sequence Protein Accession #: NP_001125

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1.5	1	11	21	31	41	51	
15	l		1	l .	1		
	MKWVESIFLI	FLLNFTESRT	LHRNEYGIAS	ILDSYQCTAE	ISLADLATIF	FAQFVQEATY	60
	KEVSKMVKDA	LTAIEKPTGD	EQSSGCLENQ	LPAPLEELCH	EKEILEKYGH	SDCCSQSEEG	120
	RHNCFLAHKK	PTPASIPLFQ	VPEPVTSCEA	YEEDRETPMN	KPIYEIARRH	PPLYAPTILL	180
	WAARYDKIIP	SCCKAENAVE	CFOTKAATVT	KELRESSLLN	QHACAVMKNF	GTRTFQAITV	240
20	TKLSOKFTKV	NPTEIOKLVL	DVAHVHEHCC	RGDVLDCLQD	GEKIMSYICS	QQDTLSNKIT	300
	ECCKLTTLER	GOCITHAEND	EKPEGLSPNL	NRFLGDRDFN	QFSSGEKNIF	LASFVHEYSR	360
	RHPOLAVSVI	LRVAKGYOEL	LEKCFOTENP	LECODKGEEE	LOKYTOESOA	LAKRSCGLFQ	420
	KLGEYYLONA	FLVAYTKKAP	OLTSSELMAI	TRKMAATAAT	CCQLSEDKLL	ACGEGAADII	480
	TOHI-CTRHEM	TPVNPGVGOC	CTSSYANRRP	CFSSLVVDET	YVPPAFSDDK	FIFHKDLCOA	540
25		EFLINLVKQK					600

Seq ID NO: 386 DNA sequence Nucleic Acid Accession #: NM_002205.1

		386 DNA sec					
20		id Accession		205.1			
30	Coding sequ	uence: 131	149				
	1	11	21	31	41	51	
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	ATGGGGAGCC	GGACGCCAGA	GTCCCCTCTC	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
35	CGCCGACCCC	CGCTSSTGCC	GCTGCTGTTG	CTGCTSSTGC	CGCCGCCACC	CAGGGTCGGG	120
-	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCCGGG	CICCITCTIC	180
	GGCLICANCI	TGGAGTTTTA	COCCCCCCCCC	ACAGACOGGG	TCACTGTGCT	GGTGGGAGCA	240
	CONTICIONS	ATACCAGCCA	CCGGCCGGGA	CTCCACCCTC	GTYCOTOTOTA	COTOTOTOCT	300
		GCCCCACACA					360
40	TGGGGTGCCA	CACTGTCCAG	GIGCACCCCC	ATTGAATTTG	MCAGCADOIGG	CICICOGCIC	420
40	CIGGAGICCI	CACTGTCCAG	CTCAGAGGGA	GAGGAGCCIG	TOGAGTACAA	GICCIIGCAG	480
	TGGTTCGGGG	CAACAGTTCG	AGCCCATGGC	TUCTUCATUT	TGGCATGCGC	TCCACTGTAC	540
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	600
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTCAG	CTGGGCAGCA	
40	GGACAGGGTT	ACTGCCAAGG	AGGCTTCAGT	GCCGAGTTCA	CCAAGACTGG	CCGTGTGGTT	660
45	TTAGGTGGAC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGTCTGCCAC	TCAGGAGCAG	720
	ATTGCAGAAT	CTTATTACCC	CGAGTACCTG	ATCAACCTGG	TTCAGGGGCA	GCTGCAGACT	780
	CGCCAGGCCA	GTTCCATCTA	TGATGACAGC	TACCTAGGAT	ACTCTGTGGC	TGTTGGTGAA	840
	TTCAGTGGTG	ATGACACAGA	AGACTTTGTT	GCTGGTGTGC	CCAAAGGGAA	CCTCACTTAC	900
	GGCTATGTCA	CCATCCTTAA	TGGCTCAGAC	ATTCGATCCC	TCTACAACTT	CTCAGGGGAA	960
50	CAGATGGCCT	CCTACTTTGG	CTATGCAGTG	GCCGCCACAG	ACGTCAATGG	GGACGGGCTG	1020
	GATGACTTGC	TGGTGGGGGC	ACCCCTGCTC	ATGGATCGGA	CCCCTGACGG	GCGGCCTCAG	1080
	GAGGTGGGCA	GGGTCTACGT	CTACCTGCAG	CACCCAGCCG	GCATAGAGCC	CACGCCCACC	1140
	CHARGO COCCUCA	CTGGCCATGA	TONCETTORC	CCATTTCCCA	CCTCCTTGAC	CCCCCTGGGG	1200
		AGGATGGCTA					1260
55		TAGTGTTTGT					1320
55		AGCCCCTGTG					1380
	CAGGTTCTGC	AGCCCCTGTG	GGCAGCCAGC	CACACCCCAG	ACTICITIGG	CICIGCCCII	1440
	CGAGGAGGCC	GAGACCTGGA	TGGCAATGGA	TATCCTGATC	TGATTGTGGG	GICCITIGGI	
	GTGGACAAGG	CTGTGGTATA	CAGGGGCCGC	CCCATCGTGT	CCGCTAGTGC	CTCCCTCACC	1500
	ATCTTCCCCG	CCATGTTCAA	CCCAGAGGAG	CGGAGCTGCA	GCTTAGAGGG	GAACCCTGTG	1560
60	GCCTGCATCA	ACCITAGCTT	CTGCCTCAAT	GCTTCTGGAA	AACACGTTGC	TGACTCCATT	1620
	GGTTTCACAG	TGGAACTTCA	GCTGGACTGG	CAGAAGCAGA	AGGGAGGGGT	ACGGCGGGCA	1680
	CIGITCCIGG	CCTCCAGGCA	GGCAACCCTG	ACCCAGACCC	TGCTCATCCA	GAATGGGGCT	1740
	CGAGAGGATT	GCAGAGAGAT	GAAGATCTAC	CTCAGGAACG	AGTCAGAATT	TCGAGACAAA	1800
	CTCTCGCCGA	TTCACATCGC	TCTCAACTTC	TCCTTGGACC	CCCAAGCCCC	AGTGGACAGC	1860
65		GGCCAGCCCT					1920
00		ACTGTGGAGA					1980
		ACCATGTGTA					2040
	COCOMICAGA	GTGAGGGTGG	CCIGGGIGAC	CONTRACTOR	GGGTCACCGC	CCCTCCAGAG	2100
	CAGAGIGIGG	CAGGACTCGT	COCCIAIGAG	CCCONGCTTC	CCACCOC	COCTCOMO	2160
70	GCTGAGTACT	CAGGACTCGT	CHURCHCCCA	GGGMACTICI	CONSCCIONS	CIGIGACIAC	2220
70	TTTGCCCTGA	ACCAGAGCCG	CCTGCTGGTG	TGTGACCTGG	GCAACCCCAT	GAAGGCAGGA	2280
	GCCAGTCTGT	GGGGTGGCCT	TCGGTTTACA	GTCCCTCATC	TCCGGGACAC	TAAGAAAACC	
	ATCCAGTTTG	ACTTCCAGAT	CCTCAGCAAG	AATCTCAACA	ACTCGCAAAG	CGACGTGGTT	2340
	TCCTTTCGGC	TCTCCGTGGA	GGCTCAGGCC	CAGGTCACCC	TGAACGGTGT	CTCCAAGCCT	2400
	GAGGCAGTGC	TATTCCCAGT	AAGCGACTGG	CATCCCCGAG	ACCAGCCTCA	GAAGGAGGAG	2460
75	GACCTGGGAC	CTGCTGTCCA	CCATGTCTAT	GAGCTCATCA	ACCAAGGCCC	CAGCTCCATT	2520
	AGCCAGGGTG	TGCTGGAACT	CAGCTGTCCC	CAGGCTCTGG	AAGGTCAGCA	GCTCCTATAT	2580
	GTGACCAGAG	TTACGGGACT	CAACTGCACC	ACCAATCACC	CCATTAACCC	AAAGGGCCTG	2640
	CACTTGGATC	CCGAGGGTTC	CCTGCACCAC	CAGCAAAAAC	GGGAAGCTCC	AAGCCGCAGC	2700
	TOTAL CONTOCAL	CGGGACCTCA	GATCCTGAAA	TOCCCGGAGG	CTGAGTGTTT	CAGGCTGCGC	2760
80	TOTALICATION	GGCCCCTGCA	DADAGAGAG	AGCCAAAGTC	TGCAGTTGCA	TTTCCGAGTC	2820
00	TGTGAGCTCG	CTTTCTTGCA	CONCARGAG	CACCCAMOTO	COCONCINC	TATACCCONCIC	2880
	TOUGCCINGA	TGAAGATGCC	GCGGGRGCAC	CHICCHITTA	accidential a	10AGGCIGIG	2940
							3000
	CAGGTGGCCA	CAGCTGTGCA	AIGGACUAAG	GCAUNUGGCA	GCTATGGCGT	CCCACTGTGG	
85		TAGCCATCCT					3060
ده		GATTCTTCAA		CCATATGGCA	CCGCCATGGA	AAAAGCTCAG	3120
	CTCAAGCCTC	CAGCCACCTC	TGATGCCTGA				

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Seq ID NO: 387 Protein sequence Protein Accession #: NP 002196.1

	Protein Acc	ession #: N	IP_002196.1				
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	MGSRTPESPL	HAVQLRWGPR TDGVSVLVGA	RRPPLLPLLL	LUCCAVAICA	WCASPTOCTP	TEFDSKGSRI.	120
	LESSLSSSEG	EEPVEYKSLQ	WFGATVRAHG	SSILACAPLY	SWRTEKEPLS	DPVGTCYLST	180
10	DNFTRILEYA	PCRSDPSWAA 'INLVQGQLQT	GQGYCQGGFS	AEPTKTGRVV	LGGPGSYFWQ	GQILSATQEQ	300
	GYVTIINGSD	IRSLYNFSGE	OMASYFGYAV	AATDVNGDGL	DDLLVGAPLL	MORTPOGRPO	360
	EVGRVYVYLQ	IRSLYNFSGE HPAGIEPTPT	LTLTGHDEFG	RFGSSLTPLG	DLDQDGYNDV	AIGAPFGGET	420
15	QQGVVFVPPG	GPGGLGSKPS PIVSASASLT	QVLQPLWAAS	HTPDPPGSAL	RGGRDLDGNG	YPDLIVGSFG	480 540
13	GPTVELOLDW	OKOKGGVRRA	LPLASROATL	TOTLLIQUE	REDCREMKIY	LRNESEFRDK	600
	LSPIHIALNP	SLDPQAPVDS	HGLRPALHYQ	SKSRIEDKAQ	ILLDCGEDNI	LRNESEFRDK CVPDLQLEVP	660
	GEONHVYLGD	KNALNLTPHA CDLGNPMKAG	QNVGEGGAYE	AELRVTAPPE	AEYSGLVRHP	GNFSSLSCDY NI.NIN COCRUV	720 780
20	SPRLSVEAGA	QVTLNGVSKP QALEGQQLLY	EAVLPPVSDW	HPRDQPQKEE	DLGPAVHHVY	ELINQGPSSI	840
	SOGVLELSCP	QALEGQQLLY	VTRVTGLNCT	TNHPINPKGL	ELDPEGSLHH	QQKREAPSRS	900
	SASSGPQILK	CPEAECFRLR LPRQLPQKER	CELGPLHQQE	SQSLQLHFRV	WAKTPLOREH	QPPSLQCEAV	960 1020
	YKLGPPKRSL	PYGTAMEKAQ	LKPPATSDA	ADDD TO TELL	11120112102	DDDODDITTO	
25							
	Nucleic Ac	388 DNA sec id Accession Lence: 261	1 #1 NM_002	1425			
30	1	11	21	31	41	51	
	1	1	1			1	60
	AAAGAAGGTA	AGGGCAGTGA GCCTATCCTC	GAATGATGCA	AGCARAGAG	GAGGACTCCA	ACAAGGATCT	120
0.5	TGCCCAGCAA	TACCTAGAAA	AGTACTACAA	CCTCGAAAAG	GATGTGAAAC	AGTTTAGAAG	180
35	AAAGGACAGT	AATCTCATTG AAGCTAGACA	TTAAAAAAAT	CCAAGGAATG	CAGAAGTTCC	TTGGGTTGGA	240 300
	TCCTGACGCTT	GGTCACTTCA	GCTCCTTTCC	TGGCATGCCG	AAGTGGAGGA	AAACCCACCT	360
	TACATACAGG	ATTGTGAATT	ATACACCAGA	TTTGCCAAGA	GATGCTGTTG	ATTCTGCCAT	420
40	TGAGAAAGCT	CTGAAAGTCT	GGGAAGAGGT	GACTCCACTC	CATGGAGACT	TTTACTCTTT	480 540
-10	TGATGGCCCA	GATATAATGA GGACACAGTT	TGGCTCATGC	CTACCCACCT	GGACCTGGGC	TTTATGGAGA	600
							660 720
	TTTGATGTAC	CATGAACTTG CCACTCTACA GGCATTCAGT	ACTCATTCAC	AGAGCTCGCC	CAGTTCCGCC	TTTCGCAAGA	780
45	TGATGTGAAT	GGCATTCAGT	CTCTCTACGG	ACCTCCCCCT	GCCTCTACTG	AGGAACCCCT	840
							900 960
	TTGGCGAAGA	GCCATCAGCA TCCCACTGGA	ACCCTGAACC	TGAATTTCAT	TTGATTTCTG	CATTTTGGCC	1020
60	CTCTCTTCCA	TCATATTTGG	ATGCTGCATA	TGAAGTTAAC	AGCAGGGACA	CCGFFFFFAT	1080
50	TTTTAAAGGA	AATGAGTTCT	GGGCCATCAG	AGGAAATGAG	GTACAAGCAG	CTGTTTCTGA	1140 1200
	CAAGGAAAAG	ACCCTGGGTT AAGAAAACAT	ACTTCTTTGC	AGCGGACAAA	TACTGGAGAT	TTGATGAAAA	1260
	TAGCCAGTCC	ATGGAGCAAG GATGCTGTAT	CCTTCCCTAG	ACTAATAGCT	GATGACTTTC	CAGGAGTTGA	1320 1380
55	ACACTTTGAG	TTTGACCCCA	ATCCCAGGAT	GGTGACACAC	ATATTAAAGA	GTAACAGCTG	1440
	GTTACATTGC	TAGGCGAGAT	AGGGGGAAGA	CAGATATGGG	TGTTTTTAAT	AAATCTAATA	1500
	ATTATTCATC	TAATGTATTA	TGAGCCAAAA	TGGTTAATTT	GAATGTTTCT	GGAATTCTTC	1560 1620
	ACTTGCTTTT	AGCCTTGCAG GAATTGCACT ATAGATGTGT	GAACAGAATT	AAGAAATACT	CATGTGCAAT	AGGTGAGAGA	1680
60	ATGTATTTC	ATAGATGTGT	TATTACTTCC	TCAATAAAAA	GTTTTATTTT	GGGCCTGTTC	1740
	CTT						
		389 Protein					
65	Protein Ace	cession #: 1	NP_002416				
	1	11	21	31	41	51	
	MILL PET MITC	LPVCSAYPLS	CAAVEDDENK	DI-MOOVI-EKY	ANT EKDAKOB	PREDSNITTUK	60
	PTO/MOVETA	LEWINGKI DED	TI. PIMPKOPC	CAMBUAGES	PROMPKWPKT	HIJTYRIVNYT	120
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	PTELACPRIS	QDDVNGIQSL	YGPPPASTEE	PLVPTKSVPS	GSEMPAKCOP	ALSFDAISTL	300
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	CAGTCCAGCA	TCTTCGGCGC	CTTCGTGGTC	TACCTCGTGG	TCCTGCTCTC	CGTAGCCTTC	720 780
40	ATGTGCTGGA	ACATGATGCA CGCAGCTGAG	GAAGTCCGAG	AGGGAAGAGA	GCAGGACCGC	CAGGAGGCAG	840
40	ACCATCATCT	TCCTGAGGCT TCATGGCTGC	GATTGTTGTG	ACATTGGCCG	TATGCTGGAT	GCCCAACCAG	900
	ATTCGGAGGA	TCATGGCTGC	GGCCAAACCC	AAGCACGACT	GGACGAGGTC	CTACTTCCGG	960 1020
	GCGTACATGA	TCCTCCTCCC	CTTCTCGGAG	ACGTTTTTCT	TOTTCGTGCA	GGTCATCAAC	1080
45	TGCCGCCTGT	CGCTGCAGCA	CGCCAACCAC	GAGAAGCGCC	TGCGCGTACA	TGCGCACTCC	1140
							1200
	TCTGCAAGGA	GAACTGAGAA AGTCATTGAG	GATTTTCTTA	AGCACTTTTC	AGAGCGAGGC	GAAACCAGCC	1320
	AATTCTGCTG	CAGAGAATGG	TTTTCAGGAG	CATGAAGTTT	GA		
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	Seq ID NO:	ession #: 1	in sequence				
	Processi Act	Leberon W.	_				
55	1	11	21	31	41	51	
22	WA COST DOOD	CSQIIDHSHV	DEFEVATURE	TTITIVVITT	PVMGLLGNSV	TIRVTOVLOK	60
	KOVLOKRVTD	HMVST-ACSDT	LVFLIGMPME	FYSIIWNPLT	TSSYTLSCKL	HTFLFEACSY	120
	ATLLHVLTLS	FERYIAICHP	FRYKAVSGPC	QVKLLIGFVW	VTSALVALPL	LFAMGTEYPL	180 240
60		CNRSSTRHHE KSQKGSLAGG					300
00	TERTMANAVE	KHDWTRSYFR	AYMILLPESE	TPPYLSSVIN	PLLYTYSSOO	PRRVFVQVLC	360
	CRLSLOHANH	EKRLRVHAHS	TTDSARFVQR	PLLFASRRQS	SARRTEKIFL	STFQSEABPQ	420
	SKSÖSPSPER	LEPNSGAKPA	NSAAENGFQB	HEV			
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	AACAGAACTG	CAACGGAGAG	ACTCAAGATG	ATTCCCTTTT	TACCCATGTT	TTCTCTACTA	60 120
	TTGCTGCTTA	TTGTTAACCC	TATAAACGCC	AACAATCATT	CCCTTCAACA	CATTTTTGGGC	180
	ACCADADAGA	AATACTTCAG	CACTTGTAAG	AACTGGTATA	AAAAGTCCAT	CTGTGGACAG	240
75	ANALOGACTO	TTTTATATGA	ATGTTGCCCT	GGTTATATGA	GAATGGAAGG	AATGAAAGGC	300
	WCCCCAGCAG	TTTWOCKERT	TOROVATOTT	TATGGCACTC	TOGGCATCGT	GGGAGCCACC	360 420
							480
	GGTTTTGGAGA	GCAACGTGAA	TGTTGAATTA	CTGAATGCTT	TACATAGTCA	CATGATTAAT	540
80	TOTAGOGA	TGACCAAGGA	CTTAAAAAAAT	GGCATGATTA	TTCCTTCAAT	GTATAACAAT	600 660
	ATCCATCCCA	ACCAGATTGC	AACAAATGGT	GTTGTCCATG	TCATTGACCG	TGCTCGAATC TGTGCTTACA	720
	CAAATTGGTA	CCTCAATTCA	AGACTTCATT	GAAGCAGAAG	ATGACCTITC	ATCTTTTAGA	780
~-	GCAGCTGCCA	TCACATCGGA	CATATTGGAG	GCCCTTGGAA	GAGACGGTCA	CTTCACACTC	840
85	THEFT	CCAATGAGGC	TTTTGAGAAA	CTTCCACGAG	GTGTCCTAGA	AAGGTTCATG	900 960
	TOTGAGTOTA	TTATGGGAGG	AGCAGTCTTT	GAGACGCTGG	AAGGAAATAC	TCTCCAGTGT AATTGAGATA	1020

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	GGATGTGACG	GTGACAGTAT	AACAGTAAAT	GGAATCAAAA	TGGTGAACAA	AAAGGATATT	1080
	GTGACAAATA	ATGGTGTGAT	CCATTTGATT	GATCAGGTCC	TAATTCCTGA	TTCTGCCAAA	1140
	CAAGTTATTG	AGCTGGCTGG	AAAACAGCAA	ACCACCTTCA	CGGATCTTGT	GGCCCAATTA	1200
							1260
5	CCATTTTCTC	ATGATACTCT AAGTAAAAGT	CACCATGGTT	CAGOGGCCTCC	TTAAATTAAT	TCTGCAGAAT	1320
-	CACAMAMMCA	AACTAAAACT	TOCCCTTAAT	GAGCTTTACA	ACCIGICADAT	ACTGGAAACC	1380
	-moogragga	AACAGCTCAG	ACTICUTA	TATOGTACAG	CTCTCTCCAT	TORRESTTOR	1440
	MICCOMMODICA	AAGGGAGTAA	CCTACCCACA	**CCCCCCCC	TTCACATATT	COGCGAGATO	1500
	TGCATGGAGA	CAGAGAAATC	CONCONON	AACCOOLOCOA	BACATRACCO	CTTTACCACC	1560
10	ATCAAGCCAG	TACTTGAAGC	CCICOTION	ANGI INVOICE	manananana	TOCAL CASC	1620
10	TTCCTCAGCC	TACTIGAAGC	TGCAGACTTG	AAAGAGCICC	TONCHCANCE	1004040100	1680
	ACATTATTTG	TGCCAACCAA	TGATGCTTTT	ANGGGAATGA	CIAGIOAAGA	A OCT CCT CTT	1740
	CTGATACGGG	ACAAAAATGC	TCTTCAAAAC	ATCATTCTTT	ATCACCTGAC	ACCAGGAGTT	
	TTCATTGGAA	ACAAAAATGC AAGGATTTGA	ACCTGGTGTT	ACTAACATTT	TAAAGACCAC	ACAAGGAAGC	1800
							1860
15	TCTGACATCA	TGACAACAAA	TGGTGTAATT	CATGITGTAG	ATAAACTCCT	CTATCCAGCA	1920
	GACACACCTG	TGACAACAAA TTGGAAATGA	TCAACTGCTG	GAAATACTTA	TAATTAAT	CAAATACATC	1980
	CAAATTAAGT	TTGTTCGTGG	TAGCACCTTC	AAAGAAATCC	CCGTGACTGT	CTATACAACT	2040
	AAAATTATAA	CCAAAGTTGT	GGAACCAAAA	ATTAAAGTGA	TTGAAGGCAG	TCTTCAGCCT	2100
	ATTATCABAA	CTGAAGGACC	CACACTABCA	AAAGTCAAAA	TTGAAGGTGA	ACCTGAATTC	2160
20	AGACTGATTA	AAGAAGGTGA	AACAATAACT	GAAGTGATCC	ATGGAGAGCC	AATTATTAAA	2220
	AAATACACCA	AAATCATTGA	TYPEACTECCT	GTGGAAATAA	CTGAAAAAGA	GACACGAGAA	2280
	CALCOLATICA	TTACAGGTCC	TCARATARA	TACACTAGGA	TTTCTACTGG	AGGTGGAGAA	2340
	ACACTACE A	CTCTGAAGAA	ATTOTACAA	CARCACCTCA	CCAAGCTCAC	CAAATTCATT	2400
	ACAGAAGAAA	ATGGTCATTT	ATTOTTACAA	CAACAAATTA	ANACACTOCT	TCAGGGAGAC	2460
25	GAAGGTGGTG	ATGGTCATTI	ATTIGORDAL	BARGETCARC	CONTORTACABO	ACCATTARGE	2520
23	ACACCCGTGA	GGAAGTTGCA CTCAGTGAAA	AGCCAACAAA	WOWII COM	OT ICINGHAG	ACCCEARCEC	2580
	GAAGGTCGTT	CTCAGTGAAA	ATCCAMANC	Chighwood	TOTTTALACA	ACCCIANGIC	2640
	AATAACCTGA	CCTTAGAAAA	TTGTGAGAGC	CAAGTTGACT	TCAGGAACIG	AAACATCAGC	
	ACAAAGAAGC	AATCATCAAA	TAATTCTGAA	CACAAATTTA	ATATTTTTT	TICIGAATGA	2700
20	GAAACATGAG	AATCATCAAA GGAAATTGTG	GAGTTAGCCT	CCTGTGGTAA	AGGAATTGAA	GAAAATATAA	2760
30	CACCTTACAC	CCTTTTTCAT	CTTGACATTA	AAAGTTCTGG	CTAACTTTGG	AATCCATTAG	2820
	AGAAAAATCC	TTGTCACCAG	ATTCATTACA	ATTCAAATCG	AAGAGTTGTG	AACTGTTATC	2880
	CCATTGAAAA	TTGTCACCAG GACCGAGCCT	TGTATGTATG	TTATGGATAC	ATAAAATGCA	CGCAAGCCAT	2940
							3000
							3060
35	CAACTAATTT	TIGCACATTT TGTACTCTCA TTCAATAAAA	GAATGTTTGT	CATATGCTTC	TTGCAATGCA	TATTTTTTAA	3120
	TOTORAROUT	TTCBATABAA	CCATTTTTCA	GATATAAAGA	GAATTACTTC	AAATTGAGTA	3180
	ATTCAGAAAA	ACTCAAGATT	TAAGTTAAAA	AGTGGTTTGG	ACTTGGGAA		
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45	 MIPFLPMFSL	LIGHTUNDIN	ANNHVOKTLA	HSR I RGRDOG	PNVCALOOII.	GTKKKYFSTC	
45	ROMARKSTOG	PPPPIANDIN	ANNHYDKILA PGYMRMEGMK	HSRIRGRDQG GCPAVLPIDH	PNVCALQQIL VYGTLGIVGA	GTKKKYFSTC TTTORYSDAS	120
45	KNWYKKSICG KLREEIEGKG	LLLLIVNPIN QKTTVLYECC SFTYFAPSNE	ANNHYDKILA PGYMRMEGMK AWDNLDSDIR	HSRIRGRDQG GCPAVLPIDH RGLESNVNVE	PNVCALQQIL VYGTLGIVGA LLNALHSHMI	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK	120 180
45	KNWYKKSICG KLREEIEGKG	LLLLIVNPIN QKTTVLYECC SFTYFAPSNE	ANNHYDKILA PGYMRMEGMK AWDNLDSDIR NGWYTWACAR	ESRIRGRDQG GCPAVLPIDH RGLESNVNVE	PNVCALQQIL VYGTLGIVGA LLNALHSHMI GVVHVIDRVL	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK TOIGTSIODF	120 180 240
45	KNWYKKSICG KLREBIEGKG NGMIIPSMYN IBABDDLGGF	LLLLIVNPIN QKTTVLYECC SFTYFAPSNE NLGLFINHYP RAAAITSDIL	ANNHYDKILA PGYMRMEGMK AWDNLDSDIR NGVVTVNCAR EALGRIGHFT	ESRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LPAPTNEAFE	PNVCALQQIL VYGTLGIVGA LLNALHSHMI GVVHVIDRVL KLPRGVLBRF	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK TQIGTSIQDF MGDKVASEAL	120 180 240 300
	KNWYKKSICG KLREBIEGKG NGMIIPSMYN IBAEDDLSSF	LLLLIVNPIN QKTTVLYBCC SFTYPAPSNB NLGLFINHYP RAAAITSDIL	ANNHYDKILA PGYMRMEGMK ANDNLDSDIR NGVVTVNCAR EALGROGHFT	HSRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LFAPTNEAFE	PNVCALQQIL VYGTLGIVGA LLNALHSHMI GVVHVIDRVL KLPRGVLBRF NGIKMUNKKO	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK TQIGTSIQDF MGDKVASEAL LUTNNGVIHL	120 180 240 300 360
45 50	KNWYKKSICG KLREBIEGKG NGMIIPSMYN IBAEDDLSSF	LLLLIVNPIN QKTTVLYBCC SFTYPAPSNB NLGLFINHYP RAAAITSDIL	ANNHYDKILA PGYMRMEGMK ANDNLDSDIR NGVVTVNCAR EALGROGHFT	HSRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LFAPTNBAFE	PNVCALQQIL VYGTLGIVGA LLNALHSHMI GVVHVIDRVL KLPRGVLBRF NGIKMUNKKO	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK TQIGTSIQDF MGDKVASEAL LUTNNGVIHL	120 180 240 300 360 420
	KNNYKKSICG KLREBIEGKG NGMIIPSMYN IBAEDDLGSF MKYHILNTLQ IDQVLIPDSA	LLLLIVNPIN QKTTVLYECC SFTYFAPSNE NLGLFINHYP RAAAITSDIL CSESIMGGAV KQVIELAGKQ	ANNHYDKILA PGYMRMEGMK AWDNLDSDIR NGVVTVNCAR EALGRDGHFT FETLEGNTIE QTTFTDLVAQ NELVWGOTLE	HSRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LPAPTNEAFE IGCDGDSITV LGLASALRPD TIGGKOLBVE	PNVCALQQIL VYGTLGIVGA LLNALHSHMI GVVHVIDRVL KLPRGVLERF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKOG	120 180 240 300 360 420 480
	KNNYKKSICG KLREBIEGKG NGMIIPSMYN IBAEDDLGSF MKYHILNTLQ IDQVLIPDSA	LLLLIVNPIN QKTTVLYECC SFTYFAPSNE NLGLFINHYP RAAAITSDIL CSESIMGGAV KQVIELAGKQ	ANNHYDKILA PGYMRMEGMK AWDNLDSDIR NGVVTVNCAR EALGRDGHFT FETLEGNTIE QTTFTDLVAQ NELVWGOTLE	HSRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LPAPTNEAFE IGCDGDSITV LGLASALRPD TIGGKOLBVE	PNVCALQQIL VYGTLGIVGA LLNALHSHMI GVVHVIDRVL KLPRGVLERF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKOG	120 180 240 300 360 420 480 540
	KNWYKKSICG RLREBIEGKG NGWIIPSMYN IBAEDDL6SF MKYHILNTLQ IDQVLIPDSA VQRLLKLILQ RNGAIHIEG FKGWTSBEKB	LLLLIVNPIN QKTTVLYECC SFTYPAPSNE NLGLFINHYP RAAAITSDIL CSESIMGGAV KQVIELAGKQ NHILKVKVGL IIKPAEKSLI LITRAEKSLI LITRAKNALO	ANNHYDKILA PGYMRMEGMK AMDNLDSDIR NGVVTVNCAR EALGRIGHFT FETLEGNTIE QTTFTDLVAQ NELYNGQILB EKLKQDKRFS NILLYHLTPG	ESRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LPAPTNEAFE IGCDGDSITV LGLASALRPD TIGGKQLRVF TPLSLLEAAD VPIGKGFEPG	PNVCALQQIL VYGTLGIVGA LLNALHSHMI GVVHVIDRVL KLPRGVLBRI NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKELLTQPGD VTNILKTTQG	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVPTNDA SKIFLKEVND	120 180 240 300 360 420 480 540
50	KOMYKKSICG KLREBIEGKG NGMIIPSMYM IBAEDDLGSF MKYHLLNTLQ IDQVLIPDSA VQRLLKLILQ RNGAIHIFRE FKGWTSEEKE TLLWELKSK	LLLLIVNPIN QKTTVLYECC SPTYPAPSNE NLGLFINHYP RAAAITSDIL CSESIMGGAV KQVIELAGKQ NHILKVKVGL IIRPAEKSLH ILLROKNALH ESDIMTTNGV	ANNHYDKILA PGYMRMEGMK ANDNLDSDIR NGVVTVNCAR EALGRDGHFT PETLEGNTIE OTTFTDLVAQ NELYNGQILE EKLKQDKRFS NIILYHLTPG HHVVDKLLYP	ESRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LPAPTNEAFE IGCDGDSITV LGLASALRPD TIGGKQLRVF TPLSILEAAD VPIGKGFEPG ADTPYGNDOL	PNVCALQQIL PNVCALQQIL VYGTLGIVGA LLNALHSHMI GVVHVIDRVL KLPRGVLBRF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKRILITQPGD VTNILKTTQG UTNILKTTQG LEILNKLIKY	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVPTNDA SKIFLKEVND IQIKFVRGST	120 180 240 300 360 420 480 540 600 660
50	KOMYKKSICG KLREBIBGKG NGMIIPSMYN IBAEDDL6SF MKYHILNTLQ IDQVLIPDSA VQRLLKLILQ RNGALHIFRB FKGMTSBEKB TLLVMELKSK	LLLLIVNPIN QKTTVLYECC SFTYFAPSNE NLGLFINHYP RAAAITSDIL CSESIMGGAV KQVIELAGKQ NHILKVKVGL IIRPAKSLH ILIRDKNALQ ESDIMTTNGV	ANNHYDKILA ANNHYDKILA PGYMRMEGMK AMDNLDSDIR NGVVTVNCAR EALGRDGHFT FETLEGNTIE QTTFTDLVAQ NELYNGQILE EKLKQDKRFS NIILYHLTPG IHVVDKLLYP	ESRIRGRDQG GCPAVLPIDH RGLESNVNVE I HGNQIATN LPAPTNEAFE IGCDGDSITV LGLASALRPD TIGGKQLRVF TPLSILEAAD VPIGKGFEPG ADTPVGNDQL	PNVCALQQIL VYGTLGIVGA LLNALHSHMI GVVHVIDRVL KLPRGVLBRF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKRILITQPGD VTNILKTTQG LEILNKLIKY KKVKIEGEPE	GTKKKYFSTC TTTQRYSDAS NKRMLTKDLK TQIGTSTQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVPTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI	120 180 240 300 360 420 480 540 600 660 720
	KNYKKSICG KLREEIEGKG NGMIIPSMYN IBAEDDL6SF MKYHILNTLQ IDQVLIPDSA VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVNELKSK FKEIPVTYYT TRVIKGEPII	LLLLIVNPIN QKTTVLYECC SFTYFAPSNE NLGLFINHYP RAAAITSDIL CSESIMGGAV KQVIELAGKO NHLKVKVGL IIRPAEKSLH ILITROKNALQ ESDIMTTNGV TKIITKVUEP KKYTKIUGV	ANNHYDKILA ANNHYDKILA PGYMRMEGMK ANDNILDSDIR NGVVTVNCAR EALGRIDGHFT FETLEGNTIB QTTFTDLVAQ NELYNGQILE EKLKQDKRFS NILLYHLTPG IHVVDKLLYP KIKVIEGSLQ PVBITEKETR	HSRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LPAPTNEAFE IGCDGDSITV LGLASALRPD TIGGKQLRVF TPLSILEAAD VPIGKGFBPG ADTPVGNDQL PII KTEGPTL ERRIITGPEI	PNVCALQQIL VYGTLGIVGA LINALHSHMI GVVHVIDRVL KLPRGVLERF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKLEGEPE KYTRISTGGG	GTKKKYFSTC TTTQRYSDAS NKRMLTEDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVFTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI FRLIKEGETLKKLL	120 180 240 300 360 420 480 540 600 660
50	KNYKKSICG KLREEIEGKG NGMIIPSMYN IBAEDDL6SF MKYHILNTLQ IDQVLIPDSA VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVNELKSK FKEIPVTYYT TRVIKGEPII	LLLLIVNPIN QKTTVLYECC SPTYPAPSNE NLGLFINHYP RAAAITSDIL CSESIMGGAV KQVIELAGKQ NHILKVKVGL IIRPAEKSLH ILLROKNALH ESDIMTTNGV	ANNHYDKILA ANNHYDKILA PGYMRMEGMK ANDNILDSDIR NGVVTVNCAR EALGRIDGHFT FETLEGNTIB QTTFTDLVAQ NELYNGQILE EKLKQDKRFS NILLYHLTPG IHVVDKLLYP KIKVIEGSLQ PVBITEKETR	HSRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LPAPTNEAFE IGCDGDSITV LGLASALRPD TIGGKQLRVF TPLSILEAAD VPIGKGFBPG ADTPVGNDQL PII KTEGPTL ERRIITGPEI	PNVCALQQIL VYGTLGIVGA LINALHSHMI GVVHVIDRVL KLPRGVLERF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKLEGEPE KYTRISTGGG	GTKKKYFSTC TTTQRYSDAS NKRMLTEDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVFTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI FRLIKEGETLKKLL	120 180 240 300 360 420 480 540 600 660 720
50	KNYKKSICG KLREEIEGKG NGMIIPSMYN IBAEDDL6SF MKYHILNTLQ IDQVLIPDSA VQRLLKLILQ RNGAIHIFRE FKGMTSEEKE TLLVNELKSK FKEIPVTYYT TRVIKGEPII	LLLLIVNPIN QKTTVLYECC SFTYFAPSNE NLGLFINHYP RAAAITSDIL CSESIMGGAV KQVIELAGKO NHLKVKVGL IIRPAEKSLH ILITROKNALQ ESDIMTTNGV TKIITKVUEP KKYTKIUGV	ANNHYDKILA ANNHYDKILA PGYMRMEGMK ANDNILDSDIR NGVVTVNCAR EALGRIDGHFT FETLEGNTIB QTTFTDLVAQ NELYNGQILE EKLKQDKRFS NILLYHLTPG IHVVDKLLYP KIKVIEGSLQ PVBITEKETR	HSRIRGRDQG GCPAVLPIDH RGLESNVNVE IIHGNQIATN LPAPTNEAFE IGCDGDSITV LGLASALRPD TIGGKQLRVF TPLSILEAAD VPIGKGFBPG ADTPVGNDQL PII KTEGPTL ERRIITGPEI	PNVCALQQIL VYGTLGIVGA LINALHSHMI GVVHVIDRVL KLPRGVLERF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKLEGEPE KYTRISTGGG	GTKKKYFSTC TTTQRYSDAS NKRMLTEDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVFTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI FRLIKEGETLKKLL	120 180 240 300 360 420 480 540 600 660 720
50 55	KNYKKSICG KLREBIEGKG NGMIIPSMYN IEAEDDLGSF MKYHLIMTLQ IDQVLIPDSA VQRLLKLILQ RNGAIHIFRE FKGMISEEKE FLLVMELKSK FKEIPVTVYT TEVIKGEPII QEEVTKVTKF Seg ID NO:	LLLLIVNPIN QKTTVLYBCC SPTTYAPSNE NIGGFINNYP RAAAITSDIL CSESIMGGA KQVIELAGKQ NHILKYKVGL IIRPARKSLH ILIRDKNALQ TKIITKVVEP KKYYKIIGGV TKIITKVVEP 402 DNA see	ANNHYDKILA PGYMMEGMK ANDMLDSDIR ANUNLDSDIR MGVVTVNCAR EALGREGHFT FFTLEGNTT FFTLEGNTT GTTEFTDLVAQ NELYNGGILE EKLLQDKRFS NIILYHLTPG HVVDKLIT KKVIEGSLQ PVBITEKSTR QUEELKRLLQG	ESRIRGRDQG GCPAVLPIDH RGLESNVAVE IIHGNQIATN LPAPTNEAFE IGCDGDSITU LGLASALRPD TIGGRQIAVF TIGGRGIRVF TPLSILEAAD VPIGKGFBPG ADTPVGNDQL PIINTEGPTL EERIITGPEI DTFVRKLQAN	PNVCALQQIL VYGTLGIVGA LINALHSHMI GVVHVIDRVL KLPRGVLERF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKLEGEPE KYTRISTGGG	GTKKKYFSTC TTTQRYSDAS NKRMLTEDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVFTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI FRLIKEGETLKKLL	120 180 240 300 360 420 480 540 600 660 720
50 55	KNYKKSICG KLREBIEGKG NGMIIPSMYN IEAEDDLGSF MKYHLIMTLQ IDQVLIPDSA VQRLLKLILQ RNGAIHIFRE FKGMISEEKE FLLVMELKSK FKEIPVTVYT TEVIKGEPII QEEVTKVTKF Seg ID NO:	LLLLIVNPIN QKTTVLYBCC SPTTYAPSNE NIGGFINNYP RAAAITSDIL CSESIMGGA KQVIELAGKQ NHILKYKVGL IIRPARKSLH ILIRDKNALQ TKIITKVVEP KKYYKIIGGV TKIITKVVEP 402 DNA see	ANNHYDKILA PGYMMEGMK ANDMLDSDIR ANUNLDSDIR MGVVTVNCAR EALGREGHFT FFTLEGNTT FFTLEGNTT GTTEFTDLVAQ NELYNGGILE EKLLQDKRFS NIILYHLTPG HVVDKLIT KKVIEGSLQ PVBITEKSTR QUEELKRLLQG	ESRIRGRDQG GCPAVLPIDH RGLESNVAVE IIHGNQIATN LPAPTNEAFE IGCDGDSITU LGLASALRPD TIGGRQIAVF TIGGRGIRVF TPLSILEAAD VPIGKGFBPG ADTPVGNDQL PIINTEGPTL EERIITGPEI DTFVRKLQAN	PNVCALQQIL VYGTLGIVGA LINALHSHMI GVVHVIDRVL KLPRGVLERF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKLEGEPE KYTRISTGGG	GTKKKYFSTC TTTQRYSDAS NKRMLTEDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVFTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI FRLIKEGETLKKLL	120 180 240 300 360 420 480 540 600 660 720
50	KNYKKSI CO KLREBIEGKO MGMIIPSMYM IBAEDDLOSF MKYHLINTLQ IDQVLIPDSA VQRLLKILLQ RRQAHIFRE FKGMTSREKE TLLVNELKSK FKEIPVTYT TEVINGEPII QEEVTKVTKP QEEVTKVTKP	ULLLIVNPIN CKTTVLYBCC SFTYFAPSNE NLGUFINNYP RAAAITSDIL CSESIMGGAV KQVTELAGKQ NHILKVKVGL IIKPAEKSLH ILIBEKNALQ ESDIMTTNGV TKLITKVEVE KKYTKIIGU IEGGDGHLFE	ANNHYDKILA PGYMRMEGMK ANDMLDSDIR RGVVTVNCAR EALGRIGHFT FETLEGNTIE FETLEGNTIE EKIKQOTEP THVTGGILB EKIKQOTEP NILLYHLTPG HIVYDKLLYP VETTEKETR DEEIKRLLQG Quence n 8: NM_000	ESRIRGRDQG GCPAVLPIDH RGLESNVAVE IIHGNQIATN LPAPTNEAFE IGCDGDSITU LGLASALRPD TIGGRQIAVF TIGGRGIRVF TPLSILEAAD VPIGKGFBPG ADTPVGNDQL PIINTEGPTL EERIITGPEI DTFVRKLQAN	PNVCALQQIL VYGTLGIVGA LINALHSHMI GVVHVIDRVL KLPRGVLERF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKLEGEPE KYTRISTGGG	GTKKKYFSTC TTTQRYSDAS NKRMLTEDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVFTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI FRLIKEGETLKKLL	120 180 240 300 360 420 480 540 600 660 720
50 55	KNYKKSI CO KLREBIEGKO MGMIIPSMYM IBAEDDLOSF MKYHLINTLQ IDQVLIPDSA VQRLLKILLQ RRQAHIFRE FKGMTSREKE TLLVNELKSK FKEIPVTYT TEVINGEPII QEEVTKVTKP QEEVTKVTKP	LLLLLVNPIN QKTTVLYEC SPTTFAPSNE NIGGFINTYP RAAAITSDIL CSESIMGGAV KQVIELAGKQ MILKYKVGL IIKPAEKSLE LLIEDKNALQ ESDIMTTNGV TKLITKVGV KKYTKIIGV IEGGGGHLFE 402 DNA see id Accessiouence: 40	ANNHYDKILA PGYMRMEGMK ANDMILGDIR MGVYTVNCAR EALGRIGHFT FETLEGNTIE GTTFTDLVAQ NELYNGQILB EKLKQDKRFS INILYHLTPO INIVUKLIYP KIKVIEGEL PVEITEKETR DEEL KRLLQG QUENCO 18: NM_002 417	HSRIRGRDOG GCPAVLPIDH RGLESNVAVE RGLESNVAVE IHENQIATN LFAPTNRAFE IGCDGDSITV LGLASALRAPD TIGGKQLRVF TFLSLLEAAD VPICKGFBBG ADTPVGNDOL PILTTEGFL EERILTGPEI DTPVRKLQAN	PNVCALQQIL VYGTLGIVGA LLNALHSHMA LLNALHSHMA LLNALHSHMA LLNALHSHMA KLPRAVLERP KUPRAVIEN LKELLTQPGD VYRTAVCIEN LEILIKLIKLIK LKYQG KKVQGSRRRL	GTKKKYFSTC TTTQRYSDAS NKRMLITGLK TQ1GTS1QDF MGDKVASEAL IVINNGVIHL NAFSDDTLSM SCHEKGSKQG WTLFVFNDA SKIFLKEVND 1Q1KFVRGST FRLI KEGET FRLI KEGET BTESTLKKLL REGRSQ	120 180 240 300 360 420 480 540 600 660 720
50 55	KNYKKSI CO KLREBIEGKO MGMIIPSMYM IBAEDDLOSF MKYHLINTLQ IDQVLIPDSA VQRLLKILLQ RRQAHIFRE FKGMTSREKE TLLVNELKSK FKEIPVTYT TEVINGEPII QEEVTKVTKP QEEVTKVTKP	LLLLIVNPIN QKTTVLYBCC SPTYFAPSNE RIGGFINHYP RAAAITSDIL CSESIMGGAV KYVIELAGKQ MHILKVKVGL ILKPAKVGL ILIRPAKSLA	ANNHYDKILA PGYMRMEGMK ANDMLDSDIR RGVVTVNCAR EALGRIGHFT FETLEGNTIE FETLEGNTIE EKIKQOTEP THVTGGILB EKIKQOTEP NILLYHLTPG HIVYDKLLYP VETTEKETR DEEIKRLLQG Quence n 8: NM_000	ESRIRGRDQG GCPAVLPIDH RGLESNVAVE IIHGNQIATN LPAPTNEAFE IGCDGDSITU LGLASALRPD TIGGRQIAVF TIGGRGIRVF TPLSILEAAD VPIGKGFBPG ADTPVGNDQL PIINTEGPTL EERIITGPEI DTFVRKLQAN	PNVCALQQIL VYGTLGIVGA LINALHSHMI GVVHVIDRVL KLPRGVLERF NGIKMVNKKD GEYTLLAPVN VYRTAVCIEN LKELLTQPGD VTNILKTTQG LEILNKLIKY TKVKLEGEPE KYTRISTGGG	GTKKKYFSTC TTTQRYSDAS NKRMLTEDLK TQIGTSIQDF MGDKVASEAL IVTNNGVIHL NAFSDDTLSM SCMEKGSKQG WTLFVFTNDA SKIFLKEVND IQIKFVRGST FRLIKEGETI FRLIKEGETLKKLL	120 180 240 300 360 420 480 540 600 660 720
50 55 60	KNNYKKSICO KLREBIEGKO NOWI PESMN IDOVILPESM VORLLKILLQ RNGALHIFRE FKGMTSEKE TILLVELKSK FKEIPUTYT TEVINGEPII QSEVTKYTKF Seq ID NO: Nucleic Ac. Coding seq	LLLLIVNPIN QKTTVLYEC SPTYFAPSNE NIGGFINTYP RAAAITSDIL CSESIMGGAV KQVIELAGKQ MILKYKVGL IIKPAEKSLE ILIRDKNALQ ESDIMTTNGV TKLITKVVEP KKYTKI IDGV IEGGGGHLFE 402 DNA sei did Accessiouence: 40	ANNHYDKILA PGYMRMEGMK ANDMILGSDIR MGVYTVNCAR EALGRIGHFT FETLEGNTIE GTTFTDLVAQ NELYNGQILB EKLKQDKRFS INILYHLFS INILYHLFS INILYHLFS LHVVDKLLYP KIKVIEGSLQ PVBITEKSTR DEEL RRLLQG QUENCE n 8: NM_00: 417	HSRIRGRDOG GCPAVLPIDH RGLESMAVVE IIHCNQIATN LPAPTNEAFE IGCDGDSITV LGLASALRAPD TIGGRQLRVF TPLSLLEAD ADTPVGNDOL PILTEGPE DTPVRKLQAN 416	PNVCALQQIL VYGTLGIVGA LLNALHSHMI LLNALHSHMI LLNALHSHMI KLPRGVLERF KLPRGVLERF KYRAVCIEN LKELLTQPGG VNTILKTTQG LKILKTQGG KKVQGSRRRL	GTKKKKYFSTC TTTORYSDAS GTKKKKYFSTC TTTORYSDAS NKRMLTRDLK TOIGTSIODF MGDKVASEAL LVTNNGVIHL NAFSDDTLSL SCHEKGSKQG SKIFLKEVND LQIKFFWSD FRLIKEGETI BTEETLKKLL REGRSQ 51	120 180 240 360 420 480 660 720 780
50 55 60	KNNYKKSICO KLREBIEGKO NUMII PSNYM I PAEDDLSSF MKYHILNTLO IDOVLI PSNYM VORLLKLILO RNCALHIRU FKGMISREKE TLLVWELKSK FKEIPVTYT TEVINGEPII GEEVYKVTKP Seq ID NO: Nucleic Ac. Coding sequ	LILLLUNPIN OKTTULYBEN STYPEAPEN STYPEAPEN NIGHPINNYP RAAAITSDIL CSBSIMGGAV RQVIELAGRQ RHILKVKVGL IIRPAEKSLR ILIRDKNALQ ESDIMTTMGV KKITKVVEP KKYYKI IDGV LEGGGGHLFE 402 DNA sei d Accessio uence: 40	ANNHYDKILA PGYMEMENK ANDNIDSDIR NGVYTVNCAR RALARDGHET PETLEGATTE QYTFTDLVAQ NELVNGQILE EKLKQDKEFS IHVVDKLLYP HILYHTPG HEVYDKLLYP PUBLIEKETR DEELKRLLQG QUENCE 4: NM_00:	HSRIRGRDOG GCDAVLPIDH RGLESMAVE I IHGMOIATN LPAPTNBAFE I IGCDGDSITV LGGASALRAPD TIGGRQLRVF TFLSLLBAAD VFICKGFBBG ADTPVGNDQL ERRIITGGEI DTPVRKLQAN 416 31	PNVCALQQIL VYGTLGIVGA LINALHSHMI GVVHVIDRVL KLPRGVLERF NGICHVNKKD GEYTLLAND UYRTAVCIEN LIKELITQEGD VINILIKTIQG LEILINKLIKT KVKIEBEPE KYTHISTGGG KKVQGSRRRL	GTKKKKYFSTC TTYORYSDAS NKRMLTRÜLK TQIOTSIQDP MGDKVASEAL NAPSDDTLSM SCHEKSIKQG WTLFVFTNOA SKIFLKEVMD IQIKFVRGST FRLI KRGETI ETESTLKKLL REGRSQ	120 180 240 360 420 540 600 600 720 780
50 55	KNNYKKSICG KLARBIEGKO KUARBIEGKO NOMITPSWAN TEAREDLASF MKYHILNTLQ LDQVLIPDSA VORLLKLILQ RNGAHIFFSF FKGMTSREKE FKGMTSREKE FKERPTYYT TEVINGSPII QEEVTKVTKF Seq ID NO: Coding sequ ATCCRATACA ATCCRATACA	LILLLIVNPIN OKITVILYBCC SPTYPAPS MIN OKITVILYBCC SPTYPAPS MIN NIGLPINNYP RAAAITSIN CSESIMGGAV OKIVELAGAV OKIVELAGAV OKIVELAGAV OKIVELAGAV OKIT OKIT OKIT OKIT OKIT OKIT OKIT OKIT	ANNHYDKILA PGYMEMENK ANDMLDSDIR RGVWTVNCAR EALGRDGIP FETLEGNTIE QTTFFTDLW RILYHLTPG HVVDKLILY RIKVIEGSL PWEITEKER DEELKRLLQG QUANCO 11 17 21 1 GGAACTCCAT GGAACTCCAT GGCAGGTCTCTG	HSR IRGRDOG GCPAVLPIDH RGLESNUAVE IIHCNOIATH ILPAPTHRAFI IGCDGSITV LGLASALBAD VPICKDFBOG ADTPVGNOG PIIKTEGPFI DTPVRKLQAN 416 31	PNVCALQQIL VYGTLGIVGA LLNALESHIGA GVVHVIDRVL KLPRGVLERF NGIROVENKO GEYTLLAPH VYRTAVCIEN LKELLTOGE VTHILKTTOGE KKVLEGERF KYTHISTEGE KKVQGSRRRL 41 I TGAAGAAAAG AAGGAAAAAG	GTKKKKYFSTC TTTORYSDAS GTKKKKYFSTC TTTORYSDAS NKRMLTRÜLK TOLGTSIODF MGDKVASEAL LVTNNGVIHL NAFSDDTLSK SCHEKGSKQG SKLFLKEVND LQLKFVRGS FRLLKEVND LQLKFVRGS FRLLKEGETI BETESTLKKLL REGRSQ 51	120 180 240 300 360 420 540 600 600 720 780
50 55 60	KNNYKKSICO KLREBIEGKO NUMII PSNYM I PAEDDLGSF MKYHILNTLO I DOVIL IPSNYM VORLLKLILO RNOAIHIPRE TLIVNELKSK FKEIFVTYT TEVINGEPII GEEVYKVTKP Seq ID NO: Nucleic Ac. Coding sequ ACCCAATACA TICCTCTING	LILLIUNPIN (KITVILYEC SPTYPAPSNE NIGUPINNYP RAAAITSIN CSESIMGGAV KYVIELAGKO NHILKVKVGL IIRPARSIL ILIRDKNALQ ESDIMTINGV TKIITKVVEP KYYKIIDF LEGGDGHLFE 402 DNA se- id Accessiouence: 40 11 GGAGTGACCTT GGAGTGACCTT GGATGACCTT GCATCATCTT	ANNHYDKILA PGYMRMENK ANDMLDSDIR MGVVTVNCAR EALGRIGHET FETLEGNTIE QTTFTDLVA NELVNGQILE EKLLQDKLPS NILLYHLTPO KIKVIEGSLQ PVETTEKST DEEL KRLLQG Quence a 8: NM_00: 117 GGAACTCCAT GGGAACTCCAT	ESRIRGRDOG GCPAVLPIDH RGLESNVAVE IHCNOIATH LPAPTHRAFE IGCDGSITV LGLSALRPD LGLSALRPD TIGGRQLRVP TFLSLLEAAD VPICKGFBPG ADTPVGNDQL PIINTEGPFIL DTPVRKLQAN 416 31 TCTATCACTA ATTOGAGIGCT	PNVCALQQIL VYGTLGIVGA LLNALESHMI GVVHVIDRVI KLPRGVLERF NGINVNKKO GEYTLLAPVN VYRTAVCIEN LKELLTOPGD VINILKTYGG LEILNKLIKY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL	GTKKKKYFSTC TTTORYSDAS NKRMLTRÜLK TOIGTSIODF MGDKVASEAL IVINNGVIHL IVINNGVIHL IVINNGVIHL IQIKFVRGST FRLIKEVED SKIFLKEVED SETESTLKKLL REGRSQ 51 I TOGGGTTCTT AGTAGTGAGA	120 180 240 360 420 540 660 720 780
50 55 60	KNNYKKSICO KLREBIEGKO NUMII PSNYM I PAEDDLGSF MKYHILNTLO I DOVIL IPSNYM VORLLKLILO RNOAIHIPRE TLIVNELKSK FKEIFVTYT TEVINGEPII GEEVYKVTKP Seq ID NO: Nucleic Ac. Coding sequ ACCCAATACA TICCTCTING	LILLIUNPIN (KITVILYEC SPTYPAPSNE NIGUPINNYP RAAAITSIN CSESIMGGAV KYVIELAGKO NHILKVKVGL IIRPARSIL ILIRDKNALQ ESDIMTINGV TKIITKVVEP KYYKIIDF LEGGDGHLFE 402 DNA se- id Accessiouence: 40 11 GGAGTGACCTT GGAGTGACCTT GGATGACCTT GCATCATCTT	ANNHYDKILA PGYMRMENK ANDMLDSDIR MGVVTVNCAR EALGRIGHET FETLEGNTIE QTTFTDLVA NELVNGQILE EKLLQDKLPS NILLYHLTPO KIKVIEGSLQ PVETTEKST DEEL KRLLQG Quence a 8: NM_00: 117 GGAACTCCAT GGGAACTCCAT	ESRIRGRDOG GCPAVLPIDH RGLESNVAVE IHCNOIATH LPAPTHRAFE IGCDGSITV LGLSALRPD LGLSALRPD TIGGRQLRVP TFLSLLEAAD VPICKGFBPG ADTPVGNDQL PIINTEGPFIL DTPVRKLQAN 416 31 TCTATCACTA ATTOGAGIGCT	PNVCALQQIL VYGTLGIVGA LLNALESHMI GVVHVIDRVI KLPRGVLERF NGINVNKKO GEYTLLAPVN VYRTAVCIEN LKELLTOPGD VINILKTYGG LEILNKLIKY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL	GTKKKKYFSTC TTTORYSDAS NKRMLTRÜLK TOIGTSIODF MGDKVASEAL IVINNGVIHL IVINNGVIHL IVINNGVIHL IQIKFVRGST FRLIKEVED SKIFLKEVED SETESTLKKLL REGRSQ 51 I TOGGGTTCTT AGTAGTGAGA	120 180 240 360 420 480 540 660 720 780
50 55 60 65	KNNYKKSICO KLREBIEGKO NUMII PSNYM I PAEDDLGSF MKYHILNTLO I DOVIL IPSNYM VORLLKLILO RNOAIHIPRE TLIVNELKSK FKEIFVTYT TEVINGEPII GEEVYKVTKP Seq ID NO: Nucleic Ac. Coding sequ ACCCAATACA TICCTCTING	LILLIUNPIN (KITVILYEC SPTYPAPSNE NIGUPINNYP RAAAITSIN CSESIMGGAV KYVIELAGKO NHILKVKVGL IIRPARSIL ILIRDKNALQ ESDIMTINGV TKIITKVVEP KYYKIIDF LEGGDGHLFE 402 DNA se- id Accessiouence: 40 11 GGAGTGACCTT GGAGTGACCTT GGATGACCTT GCATCATCTT	ANNHYDKILA PGYMRMENK ANDMLDSDIR MGVVTVNCAR EALGRIGHET FETLEGNTIE QTTFTDLVA NELVNGQILE EKLLQDKLPS NILLYHLTPO KIKVIEGSLQ PVETTEKST DEEL KRLLQG Quence a 8: NM_00: 117 GGAACTCCAT GGGAACTCCAT	ESRIRGRDOG GCPAVLPIDH RGLESNVAVE IHCNOIATH LPAPTHRAFE IGCDGSITV LGLSALRPD LGLSALRPD TIGGRQLRVP TFLSILEAAD VPICKGFBPG ADTPVGNOQL PIINTEGPFIL DTPVRKLQAN 416 31 TCTATCACTA ATTOGAGIGCT	PNVCALQQIL VYGTLGIVGA LLNALESHMI GVVHVIDRVI KLPRGVLERF NGINVNKKO GEYTLLAPVN VYRTAVCIEN LKELLTOPGD VINILKTYGG LEILNKLIKY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL	GTKKKKYFSTC TTTORYSDAS NKRMLTRÜLK TOIGTSIODF MGDKVASEAL IVINNGVIHL IVINNGVIHL IVINNGVIHL IQIKFVRGST FRLIKEVED SKIFLKEVED SETESTLKKLL REGRSQ 51 I TOGGGTTCTT AGTAGTGAGA	120 180 240 360 420 540 660 720 780
50 55 60 65	KNNYKKSICO KLREBIEGKO NGWIIPSNYM IEAEDDLGSF MKYHINTLO IDQVLIPDSA VORLLKLILO RNGALHIPSF FKGWITSHEKE FKEIPVTYT TEVINGSPII GEVYKVTKF Seq ID NO. Nucleic Ac. Coding seq 1 ATCCAATACA TTCTCTTMG AAGGOTGGCT GACCTTAACA AAGAGTGGCG	LULLILVAPIN QKTTULVECC STYPEAPS WE STYPEAP	ANNHYDKILA PGYMRMEGHK AUDNINGDSIR NGWYTYMCAR REJARDGHTH FETLEGGTIE GYTFPILVAG NELYNGGILB EKIKGDKRES NILYHLTPG INVOKLIP LUNYKLIP LUNYKLIP LUNYKLIP GENGRICAN LUNYKLIP GENGRICAN LUNYKLIP LUNYKLIP GENGRICAN LUNYKLIP LUNYKLIP GENGRICAN LUNYKLIP LUNYKLIP GENGRICAN LUNYKLIP LUNYKLI LUNYKLIP LUNYKLIP LUNYKLIP LUNYKLIP LUNYKLIP LUNYKL	ERRIRGRDG GCPAVLPIDR GCPAVLPIDR GCJESNOVIE LIHGNGIATN LIHGNGIATN LIHGNGIATN LIHGNGIATN LIHGNGIATN LIHGNGIATN TUGGGGGT TUGGGGGGT TUGGGGGT TUGGGGGT TUGGGGGT TUGGGGGT TUGGGGGT TUGGGGGGG TUGGGGGGGG	PRIVCALQOIL VYGTLGTVGA LINALESHBI GVVHYLORVI KUPRGVLEBI GEYTLLAFW GVSTYLORVI KUPRGVLEBI GEYTLLAFW VYRTAVCI SI LUGSLITQBGI TRVKLBGBEP KKVQGSERRL 41 TGAAGANAAG AAGGAACCCC TTGAAGANAAG	GTKKKYFSTC TTTORYSDAS MINEMITROLI TOTORYSDAS MORDIVASEAL TOTORYSDAS MORDIVASEAL TVINNOYIBL MAPSDOTISM SCIEKKSKQG WILPYPTNOS SKIELLENYM LOUIFFVRST FELLIKSKET FELLIKSKET TESTIKKUL REGRSQ 51 TOTORYSTCTT ACTACTICADA TCCTTCADA TCCTCACACT ACTCACTACAC	120 180 240 360 420 480 540 660 720 780
50 55 60	KNNYKKSICO KLREBIEGKO NGULIFSHIN IEAEDDLSSF MKYHLINTLO INOVLIFDSA MKYHLINTLO RECALLIFES RECALLIFES RECALLIFES RECALLIFES RECALLIFES TELVITYT TEVIMOEPII TOVLIGE ACCITAGA AAGATACAA	LILLLILYNPIN OKTTULVECC SPTYPAPSIN STYPTAPSIN NGBUTUHTP CASSINGAN LIKPARSIA	ANNIYOKILA PGYREMEGHK ANDINLEDEL RAMINLEDEL RAMINLEDEL REALEMICHIE PETLEGITLE CHEFTHOLIC REALEMICHE REALEMICHE REALEMICHE REALEMICHE PUBLISHER REALEMICH PUBLISHER REALEMICH REA	ERRIRORDOG GCPAVLPIDR GCPAVLPIDR GCLESNNYE LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNGIATN L	PRIVCALQOIL VYSTLGTVGA LUNIAISSHI GVVRYIDRI KLINALASSHI GVVRYIDRI KLINALASSHI GETTLLAPVN VYSTLAVCIS LUSILITOPOG VYSTLAVCIS KKVQGSEREL 41 1 1 1 1 1 1 1 1 1	GTKKKYFSTC TTTORYSDAS NKRPLETOLE TTTORYSDAS NKRPLETOLE TOTORYSDAS NKRPLETOLE TOTORYSTE TOTORYSTE SESSON SKIFLKENDE SKIFLKENDE STEETLINGL REGRSQ 51 1 TOTORYSTCT TOTORYSTCT TOTORYSTCT TOTORYSTCT ACTACATOR ACTORADAS ACCOTTAGAAS	120 180 300 360 420 480 600 600 780 120 180 240 360 360
50 55 60 65	KNNYKKSICO KLREBIEGKO NGULIFSHIN IEAEDDLSSF MKYHLINTLO INOVLIFDSA MKYHLINTLO RECALLIFES RECALLIFES RECALLIFES RECALLIFES RECALLIFES TELVITYT TEVIMOEPII TOVLIGE ACCITAGA AAGATACAA	LILLLILYNPIN OKTTULVECC SPTYPAPSIN STYPTAPSIN NGBUTUHTP CASSINGAN LIKPARSIA	ANNIYOKILA PGYREMEGHK ANDINLEDEL RAMINLEDEL RAMINLEDEL REALEMICHIE PETLEGITLE CHEFTHOLIC REALEMICHE REALEMICHE REALEMICHE REALEMICHE PUBLISHER REALEMICH PUBLISHER REALEMICH REA	ERRIRORDOG GCPAVLPIDR GCPAVLPIDR GCLESNNYE LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNQIATN LIHGNGIATN L	PRIVCALQOIL VYSTLGTVGA LUNIAISSHI GVVRYIDRI KLINALASSHI GVVRYIDRI KLINALASSHI GETTLLAPVN VYSTLAVCIS LUSILITOPOG VYSTLAVCIS KKVQGSEREL 41 1 1 1 1 1 1 1 1 1	GTKKKYFSTC TTTORYSDAS NKRPLETOLE TTTORYSDAS NKRPLETOLE TOTORYSDAS NKRPLETOLE TOTORYSTE TOTORYSTE SESSON SKIFLKENDE SKIFLKENDE STEETLINGL REGRSQ 51 1 TOTORYSTCT TOTORYSTCT TOTORYSTCT TOTORYSTCT ACTACATOR ACTORADAS ACCOTTAGAAS	120 180 300 360 420 480 600 600 780 120 180 240 360 360
50 55 60 65	ENNYKKIOO KLASSINGKA KUASILORU KUASI	LULLILYNPIN OKTTULVECC STYPEASSE NIGHEISHTP REAARTEDIL CESSINGAN THE MOGIL LIKPARSIGH LI	ANNHYDKILA PGYMEMEGHK ANDHLOSDIK ANDHLOSDIK PGYMEMEGHK NGWYTVICAR EALGEICHT FETLEGITLE GUTPTIDLAN GUTPTIDLAN HILLMITTE HILLDGRIFT HIVVOKLLYP KIKVI GOSIG PWSITENETR DEEL KRILJG GUACTCCAT GGACTCCAT GGGACTCCAT GGGACTCCAT CAGCACCAC AAGCCCTTC CAGCACCAC AAGCCCTTC CAGCACCAC AAGCCCTTC CCAAAACCAA AAAACTCCAT	ERRIRGEDGG GCPAVLPIDR ERRIRGEDGGGCAVLPIDR GCGCAVLPIDR GCGCAVLPIDR GCGCAVLPIDR ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET	PRIVCALQOIL VYSTLGTVGA LUNALSSHOR GVVRIVIDRIA KURRGVLERR KURRGVL	GTKSKYPSTC TTTGKYSDAS RRGHITTOLK	120 180 300 300 420 480 540 720 780 60 180 240 360 420
50 55 60 65	ENNYKKIOO KLASSINGKA KUASILORU KUASI	LULLILYNPIN OKTTULVECC STYPEASSE NIGHEISHTP REAARTEDIL CESSINGAN THE MOGIL LIKPARSIGH LI	ANNHYDKILA PGYMEMEGHK ANDHLOSDIK ANDHLOSDIK PGYMEMEGHK NGWYTVICAR EALGEICHT FETLEGITLE GUTPTIDLAN GUTPTIDLAN HILLMITTE HILLDGRIFT HIVVOKLLYP KIKVI GOSIG PWSITENETR DEEL KRILJG GUACTCCAT GGACTCCAT GGGACTCCAT GGGACTCCAT CAGCACCAC AAGCCCTTC CAGCACCAC AAGCCCTTC CAGCACCAC AAGCCCTTC CCAAAACCAA AAAACTCCAT	ERRIRGEDGG GCPAVLPIDR ERRIRGEDGGGCAVLPIDR GCGCAVLPIDR GCGCAVLPIDR GCGCAVLPIDR ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET ERRIRGET	PRIVCALQOIL VYSTLGTVGA LUNALSSHOR GVVRIVIDRIA KURRGVLERR KURRGVL	GTKSKYPSTC TTTGKYSDAS RRGHITTOLK	120 180 360 420 480 660 660 720 780 120 120 1240 360 420 480
50 55 60 65 70	ENNYKKIOO KLASSINGKA KUASILORU KUASI	LULLILYNPIN OKTTULVECC STYPEASSE NIGHEISHTP REAARTEDIL CESSINGAN THE MOGIL LIKPARSIGH LI	ANNHYDKILA PGYMEMEGHK ANDHLOSDIK ANDHLOSDIK PGYMEMEGHK NGWYTVICAR EALGEICHT FETLEGITLE GUTPTIDLAN GUTPTIDLAN HILLMITTE HILLDGRIFT HIVVOKLLYP KIKVI GOSIG PWSITENETR DEEL KRILJG GUACTCCAT GGACTCCAT GGGACTCCAT GGGACTCCAT CAGCACCAC AAGCCCTTC CAGCACCAC AAGCCCTTC CAGCACCAC AAGCCCTTC CCAAAACCAA AAAACTCCAT	ERRIRGEDGG GCPAVLPIDR ERRIRGEDGGG GCPAVLPIDR GCGGGGANT EIRGEGGGGT EIRGEGGGGGT EIRGEGGGGGGT EIRGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	PRIVCALQOIL VYSTLGTVGA LUNALSSHOR GVVRIVIDRIA KURRGVLERR KURRGVL	GTKSKYPSTC TTTGKYSDAS RRGHITTOLK	120 180 300 420 480 540 600 720 780 120 180 240 360 420 480 560 600
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50 55 60 65 70	ENNYKKSICO KLASSIEGGI NGWIIPSMYN ISABORISH KRISHIEGGI NGWIIPSMYN KRISHIEGGI K	LULLILYNPIN OKTYULYECC STYTEMSEN STYTEMSEN STYTEMSEN STYTEMSEN RAAATTSDIL CSSSIMGGAN KOVIELAGN KOVIELAGN KOVIELAGN KOVIELAGN TRITTKYVEP KRYKKI IDO I EKONOMIC I EKONO	ANNHYDKILA ROYMENDGHK MANDHODSIK MANDHODSIK MANDHODSIK MANDHODSIK BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET BALGRICHET GGAACTCCAT CAGCCCAC AGCCCCAC CAGCCCCAC CAGCCCAC CAGCCCAC CAGCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCAC CAGCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCAC CAGCCCCCAC CAGCCCCAC CAGCCCCCCCAC CAGCCCCCCCCCC	ERRIRGEDOG GCRAVLPIDE ERRIRGEDOG GCRAVLPIDE ERRIRGEDOG GCRAVLPIDE ERRIRGEDGE GCRAVLPIDE ERRIRGEDGE GCRAVLPIDE ERRIRGEDGE GCRAVLPIDE	PRIVOLIGO ILI VYETILGI VIGA GIVINI VIGA VIGA VIGA GIVINI VIGA VIGA VIGA VIGA VIGA VIGA VIGA VIGA	GTRENCYPSTC TTTORYSDAS MNOWLTEDLO GTRENCYPSTC TTTORYSDAS MNOWLTEDLO GTRENCYPSTC MODIVASERAL TUTNINGVIEL MAPEDDITISM SCICKRESSEQ SILFIAGRA SELFIAGRA SELFIAGRA TEGET TOGTOTTCT TOGTOTT TOGTOTTCT TOGTOTT 120 180 300 420 480 540 660 720 780 180 240 480 360 480 540 660 660 660 660 660 660 660 660 660 6	
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50 55 60 65 70	ENNYRESI CO KLASSI ISONO KLASSI ISONO KKYHLLATIA IDWILLIDIA INWILLIDIA INWINISIA ILIVIELINI INWINISIA ILIVIELINI INVINISIA INVINISIA INCONTRALIA INCON	LULLILLYNPIN GRTVLITECC GRTVLITECC GRTVLITECC GRTVLITECC GRTVLITECC GRESIMGAN ROVIELLAGO	ANNHYDKILA ROYNEWGOK	ERRIEGEDOG GCDAVLPIDE GCTAVLPIDE	I TOTAL COLOR OF TOTA	TOTORYSON OF THE CONTROL OF THE CONT	120 180 300 420 480 540 600 600 720 780 180 240 360 480 540 600 660 660 660 660 660 660 660 660 6
50 55 60 65 70 75	ENNYRESI CO KLASSI ISONO KLASSI ISONO KKYHLLATIA IDWILLIDIA INWILLIDIA INWINISIA ILIVIELINI INWINISIA ILIVIELINI INVINISIA INVINISIA INCONTRALIA INCON	LULLILLYNPIN GRTVLITECC GRTVLITECC GRTVLITECC GRTVLITECC GRTVLITECC GRESIMGAN ROVIELLAGO	ANNHYDKILA ROYNEWGOK	ERRIEGEDOG GCDAVLPIDE GCTAVLPIDE	I TOTAL COLOR OF TOTA	TOTORYSON OF THE CONTROL OF THE CONT	120 180 240 300 420 420 660 660 6720 780 120 180 300 340 420 420 480 540 660 720 780 960 960 960 960 960 960 960 960 960 96
50 55 60 65 70 75	ESNYTKESI CO KLASSI SOMO PROPERTY OF THE ACCOUNTY OF THE ACCOU	LILLILIVAPIN GRTVALVECC GRTVALVECC GRTVALVECC GRTVALVECC GRTVALVECC GRTVALVECC GRSSIMGGAN ROUSELAGRO ROUSELAGR	ANNHYDKILA ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK ROYMENGAK RIKURITAN	ERRIEGEDOG GCDAVLPIDE	PRIVENCIAGE	GREACYPSTC TTTOKYSOAS GREACYPSTC TTTOKYSOAS GREACYPSTC TTTOKYSOAS GREACYPSTC TTTOKYSOAS GREACYPSTC TTTOKYSOAS GREACYPSTC TTTOKYSOAS GREACYPSTC TTTOKYSOAS GREACYPSTC TOKYSOAS STATE TOKYSOAS STATE TOKYSOAS TOKYSO	120 240 300 300 420 480 540 660 660 720 780 120 360 420 360 420 360 420 780 660 780 860 860 960 960 960 960 960 960 960 960 960 9
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50 55 60 65 70 75	ESHYTKESI CO KARANGANA AGANAAATAA AGANAAATAA AGANAATAA A AGANAATAAA AGANAATAAA AGANAATAAA AGANAATAAA AGANAATAAA AGANAATAAAA AGANAATAAAATAA	LULLIVEPIN GETTALTECT OF THE ACT	ANNHYDKILA PRYMEMBORK MONYTHINGAS EALGRICHET FETLEGATIE MELHAGOTIS MELHAGOTIS PETLEGATIE MELHAGOTIS PETLEGATIE MELHAGOTIS PETLEGATIE MELHAGOTIS PETLEGATIE PETLEGATIE OGAGACCOAT GOGACTOAT GOGAC	ERRIEGEDOG GCGAVALPIDHE HERRIEGEDOG GCGAVALPIDHE HERRIEGEDOG GCGAVALPIDHE HERRIEGEDGE HERR	NUTLINGS ILL PROVIDED TO THE	TOTAL STATE OF THE	120 240 360 360 480 660 720 780 660 120 180 300 340 340 420 480 480 660 720 780 180 180 180 180 180 180 180 180 180 1
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	AGATTGTCAG	CTCCTTGAGG	GCAAGAGCCA	CAGTATATTT	CCCTGTTTCT	TCCACAGTGC	1440
	CTAATAATAC	TOTOGRACTA	GGTTTTAATA	ATTTTTTAAT	TGATGTTGTT	ATGGGCAGGA	1500
	TGGCAACCAG	ACCATTGTCT GTAACCTCTT	CAGAGCAGGT	GCTGGCTCTT	TCCTGGCTAC	TCCATGTTGG	1560 1620
5	CTAGCCTCTG	CCTTGTCTTT	TTATGACAGG	ATGTTTGCTC	AGCTTCTCCA	ACAATAAGAA	1680
-	GCACGTGGTA	AAACACTTGC	GGATATTCTG	GACTGTTTTT	ATATAAAAAA	CAGTTTACCG	1740
							1800
	CCAACCATAC	AAAAATTCCT AACAAGATAG	TTTCCCGAAG	GAAAAGGGCT	TTCTCAATAA	CCCCAGCIT	1860
10	ACTITITATING	TOTTTACT	TGTTTCAGAG	TTTGTATTGT	GATTATCAAT	TACCACACCA	1980
	TCTCCCATGA	AGAAAGGGAA	CGGTGAAGTA	CTAAGCGCTA	GAGGAAGCAG	CCAAGTCGGT	2040
	TACTEGRADEC	ATGATTGGTG	CCCAGTTAGC	CTCTGCAGGA	TGTGGAAACC	TCCTTCCAGG	2100
	GGAGGTTCAG	TGAATTGTGT TTGAATCACT	AGGAGAGGTT	CTCATCATC	AGAGTGCTGT	CCCGTGGAGA	2220
15	TOTOROGIA	ACCITCTTATC	TARTCATGAA	ACTCCCTAGT	TCCTTCATGT	AACTTCCCTG	2280
	AAAAATCTAA	CTCTTTCATA	DADASTTTAA	TCTGTGACCC	ACTTACCTTG	CATCTCACAG	2340
	GTAGACAGTA	TATAACTAAC	AACCAAAGAC	TACATATTGT	CACTGACACA	CACGITATAA	2400
	TCATTTATCA	TATATATACA GACTTGTATA	TACATGCATA	CACTCTCAAA	GCAAATAATT TCTTTGTTAA	AATAGAATGG	2520
20	TATCAATAAA	TAGACCATTA	ATCAG	10/00/1/11/11			
	Seq ID NO: Protein Acc	403 Proteir	sequence				
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	MKKSGVLPLL	GIILLVLIGV	QGTPVVRKGR	CSCISTNOGT	IHLQSLKDLK	QFAPSPSCEK	120
	OKKTT	VQTCLNPDSA	DAKELIKKME	KQVSQKKKQK	MUKKHUKKKV	LKVKKSQKSK	120
30	QREII						
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35	1	11	21	31	41	51	
		CCCTCCGGGC		Chaccattered	I conceanance	GTCCCPGCCC.	60
	AGCTCCCGGG	AAACGCGAGC	CGCGATGCCT	GGGGGGTGCT	CCCGGGGCCC	CCCCCCCCCCC	120
	GACGGGGGGTC	TGCGGCTGGC	GCGACTAGCG	CTGGTACTCC	TGGGCTGGGT	CTCCTCCTCT	180
40	TCTCCCACCT	CCCCGCTGCC	CTCCTTCTCC	TCCTCGGCGC	CCTTCCTGGC	TTCCGCCGTG	300
	TOCGCCCAGC	AGTGCGTTAA	COSCANTOTO	ACCORDIGATOR	CCACGGACCT	GCCCGCCTAC	360
	GTGCGCAACC	TCTTCCTTAC	CGGCAACCAG	CTGGCCGTGC	TCCCTGCCGG	CCCCTTCCCC	420
4.0	CGCCGGCCGC	CGCTGGCGGA	GCTGGCCGCG	CTCAACCTCA	GCGGCAGCCG	CCTGGACGAG	480
45	GTGCGCGCGG	GCGCCTTCGA ACCTCAGTCC	GCATCTGCCC	AGCCTGCGCC	AGCTCGACCT	CAGCCACAAC	540 600
	AGTCCCCTTG	TGGAACTGAT	CCTGAACCAC	ATCGTGCCCC	CTGAAGATGA	GCGGCAGAAC	660
	CCCACCTTCC	AGGGCATGGT	GGTGGCGGCC	CTGCTGGCGG	GCCGTGCACT	GCAGGGGCTC	720
50	CGCCGCTTGG	AGCTGGCCAG TCAGGCACCT	CAACCACTTC	CTTTACCTGC	CGCGGGGATGT	GCTGGCCCAA	780 840
30							900
	CTTCACAATG	GCACCCTGGC	TGAGTTGCAA	GGTCTACCCC	ACATTAGGGT	TTTCCTGGAC CAAGGAAACA	960
	AACAATCCCT	GGGTCTGCGA	CTGCCACATG	GCAGACATGG	TGACCTGGCT	CAAGGAAACA	1020
55	GAGGTAGTGC	AGGGCAAAGA AACTCAACAG	CCGGCTCACC	TGTGCATATC	CGGAAAAAAT	GAGGAATCGG	1080
33	CAAACCTCTT	ATGTCTTCCT	GGGTATTGTT	TTAGCCCTGA	TAGGCGCTAT	TTTCCTCCTG	1200
	GITTTGTATT	TGAACCGCAA	GGGGATAAAA	AAGTGGATGC	ATAACATCAG	AGATGCCTGC	1260
	AGGGATCACA	TGGAAGGGTA	TCATTACAGA	TATGAAATCA	ATGCGGACCC	CAGATTAACA	1320 1380
60	AACCTCAGTT	CTAACTCGGA-	TGTCTGAGAA	CTACCCTTCC	TCCACTTTCA	TCCTCCACTA	1440
30	TAGATACAAC	CCACTTTGAC	TAAAAGCAGT	GAAGGGGATT	TECTTCCTTG	TTATGTAAAG	1500
	mmoreocc	THE PROPERTY AND ADDRESS OF THE PARTY AND ADDR	ATTENACACE	ATGRACAGTT	CTGTATAGTG	TTTTACCCTC	1560
	TTCTTTTTCT	TGGAACTCCT	CAACACGTAT	GGAGGGATTT	TTCAGGTTTC	GTGTACCCAC	1620
65	ACAGATAGCA	TTCAACAAAA	GCTGCCTCAA	CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	AAAAATACTT	TATTCATAAA	1740
••	TATEMETTT	ATTOTCATGT	ACCTAAGTTG	TGGAGAAAAT	AATTGCATCC	TATAAACTGC	1800
	CTGCAGACGT	TAGCAGGCTC	TTCAAAATAA	CTCCATGGTG	CACAGGAGCA	CCTGCATCCA	1860
	AGAGCATGCT	TACATTTTAC	TGTTCTGCAT	ATTACAAAAA	ATAACTIGCA	ACTICATARC	1920
70	TTTTAATAAA	CTGCATCGAG	ATCCAACCGA	CTGAATTGTT	AAAAAAAAA	ACTGATTTTT AAAAATAAAG	2040
	ATTCTTAAAA	GAA					
75	Seq ID NO: Protein Ac	405 Proteincession #: 1	n sequence NP_006661				
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	MPGGCSRGPA	AGDGRLRLAR	LALVLLGWVS	SSSPTSSASS	PSSSAPFLAS	AVSAQPPLPD	60 120
80	AALNLSGSPI.	DEVRAGAPEH	LPSLROLDIA	HNPLADLSPF	AFSGSNASVS	PARRPPLAEL APSPLVELIL	180
	NHIVPPEDER	ONRSFEGMVV	AALLAGRALO	GLRRLELASN	HFLYLPRDVL	AQLPSLRHLD	240
	LSNNSLVSLT	YVSFRNLTHL	BSLHLEDNAL	KVLHNGTLAE	LOGLPHIRVE	LDNNPWVCDC	300
	HMADMVTNLK	ETEVVQGKDR LLVLYLNRKG	LTCAYPERMR	NKVLLKLNSA	PPDCDATED	SLOTSYVFLO	360
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5	ATGCCTGGGG	GGTGCTCCCG	GGGCCCCGCC	GCCGGGGACG	GCCGTCTGCG	GCTGGCGCGA	60
-	CTAGCGCTGG	TACTCCTGGG	CTGGGTCTCC	TOGTCTTCTC	CCACCTCCTC	GGCATCCTCC	120
	TTCTCCTCCT	CGGCGCCGTT	CCTGGCTTCC	GCCGTGTCCG	CCCAGCCCCC	GCTGCCGGAC	180
	CAGTGCCCCG	CGCTGTGCGA AGGTGCCCAC	GTGCTCCGAG	GCAGCGCGCA	CAGTCAAGTG	CGTTAACCGC	240 300
10	AATCTGACCG	CCAGCAACCA	GGACCTGCCC	GCCTACGTGC	BECTCCTCCT	CCTTACCGCC	360
10	AACCAGCTGG	ACCTGGACTT	ANOTANTANT	TOCOTOCTCA	CCTCACCTA	CONSTRUCTE	420
	CCCAACCTGA	CACATCTAGA	AAGCCTCCAC	CTGGAGGACA	ATGCCCTCAA	GGTCCTTCAC	480
	AATGGCACCC	TYGGTTGAGTT	GCAAGGTCTA	CCCCACATTA	GGGTTTTCCT	GGACAACAAT	540
	CCCTGGGTCT	GCGACTGCCA	CATGGCAGAC	ATGGTGACCT	GGCTCAAGGA	AACAGAGGTA	600
15	GTGCAGGGCA	AAGACCGGCT	CACCTGTGCA	TATCCGGAAA	AAATGAGGAA	TCGGGTCCTC	660
	TTGGAACTCA	ACAGTGCTGA	CCTGGACTGT	GACCCGATTC	TTCCCCCATC	CCTGCAAACC	720
	TCTTATGTCT	TCCTGGGTAT	TGTTTTAGCC	CTGATAGGCG	CTATTTTCCT	CCTGGTTTTG	780 840
	TATTTGAACC	GCAAGGGGAT	AAAAAAGTGG	ATGCATAACA	TCAGAGATGC	PACHAGGGAT	900
20	CACATGGAAG	GGTATCATTA CGGATGTCCT	CAGATATGAA	ATCMTGCGG	ACCCCAGATT	AACAMCCIC	300
20	AGTTCTAACT	CGGMIGICCI	COMOTON				
	Sec ID NO:	407 Protein	sequence				
	Protein Acc	ession #: 1	os sequence	:			
25							
25	1	11	21	31	41	51	
	1	AGDGRLRLAR	1	CCCDTCCACC	Peccanpr.se	AVENODDI.DD	60
	MPGGCSRGPA	AARTVKCVNR	PATABLE MAS	PARTITIONS	NOT A CHILDT V	L.DDDVIT.AOT.D	120
	GCPALICECSE	SLVSLTYVSF	DMI-TUT-PGI-H	LEDNALKULH	NOTIARLOGIA	PHIRVPLDNN	180
30	DEVICTORIMAN	MUTWLKETEU	VOGKORLICA	YPEKMRNRVL	LELINSADLDC	DPILPPSLQT	240
-	SYVPLGIVIA	LIGATPLLVL	YLNRKGIKKW	MINIRDACED	HMEGYHYRYE	INADPRETNE	300
	SSNSDVLE						
35	Seq ID NO:	408 DNA sec	quence				
23	Nucleic Ac	id Accession	1 #: NM_UUC	1095.1			
	Coaing seq	dence: 26	2233				
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40	CAGCACCCAG	CTCCCCGCCA	CCGCCATGGT	CCCCGACACC	GCCTGCGTTC	TTCTGCTCAC	60
	CCTGGCTGCC	CTCGGCGCGT	CCGGACAGGG	CCAGAGCCCG	TTGGGCTCAG	ACCTGGGCCC	120
							180
	GCGGCAGCAG	GTCAGGGAGA CAGTCAGTAC	TCACGTTCCT	GAAAAACACG	GTGATGGAGT	GTGACGCGTG	240 300
45	CGGGATGCAG	TGCTTCCCCG	GCACCGGCCT	ACCCAGCGTG	CGGCCCCTGC	CCCCCCCCCCCC	360
43	**********	acceptance.	CCCCCA A CCC	CECCECACTOC	ACCCACCTCA	ACGRETECAA	420
	CCCCTGCCCC	TGCTTCCCCC CCGGGGTACA	GAGTCCGCTG	TATCAACACC	AGCCCGGGGT	TCCGCTGCGA	480
	COCCUTACOCC	COGGGGTACA	GCGGCCCCAC	CCACCAGGGC	GTGGGGCTGG	CTTTCGCCAA	540
							600
50	CCCCS ACTCC	CTTTTCCATCA	ACACCCGGGG	CTCCTTCCAG	TGCGGCCCGT	GCCAGCCCGG	660
	CTTCGTGGGC	GACCAGGCGT	CCGGCTGCCA	GCGCGGCGCA	CAGCGCTTCT	GCCCCGACGG	720 780
	CTCGCCCAGC	GAGTGCCACG	AGCATGCAGA	CTGCGTCCTA	GAGCGCGATG	BON COCK CCT	840
	GTGCGTGTGT	COGGACGAGA	ACCICCOCCIO	CCCCCGACCCC	CAGTGCCCTA	ACGUCACCE	900
55	COTTON CTICTO	CCCAACTCAG	GCCAGGAGGA	TGTGGACCGC	GATGGCATCG	GAGACGCCTG	960
-	CONTOCCAT	CCCCACGGGG	ACGGGGTCCC	CAATGAAAAG	GACAACTGCC	CGCTGGTGCG	1020
	GAACCCAGAC	CAGCGCAACA	CGGACGAGGA	CAAGTGGGGC	GATGCGTGCG	ACAACTGCCG	1080
	GTCCCAGAAG	AACGACGACC	AAAAGGACAC	AGACCAGGAC	GGCCGGGGGCG	ATGCGTGCGA	1140
	CGACGACATC	GACGGCGACC	GGATCCGCAA	CCAGGCCGAC	AACTGCCCTA	GGGTACCCAA	1200
60	CTCAGACCAG	AAGGACAGTG	ATGGCGATGG	TATAGGGGAT	GCCTGTGACA	ACTGTCCCCA	1320
	GAAGAGCAAC	CCGGATCAGG	CGGATGTGGA	CCACGACTT	CACAACTCTC	CCACCGTGCC	1380
	TARCACTOC	CAGGAGGACT	CAGACCACGA	TGGCCAGGGT	GATGCCTGCG	ACGACGACGA	1440
	CONCANTGAC	GGAGTCCCTG	ACAGTCGGGA	CAACTGCCGC	CTGGTGCCTA	ACCCCGGCCA	1500
65	GGAGGACGC	GACAGGGACG	GCGTGGGCGA	CGTGTGCCAG	GACGACTTTG	ATGCAGACAA	1560
	COTOGTAGAC	AAGATCGACG	TGTGTCCGGA	GAACGCTGAA	GTCACGCTCA	CCGACTTCAG	1620
	GGCCTTCCAG	ACAGTCGTGC	TGGACCCGGA	GGGTGACGCG	CAGATTGACC	CCAACTGGGT	1680
	GGTGCTCAAC	CAGGGAAGGG	AGATOGTGCA	GACAATGAAC	AGCGACCCAG	GCCTGGCTGT	1740
70	GGGTTACACT	GCCTTCAATG	GCGTGGACTT	CGAGGGCACG	TTCCATGTGA	ACACGGTCAC	1860
70	GGATGACGAC	CAGATGGAGC	TCATCTTTGG	CTACCAGGAC	AGCICCAGCI	CTCTCCCCCA	1920
	CATGIGGAAG	CAACTCAAGG	CTCTCALACTC	TTCCACAGGC	CCCGGGGAAC	AGCTGCGGAA	1980
	CCTCTCTCTC	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCGCG	2040
	AAACGTGGGT	TGGAAGGACA	AGAAGTCCTA	TCGTTGGTTC	CTGCAGCACC	GGCCCCAAGT	2100
75	GGGCTACATC	AGGGTGCGAT	TCTATGAGGG	CCCTGAGCTG	GTGGCCGACA	GCAACGTGGT	2160
	CTTCCACACACA	ACCATGOGGG	GTGGCCGCCT	GGGGGTCTTC	TGCTTCTCCC	AGGAGAACAT	2220
	CATCTGGGCC	AACCTGCGTT CAAGCCTAGG	ACCCCTGCAA	TGACACCATC	CCAGAGGACT	ATGAGACCCA	2280
	TCAGCTGCGG	CAAGCCTAGG	GACCAGGGTG	AGGACCCGCC	GGATGACAGC	CACCCTCACC	2340 2400
80	GCGGCTGGAT	GGGGGCTCTG	CACCCAGCCC	AAGGGGTGGC	CUTCUTGAGG	GOGAAGTGAG	2400
OU	AAGGGCTCAG	AGAGGACAAA	ATAAAGTGTG	1910CHUGG			
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	NGSHCTDVNE	CNAHPCFPRV	RCINTSPGFR	CEACPPGYSG	PTHOGVGLAF	AKANKOVCTD	180
	INECETGOEN	CVPNSVCINT	RGSFOCGPCO	PGFVGDOASG	CORGAORFCP	DGSPSECHEH	240 300
5	ADCVLERDGS	RSCVCRVGWA ACDPDADGDG	UDNESCONCEL.	DEDGFPDEKL	RCPEPQCRKD	CRSOKNDDOK	360
,	DTDODGRGDA	CDDDIDGDRI	RNQADNCPRV	PNSDQKDSDG	DGIGDACONC	PQKSNPDQAD	420
	VDHDFVGDAC	DSDQDQDGDG	HODSRDNCPT	VPNSAQEDSD	HDGQGDACDD	DDDNDGVPDS	480 540
	RDNCRLVPNP	GQEDADRDGV WVVLNQGREI	GDVCQDDFDA	DKVVDKIDVC	PENAEVTLTD	FRAFQTVVLD	540 600
10	PGYODSSSEY	VVMWKOMEOT	YWOANPFRAV	AEPGIOLKAV	KSSTGPGEOL	RNALWHTGDT	660
	RSOVRLLWKD	PRNVGWKDKK	SYRWPLOHRP	OVGYIRVRFY	EGPELVADSN	VVLDTTMRGG	720
	RLGVFCFSQE	NIIWANLRYR	CNDTIPEDYE	THQLRQA			
	Sea ID NO:	410 DNA sec	ruence				
15	Nucleic Aci	d Accession	#: NM 001	565.1			
	Coding sequ	ence: 673	163				
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20	GAGACATTCC	TCAATTGCTT ATCAAACTGC	AGACATATTC	TGAGCCTACA	GCAGAGGAAC	CTCCAGTCTC	60 120
	AGCACCATGA	TACCTCTCTC	TAGRACCOTA	CGCTGTACCT	GCATCAGCAT	TAGTAATCAA	180
	CCTGTTAATC	CAAGGTCTTT	AGAAAAACTT	GAAATTATTC	CTGCAAGCCA	ATTTTGTCCA	240
25	CCTCTTGAGA	TCATTGCTAC	AATGAAAAAG	AAGGGTGAGA	AGAGATGTCT	GAATCCAGAA	300 360
25	*******	TCAAGAATTT GGGGAGCAAA	ATTOCATOCAG.	TOCTTOCK NO.	CATGGACCAC	DOMORAGA A	420
	CCTCTCCCAT	CACTTCCCTA	CATGGAGTAT	ATGTCAAGCC	ATAATTGTTC	TTAGTTTGCA	480
							540 600
30	GGTTAATGTT	CATCATCCTA	AGCTATTCAG	TAATAACICT	CTGCTTCAAA	TATTATCCCTC	660
50	ACCTTTCCCA	GGTGCTATGT TCTTCCAAGG	GTACTAAGGA	ATCTTTCTGC	TTTGGGGTTT	ATCAGAATTC	720
	TCAGAATCTC	DARTARCTAR	AAGGTATGCA	ATCAAATCTG	CTTTTTAAAG	AATGCTCTTT	780
	ACTTCATGGA	CTTCCACTGC CAAACACATA	CATCCTCCCA	AGGGGCCCAA	ATTCTTTCAG	TGGCTACCTA	840 900
35	CATACAATTC	GAAAGACTGT	ACAAAGTATA	AGTCTTAGAT	GTATATATTT	CCTATATTGT	960
	THECACTETA	CATGGAATAA	CATGTAATTA	AGTACTATGT	ATCAATGAGT	AACAGGAAAA	1020
	TAAAAATTT	ACAGATAGAT AAAATGAGGT	ATATGCTCTG	CATGTTACAT	AAGATAAATG	TGCTGAATGG	1080
	TTTTCAAATA	AAAATGAGGT	ACTOTOCOGG	AMIAIIAG			
40	Seq ID NO:	411 Protein	sequence				
	Procein Acc	cession #: 1	MP_001556.1				
	procein Acc	cession #:	21	31	41	51 .	
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45	1 MNOTAILICC	11 - LIPLTLSGIQ	21 GVPLSRTVRC	TCISISNQPV	1	ī '	60
45	1 MNQTAILICC EIIATMKKKG	11 LiflTLSGIQ EKRCLNPESK	21 GVPLSRTVRC AIKNLLKAVS	TCISISNQPV	1	ī '	60
45	1 MNQTAILICC EIIATMKKKG Seq ID NO:	11 LIFLTLSGIQ EKRCLNPESK	21 GVPLSRTVRC AIKNLLKAVS	TCISISNQPV KEMSKRSP	1	ī '	60
	1 MNQTAILICC EIIATMKKKG Seq ID NO: Nucleic Ac.	11 LIFLTLSGIQ EKRCLNPESK 412 DNA second Accession	21 GVPLSRTVRC AIKNLLKAVS Quence 1 #: XM_05	TCISISNQPV KEMSKRSP	1	ī '	60
45	1 MNQTAILICC EIIATMKKKG Seq ID NO: Nucleic Ac.	11 LIFLTLSGIQ EKRCLNPESK	21 GVPLSRTVRC AIKNLLKAVS Quence 1 #: XM_05	TCISISNQPV KEMSKRSP	nprsleklei	I PASQFCPRV	60
	1 MNQTAILICC EIIATMKKKG Seq ID NO: Nucleic Ac.	11 LIFLTLSGIQ EKRCLNPESK 412 DNA second Accession	21 GVPLSRTVRC AIKNLLKAVS Quence 1 #: XM_05	TCISISNQPV KEMSKRSP	1	ī '	60
50	1 MNQTAILICC EIIATMKKKG Seq ID NO: Nucleic Ac. Coding sequence 1	11	21	TCISISNOPV KEMSKRSP	NPRSLEKLEI 41 AGCCTGGGGG	I I I I I I I I I I I I I I I I I I I	60
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50	1 MNQTAILICC EIIATMKKKG Seq ID NO: Nucleic Ac. Coding sequ 1 GGGAGGGAGA GCGGCGGAGA	LIFLTLSGIQ EKRCLNPESK 412 DNA see id Accession uence: 143. 11 GAGGCGCGCG CCAGACGCTG	21	TCISISNOPV KEMSKRSP 7014 31 GCATTGATGC TCTCCTCGGT TCACGGCCCC	41 AGCCTGCGGC CCCCCTCCCC	I IPASQFCPRV 51 GGCCTCGGAG TCCAGCTCCG CGCAGCGGCT	60 120 180
50	MOTATLICC EITATMKKKG ENGID NO: Nucleic Ac. Coding sequil GGGAGGGAGA GGGGGGGAGAGA GGGGGGGAGAGAGA	11 LIFLTLEGIQ EKRCLNPESK 412 DNA see 414 ACCESSION LUCKES 143. 11 GAGGCGCGCG CCAGACGCTG CAGCCGGGAG	21 GVPLSRTVRC AIRNLLKAVS PLENCE 1 #: XM_05' .874 21 GGTGAAAGGC ACCAGTTCC CCATGGGACC	TCISISNOPV KEMSKRSP 7014 31 GCATTGATGC TCTCCTCGGT CCAGGGCCCC GCTGCTGCGG	41 AGCCTGOGGC GCGGCTCCGCC	51 GGCCTCGGAG TCCAGCTCCG CGCAGCGGCT CCTCTGGAGT	60 120
50 55	1 MAGTAILICE EIIATMKKKG Seq ID No: Nucleic Ac. Coding seque	11 LIFLTLSGIQ EXECUMPESK 412 DNA seid Accession uence: 143. Jagggggggg CCAGACGCTG CAGCCGGGAG CTGCTGCTCC AAGCGCAAAGG	21 GVPLSRTVRC AIRNLLKAVS QUENCE 1 #: XM_05' 874 21 GGTGAAAGGC ACCACGTTCC CCATGCGACC CGAGGCTCCG CGAGGCTCCG CAGGAGTGCC	TCISISNOPV KEMSKRSP 7014 31 GCATTGATGC TCTCCTGGT TCTCCTGGGCCCC GCTGCCCGCG GCAGAGGGAG TGGTCGAGAGC	41 Agecraeage crereage crereage geogetee correage graeroage graeroage	51 GGCCTCGGAG TCCAGCTCCG GGCAGCGGCT CCTCTGAGAT TGTATAATGG GGGCCAATGG	60 120 180 240 300 360
50	1 MNQTAILICC EIIATMKKKG Seq ID NO: Mucleic Ac. Coding seq: 1 GGGAGGAGA 1 GGGAGGAGAGA GGGGGGGCTC CCCCAAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGTTA	11 LIFLTLSGIQ EKRCLNPESK 412 DNA seid Accession uence: 143. 11 GAGGGGGGG CAGCAGGGGGGGGGGGGGGGGGGGGGGGG	21 GVPLSRTVRC AIRNILKAVS QUENCE 4 XM_05' 874 3 3 3 3 3 3 3 3 3 3	TCISISNOPV KEMSKRSP 7014 31 GCATTGATGC CCAGGGCCCC GCTGCCGCG GCAGAGGGAG GGATGAATC	41 	51 GGCCTCGGAG GCCTCGGAG TCCAGCTCCG CGCAGCGCT CTCTTAGAT TGTATAATGG GGCCAATGG	60 120 180 240 300 360 420
50 55	1 MNQTAILICC EIIATMKKKG Seq ID NO: Mucleic Ac. Coding seq: 1 GGGAGGAGA 1 GGGAGGAGAGA GGGGGGGCTC CCCCAAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGGAATAGGGTTA	11 LIFLTLSGIQ EKRCLNPESK 412 DNA seid Accession uence: 143. 11 GAGGGGGGG CAGCAGGGGGGGGGGGGGGGGGGGGGGGG	21 GVPLSRTVRC AIRNILKAVS QUENCE 4 XM_05' 874 3 3 3 3 3 3 3 3 3 3	TCISISNOPV KEMSKRSP 7014 31 GCATTGATGC CCAGGGCCCC GCTGCCGCG GCAGAGGGAG GGATGAATC	41 	51 GGCCTCGGAG GCCTCGGAG TCCAGCTCCG CGCAGCGCT CTCTTAGAT TGTATAATGG GGCCAATGG	60 120 180 240 300 360 420 480
50 55	MNOTAILICE EIIATMKKKG Seq ID NO: Nucleic Ac Coding seq: 1 00000000000000000000000000000000000	11	21 GVPLSRTVRC AIRALLKAVS quence 1 #: XM_05' 874 21 GGTGAAAGC ACCACGTTCC ACCACGTTCC ACCACGTCC CAGAGTCCC TGCTGCTGCA CTCCAGGTCC TCCCAGGTCC TCCCAGGTCC TTCGGAAAT	TCISISMOPV KEMSKRSP 7014 31	41 AGCTTGCGC CTCCTCGCC GCGCCTCCC GCGCCTCCC GGGGCCCTC AAGCGGTGTTGCACC AAGCAGTGTT ACATTTACAA	51 IPASQFCPRV 51 GGCCTCGGAG TCCAGCTCCG CGCAGCGCCT CCTCTGAGAT TGTATAATGG GGGCCAATGA AGGGGGAATG AGGGGGATGA AGGGGGATGA AGGGGATTC AGATGCATCA	60 120 180 240 300 420 480 540 600
50 55 60	MNOTAILICE EIIATMKKKG Seq ID NO: Nucleic Ac Coding seq: 1 00000000000000000000000000000000000	11	21 GVPLSRTVRC AIRALLKAVS quence 1 #: XM_05' 874 21 GGTGAAAGC ACCACGTTCC ACCACGTTCC ACCACGTCC CAGAGTCCC TGCTGCTGCA CTCCAGGTCC TCCCAGGTCC TCCCAGGTCC TTCGGAAAT	TCISISMOPV KEMSKRSP 7014 31	41 AGCTTGCGC CTCCTCGCC GCGCCTCCC GCGCCTCCC GGGGCCCTC AAGCGGTGTTGCACC AAGCAGTGTT ACATTTACAA	51 IPASQFCPRV 51 GGCCTCGGAG TCCAGCTCCG CGCAGCGCCT CGCAGCATGA AGGGGGAATGA AGGGGGAATGA AGGGGGATGA AGGGGGATGA AGGGGGATGA AGGGGATTCA AGATGCATCA GABATGCATGA	60 120 180 240 300 360 420 480 540 660
50 55	1 MNOTAILICC EIIATMKKKG Seq ID NO: Nucleic Ac Coding sequity of the coding sequity of	11	21	I TCISISNOPV KEMSKRSP 7014 31 GCATTGATGC TCTCCTGGGT CCAGGGCCGGG GCAGAGGGAG GGATGGATTC TGCGGGGGTTGATTCTTGCGGGGGGGGGG	41 AGCCTGCGGC GCGCCTCCC COTCGAGG GTGGTGGACC GTGGTGGACC AAGCAGTGTT ACATTTACAA CTAAAATGA TCAGGACTC	51 	60 120 180 240 300 360 420 480 540 660 660
50 55 60	1 MNOTAILICE EILATMICKG Seq ID NO: Nucleic Ac. Coding seq: 1 GOGAGOGATA GOGGGGGCTC CCCCAAGGG ANTGGGTTA AATTAGTGCTT AAATAGTGCT TGTCAGGGA AGCTATAATT	11	21	TGISISROPV KEMSKRSP 7014 31	41 AGCORDAGE GEOGRAPHICA AGCORDAGE GEOGRAPHICA ALIANTIACA CIAANTIACA	51 	60 120 180 240 300 360 420 480 540 660 720 780 840
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50 55 60	1 MANDYALLICC ELIATMENGS Seq ID NO. NULleic Ac Coding seq 1 1 1 0 0 0 0 0 0 0	11 LIFLITLEGIQ ERRCLEMPER 412 DNA se- tid Accession uence: 143. 11 GAGGGGGGGG CCAGAGGCTGCA CCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	21 GVPLSRTVRC ATROLLERV9 Weence 1	TCISISNOPV KEMSKRSP 7014 31	41	S1	60 120 180 240 360 420 540 660 720 840 900 960 1020
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50 55 60 65	1	11 LIFL/TLBGIQ ERRCLE/PEEK 4/12 DNA see 1d Accession uence: 143. 11 LIFL/TLBGIQ ERRCLE/PEEK 4/12 DNA 11 LIFL/TLBGIQ ERRCLE/PEEK 143. 11 LIFL/TLBGI	21 OVPLORTYRC ATROLLEAVY PURPOR 1 B: 874 21 OVPLORTYRC 1 B: 874 21 OVPLORTYRC CONTROL CO	I TICISISMOPV KENSKREP 7014 31 I GUTTORATOC TOCCOCOSI GORGOCOCOC GORGOCOCOC GORGOCOCOC GORGOCOCOC GORGOCOCOC TOCCOCOC TOCCOC TOCCOCOC TOCCOC TOCC	41 AGCCTGGGGG CTCCTCGGGG GTGGTGGGGC CTCCTCGGGG GGGGGCCTCC CGGGGGGCCTC CGGGGGGCCTC CGGGGGCCTC CGGGGGCCTC CGGGGGCCTC CGGGGGCCTC CGGGGGCCTC CGGGGGCCTC CGGGGGTGTT CTAGGGCCT TCAGGGCT TCAGGGCT TCAGGGCT TCAGGGCT TCAGGGTT TCAGGGCT TCAGGGTT TCAGGTT TCAGGGTT TCAGGTT TCAGGGTT TCAGGGTT TCAGGGTT TCAGGGTT TCAGGGTT TCAGGGTT TCAGGGT TCAGGGTT CAGGTT TCAGGGT TCAGGT S1 S1 SCHOOLSE STORE STO	60 120 180 240 300 480 540 660 720 840 900 960 1080 1180	
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35		GAGCAGACTC	ACABGAGCCC	TOCCACTTTG	ATTCTCAGCA	CCCTCCAGTC	TTGGAAGAAG	1680
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CTCACAGTCA GAGCAGGGG TACTCTCGGG AGGGCGAA AGATGCGGGG GTGCCACTT 1920		TTCACCACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCACCAA	AACCACCATC	1860
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### TITTCAMGAA CTAGACAGGT TATTCCTATA CUGARITTA GUTCCTATA GAACTGCTGG 2760 ####################################	50	TATTCTATCT	IGGAGATAAA	AICIGIAIGI	TA DOMITTONCO	CCANADATCE	CTTTTAATCCT	
TOTTROGIA TARGANTOT CATRAGECT AMANICON GIAMGOTIAT ACTGAMTTA 2020		TAAACAAGAG	ATTTGGCATG	ACATGITCIG	CONCOMPORTO	CCTCTCTCTA	CANCEGCEG	
AGCAMAGNA TAMAGGMAN AMGRANAN TCTRARATT GGGGRGGGT RARTCETTAT 2880 AMANACCA MANTETTAT TAMATRAGG GGGGGAGNAT TAMATCETTAT 2880 CMARATRAT TAMAGRACA TACATTANAC GGGGGAGNAT TAMATCHAT 2880 CMARATRAT TAMAGTACA TACATTANAC GGGGGAGNAT TAMATCHAT 2880 AMATATATT TAMATCA AGCAMATATA CATTITUTCA GGATHATTIC CCGTAMANC 3000 GARGAGGAC CTCCTATATA CATATTANAC TACATTANAC TITUTATATA CAGAMATCH 3120 TOTOGGGGG THATATATACA GGANAGATA GATTACCA GAMATCHA ATTICATATAT AGCATCAMATCH 2880 CAMATTATT AMGRATACA GATAGATACA CTGTAGATA TAMATCHA ACCTUANACT 3120 CAMATTATT AGGATAGA ACCTTAGATA ACCTTAGATA TAMATCHA CAGAMATCH 2880 CAMATTATC AGGATAGA ACCTTAGATA ACCTTAGATA CAGAMATCHA CAGAMATCH 2880 CAMATTATC AGGATAGA ACCTTAGATA CAGAMATCHA TAMATCHA CAGAMATCH 2880 CAGAMATCH CTTANATACA GGATACATAGA CAGAMATCHA CAGAMATCH 2880 CAGAMATCH CTTANATACA GGATACATAGA CAGAMATCHA CAGAMATCH 2880 CAGAMATCH CTTANATACA GGATACATAGA CAGAMATCHA CAGAMATCH 2880 AGGATACTATATATACA GGATACATAGA CAGAMATCHA CAGAMATCH 2880 CAGAMATCH CTTANATACA GGATACATAGA CAGAMATCHA CAGAMATCH 2880 CAGAMATCH CTTANATACA GGATACATAGA CAGAMATCHA CAGAMATCH 2880 CAGAMATCH CTTANATACA GGATACATAGA CAGAMATCHA CAGAMATCH 2880 AGGATACHA TAMATCHA TAMATCHA TAMATCHA TAMATCHA CAGAMATCH 2880 AGGATACHA TAMATCHA TAMATCHA TAMATCHA TAMATCHA CAGAMATCH 2880 CAGAMATCHA CTTANATACA GGATACATAGA CAGAMATCHA TAMATCHA TAMATC		TTTTCAAGAA	CIMACACAGI	TATICCIAIA	CIGGRIIIIA	CARACCTTAT	ACTORACTOR	
55 AAAAATCACA AAATTATTO TAAATTAGAG GGGGGAATT TAGAATTAGA TATAAAAGG 2946 CAGAATTAGA TAAGAGTAGAA TICATTAGAAC AATTATAGAT GAGATTAGA CAGAAAGC GTAGTGGGCA COCCATATA CHATTAGATC ATATTAGAC TATATAGAA CAGAAACC GTAGTGGGCA COCCATATA CHATTAGATC TACATTAGA TATATAGA CAGAAACCC TACATTAGACA CAGAAGCCT TACATTAGA TATATAGACA CAGAACTGGGT 1320 CAGAATTAC KAGAGTAGA AACTTGGAA TATATAGAGA TACATAGAACA CAGAACCCC CAGAATTAC KAGAGTAGA AACTTGGAA TATATAGAGA TACATAGAACA 1346 CAGAATTAC CAGATCAGAA AACTTGGAA TATATAGACA CACATAGATA 1360 GGCCATAGTCC CAGATCAGAA CAGTCAGAACCCC CAGATCAGACA 1360 GGCCATAGTCC CAGATCAGAA CAGTCAGAACCC CAGATCAGACA 1360 GGCCATAGTCC CAGATCAGAC CAGATCAGACA CAGATCAGACA 1360 GGCCATAGTCC CAGATCAGACACCCC CAGATCAGACACCCC CAGATCAGACACCCC CAGATCAGACACCC CAGATCAGACACCCC CAGATCAGACACCC CAGATCAGACACCC CAGATCAGACACCC CAGATCAGACACCC CAGATCAGACACCC CAGATCAGACACCC CAGATCAGACACCC CAGATCAGACACCC CAGATCAGACACCC CAGATCAGACACCCACACCC CAGATCAGACACCC CAGATCAGACACCACACC		TGTTTAGGAA	TAAGAATGTG	CATGAMGCCT	AAAATACCAA	COCCUTAT	ACTOMATTIA	
CMARATREET ARAGAGRACA TECATTANAC RITTUTICA GORITANTIC COGTANANAC GARGAGRACA CECCALATAR CALATRAGA TECATAGA TECATAGA TECATAGA TECATAGA TETATAGA TECATAGA TECATAGA TETATAGA TECANATCI 1800 AMATRATICT ARAGAMICA GARGAGRACA CHURACCAS GARATTOGA TETATAGA CHURACAG GARGAGRACA CHURACAGA TANTANCAC COMANGUET DATURCOGA TETATAGA ACCUTAGA TANTANCAC ATATARAGAC ACATAGA ACTUTAGA TANTANGAC ATATARAGAC ACATAGA COMANGUET CHURACAGA TANTANGAC ATATARAGAC ACATAGA COMANGUET CONTINUA TANTANGAC ATATARAGAC ACATAGA COMANGUET CONTINUA TANTANGAC ATATARAGAC ATATARAGACA	55	AGCAAAGAAA	TAAAGGAGAA	AAGAGAAGAA	TCTGAGAATT	COGGAGGCA1	MUMITETIAL	
GRATTAGGC CETCHATAT CHAFTMOTO TACATITAGC TITUTATATA CARAMATU 3000 AMATUTATUT ANUMATURA AGAINATUGA CAUTUMCAA AGAINTEGGA TITUCADARU 3130 60 TAMTOCOMO TATATATUGA AGAINATUGA TATATAGA AGAINTEGGA TITUTAGANTO CANAMACHU DAVIGUCOMO TATATATUGA CANAMACHU DAVIGUCOMO TATATAGAUC AGAINTAGA AGAINTAGA TATATAGAGA TATATAGACHA AACTAGATA TATATAGACH AACTAGATA TATATAGACH ACTAGATAGA TATATAGACH AGAINTAGA CHACATAGA CHA	33	AAAAATCACA	AAATTTGTTG	TAAATTAGAG	GGGAGAAATT	TAGAATTAAG	THIMOUNDS	
AMATATATT AATGMATTCA MGCANTATAC ACTURACCAA GAMATTGGAA TITCAMANTO 3120 TOGTOGGGG THATATACCA GATGGATGAC GRUGHTGATT TANTATACCA CAGACTGGGT 3124 60 TATTGCCAAG THATATACCA COAMAGUTO TATGGTGGA TATTGTCAAG TATATAGACT ACACTAMITA 3240 CAMATTATCA GAGGTGATA ACCTTGTAAT ATATAGACTA ACATTGAAT 3240 TCATTGTATT CANTEGARA ACTTGTAAT ATATAGACTACA ATATAGAACT ACACTAMITA 3140 GAGGTTGTT GATTCAGAA ATATACTGCT ATATGGAGT COCTUCTOTO GCATTCTCTA 3420 GAGGTTGTT TITTACAGAA TATATCTCT ATATGGAGT CA		CAGAATTAGT	ATAGAGTACA	TTCATTAAAC	ATTTTTGTCA	GGATTATTIC	CCGTAAAAAC	
TOOPGOOSE THANHACCA GARGATECA GRAGITAGIT TARGATACA CAGACGGOT 3180 TATGOCOM THANHACCA CAMAGGOT PARGACGGA HUTCHOSTA SCACTOGATTA CAMAMITATE ANGERGITA ANCTITIGATA TATATAGAGA HATHAMACI ACACHAGTA CAMAMITATE ANGERGITA ANCTITIGATA TATATAGAGA HATHAMACI ACACHAGTA TATATAGAT GARTAGAGA ANGENTETAG		GTAGTGAGCA	CTCTCATATA	CTAATTAGTG	TACATTTAAC	TTTGTATAAT	ACAGAAATCT	
60 TATTGCCAMG TRATATATCA COAMAGGTO TATGGCTGGA TGTTCTGGTT ACCTGGTTTA 3240 CAMATTATCA GAGGTGATA AACTTGGATA TATGTGGGGA TGTTGAGTGAT ACACTMGGTTA 3240 CAGTTGGATT CGATTGAGAA AGTGTTGA TATGTCTGGG TGTTCAGTG CACATMGTAT 3140 CAGCAGTTGT CTTATGTATCA GGTACTGAGA CCATACTGGG CCCTTCTGGG GCATCCTGT 3420		AAATATATTT	AATGAATTCA	AGCAATATAC	ACTTGACCAA	GAAATTGGAA	TTTCAAAATG	
CAAAATTATC AGAGTAGTAA AACTITGATA TATATGAGGA TATTAAAACT ACACTAAGTA 3300 TCATTGATT GGATTCAGAA AGACTTGAA TATCCTCAGA TGCTTCAGT CTGTCAGTTG 1360 GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420 GATGTTCTT TTTATACACAA TAMATTCCTT AATATCAGCTT GA	60	TTCGTGCGGG	TTATATACCA	GATGAGTACA	GTGAGTAGTT	TATGTATCAC	CAGACTGGGT	
TCATTIGATI CGATICAGAA AGIACTITGA TATCICTCAG TGCTICAGTO CTATCATTGI 3360 GGICGATTGI CTITATATAC GGIACTGIAG CCATACTAGG CCTGTCTGIG GCATTCTCIA 3420 GATGITICTI TITTACACAA TAAATTCCTI ATATCAGGT G	OU	TATTGCCAAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTGGTT	ACCTGGTTTA	
GAGCAATTGT CITTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420 GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G		CAAAATTATC	AGAGTAGTAA	AACTTTGATA	TATATGAGGA	TATTAAAACT	ACACTAAGTA	
GATGETECTT TITTACACAA TAAATICCIT ATATCAGCTT G		TCATTTGATT	CGATTCAGAA	AGTACTTICA	TATCTCTCAG	TGCTTCAGTG	CTATCATTGT	
65 GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G		GAGCAATTGT	CTTTATATAC	GGTACTGTAG	CCATACTAGG	CCTGTCTGTG	GCATTCTCTA	3420
05		GATGTTTCTT	TTTTACACAA	TAAATTCCTT	ATATCAGCTT	G		
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		415 Protei					
70	1	11	21	31	11	51 I	
, ,	MADKT-SVIII.T	LTFALSVIND	LHRI-KAAAFP	OTTRKISPNW	RSGINVDLAI	STROYHLOOL	60
	EABAGEMNS!	SVEGFRELLQ	NIGIDKIKRI	HIHHDHDHHS	DHEHHSDHER	HSDHEHHSDH	120
	ENHSDNDHHS	HHNHAASGKN	KRKALCPDHD	SDSSGKDPRN	SOCKGAHRPE	HASGRRNVKD	186
	SVSASEVTST	VYNTVSEGTH	PLETIETPRP	GKLPPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
75	NESVSEPRKG	FMYSRNTNEN	POECFNASKL	LISHGMGIQV	PLNATEFNYL	CPAIINQIDA	300
	RSCLIHTSEK	KAEIPPKTYS	LOIAWVGGFI	AISIISFLSL	LGVILVPLMN	RVFFKFLLSF	36
	LVALAVGTLS	GDAPLHLLPH	SHASHHHSHS	HEEPAMEMKR	GPLFSHLSSQ	NIEESAYPDS	420
	TWKGLTALGG	LYFMFLVEHV	LTLIKOPKOK	KKKNOKKPEN	DDDARIKKOT	SKYESQLSTN	486
	EEKVDTDDRT	EGYLRADSOE	PSHFDSQQPA	VLEEEEVMIA	HAHPQEVYNE	YVPRGCKNKC	540
80	HSHFHDTLGO	SDDLIHHHHD	AKHIPHKKHH	QNHHPHSHSQ	RYSREELEDA	GVATLAWMVI	60
	MCDGLHNFSD	GLAIGAAFTE	GLSSGLSTSV	AVECHELPHE	LGDFAVLLKA	GMTVKQAVLY	66
	NALSAMLAYL	GMATGIFIGH	YABNVSMWIF	ALTAGLENYV	ALVDMVPEML	HNDASDHGCS	72
	PWGYPPLONA	GMLLGFGIML	LISTFRHKIV	FRINF			

Seq ID NO: 416 DNA sequence
Nucleic Acid Accession 8: NM_015419.1
Coding sequence: 1..8487

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	1	!	1	1	1	TTGGGGCCAT CGAGGTCCAC GGAAAGAATC ACTGACCAAG AGCTTTAAGA GATCACAGGA CAAGATCGAG TTTGGAAGGA CGATTATTTC	60
5	ATGCCCAAGC	GCGCGCACTG	GGGGGCCCTC	TCCGTGGTGC	TGATCCTGCT	TIGGGGGCCAT	120
,	TOCACOTTOC	CATCCCTGGC	TTCCGTGCCC	GCTGGCATTG	CTAGACACGT	GGAAAGAATC	180
	AATTTGGGGT	TTAATAGCAT	ACAGGCCCTG	TCAGAAACCT	CATTTGCAGG	ACTGACCAAG	240
	TTGGAGCTAC	TTATGATTCA	CGGCAATGAG	ATCCCAAGCA	TCCCCGATGG	AGCTTTAAGA	300
10	GACCTCAGCT	CTCTTCAGGT	TTTCAAGTTC	AGCTACAACA	AGCTGAGAGT	GATCACAGGA	360 420
10	CAGACCCTCC	AGGGTCTCTC	CAACCCCCTTA	AGGCTGCACA	GGCTACTCCA	TTTGGAAGGA	480
	AATCTCCTCC	ACCAGCTGCA	CCCCAGCACC	TTCTCCACGT	TCACATTTTT	GGATTATTTC	540
	AGACTCTCCA	CCATAAGGCA	CCTCTACTTA	GCAGAGAACA	TGGTTAGAAC	TCTTCCTGCC	600
10	AGCATGCTTC	GGAACATGCC	GCTTCTGGAG	AATCTTTACT	TGCAGGGAAA	TCCGTGGACC	660
15	TGCGATTGTG	AGATGAGATG	GTTTTTGGAA	TGGGATGCAA	AATCCAGAGG	CACTCCAAG	720 780
	TGTAAAAAGG	CTCAAGCTTT ACCAGCTGCA CCATAAGGCA GGAACATGCC AGATGAGATG	ACACAAGCTG	AAGGACATGA	CTTGTCTGAA	GCCTTCAATA	840
	GAGTCCCCTC	TGAGACAGAA	CAGGAGCAGG	AGTATTGAGG	AGGAGCAAGA	ACAGGAAGAG	
	GATGGTGGCA	GCCAGCTCAT	CCTGGAGAAA	TTCCAACTGC	CCCAGTGGAG	CATCTCTTTG GNANCCATTG ANATGCANCA ATGGAACA ATGGAACA CTACACAGGT AGATATCCAG CCAGTATTCT AATGATTGAG CGAGTTGAGC TGGCTCCATT TGGCTCGCT TCAAGTGAGG TCAAGTGAGG TCAAGTGAGG AGATTATCAAGA AGAGCAGAC ATGGATGAGA AGAGCAGAC AGATTATTAAGA AGAGCAGAC AGATTATTAATTAAT AGATTAAAA AGAGCAGAAAA AGAGCAAAAA AGAGCACAAAA	960
20	AATATGACCG	ACGAGCACGG	GAACATGGTG	AACTTGGTCT	GTGACATCAA	GAAACCAATG	1020
	GATGTGTACA	AGATTCACTT	TCCAATGACG	CCACAAAAACT	ATGRADAGCT	ATTGGAAATTG	1140
	ATAGCATACT	ACAGTGAAGT	TCCCGTGAAG	CTACACAGAG	AGCTCATGCT	CAGCANAGAC	1200
	CCCAGAGTCA	GCTACCAGTA	CAGGCAGGAT	GCTGATGAGG	AAGCTCTTTA	CTACACAGGT	1260
25	GTGAGAGCCC	AGATTCTTGC	AGAACCAGAA	TGGGTCATGC	AGCCATCCAT	AGATATCCAG	1320
	CTGAACCGAC	GTCAGAGTAC	GGCCAAGAAG	CCTCCCCCCC	COTACTACAC	AATGATTGAG	1440
	CCTACTCCAC	CTGTGCAAAG	AGATCAGACT	GTCCTGGAAG	GGGGTCCATG	CCAGTTGAGC	1500
	TGCAACGTGA	AAGCTTCTGA	GAGTCCATCT	ATCTTCTGGG	TGCTTCCAGA	TGGCTCCATC	1560
30	CTGAAAGCGC	CCATGGATGA	CCCAGACAGC	AAGTTCTCCA	TTCTCAGCAG	TGGCTGGCTG	1620
	AGGATCAAGT	CCATGGAGCC	ATCTGACTCA	GGCTTGTACC	AGTGCATTGC	TCAAGTGAGG	1740
	GATGAAATGG	CACTGACAAT	TGGCAAGAAC	CTAGGGGAGT	CGGTGACATT	GCCTTGCAAT	1800
	GCTTTAGCAA	TACCCGAAGC	CCACCTTAGC	TGGATTCTTC	CAAACAGAAG	GATAATTAAT	1860
35	GATTTGGCTA	ACACATCACA	TGTATACATG	TTGCCAAATG	GAACTCTTTC	CATCCCAAAG	1920
	GTCCAAGTCA	GTGATAGTGG	TTACTACAGA	TGTGTGGCTG	TCAACCAGCA	CARAGRACIAC	1980 2040
	ACTOCCCCAC	CTCCAAACCC	TCTTTCCAGA	GTCAGAGAAG	ACATOGTGGA	GGATGAAGGG	2100
	GGCTCGGGCA	GTGATAGTGG TGGGAATCAC GTGCAAAGGC TGGGAGATGA	AGAGAACACT	TCAAGGAGAC	TTCTGCATCC	AAAGGACCAA	2160
40							2220
	AGAAGAAAGC	TGAAACTCTG	GAAGCATTCG	GAAAAAGAAC	CAGAGACCAA	TOTTIGCAGAA GATTAATCOG GGGCACAGAA CACACCACT TGCTGAAGAA CATTTCCTCA TGAAGTAACA GATTACATCA GATTACATCA GATTACATCA CTTTTGAACCA AGAGACGGCA CATTTGACCA ATTTGAGCAC ATTTGAGCAC AAGAGACAAC AAGGGTATG GACAGACAAC CACACACTCC CTCCACACTC	2280 2340
	GGTCGCAGAG	TGTTTGAATC	MCCCAAAGG	COTTOCODADA	ATCTCCCTAA	GGGCACAGAA	2400
	GTACCCCCGT	TGATTAAAAC	CACAAGTCCT	CCATCCTTGA	GCCTAGAAGT	CACACCACCT	2460
45	TTTCCTGCTG	TTTCTCCCCC	CTCAGCATCT	CCTGTGCAGA	CAGTAACCAG	TGCTGAAGAA	2520
	TCCTCAGCAG	ATGTACCTCT	ACTTGGTGAA	GAAGAGCACG	TTTTGGGTAC	CATTTCCTCA	2580 2640
	GCCAGCATGG	GGCTAGAACA	CAACCACAAT	CTTTCTGAGA	AGACTGAGGA	GATAACTTCC	2700
	ACTGAAGGAG	ACCTGAAGGG	GACAGCAGCC	CCTACACTTA	TATCTGAGCC	TTATGAACCA	2760
50	TCTCCTACTC	TGCACACATT	AGACACAGTC	TATGAAAAGC	CCACCCATGA	AGAGACGGCA	2820
	ACAGAGGGTT	GGTCTGCAGC	AGATGTTGGA	TCGTCACCAG	AGCCCACATC	CAGTGAGTAT	2880 2940
	GAGCCTCCAT	TGGATGCTGT	ACCAGATGAG	GATAAGATGA	AAGAAGACAC	CTTTGCACAC	3000
	CTTACTCCAA	CCCCACCAT	CTGGGTTAAT	GACTCCAGTA	CATCACAGTT	ATTTGAGGAT	3060
55	TCTACTATAG	GGGAACCAGG	TGTCCCAGGC	CAATCACATC	TACAAGGACT	GACAGACAAC	3120
	ATCCACCTTG	TGAAAAGTAG	TCTAAGCACT	CAAGACACCT	PACTGATTAA	CACACACTCC	3180 3240
	AAAGAGATGT	ACRETERECE	CCAAGAGAGG	AAATCCATCA	CTTTGCCTGA	CTCCACACTG TGGTACCCTC TCCGTCATCC	3300
	GGTATAATGA	GCAGTATGTC	TCCAGTTAAG	AAGCCTGCGG	AAACCACAGT	TGGTACCCTC	3360
60	CTAGACAAAG	ACACCACAAC	AGTAACAACA	ACACCAAGGC	AAAAAGTTGC	TCCGTCATCC	3420
	ACCATGAGCA	CTCACCCTTC	TCGAAGGAGA	CCCAACGGGA	GAAGGAGATI	ACACACTETE	3540
	TOTACTORAC	CARCTCARGO	ACCTGACATT	AAGATTTCAA	GTCAAGTGGA	GAGTTCTCTG	3600
	GTTCCTACAG	CTTGGGTGGA	TAACACAGTT	AATACCCCCA	AACAGTTGGA	AATGGAGAAG	3660
65	AATGCAGAAC	CCACATCCAA	GGGAACACCA	CGGAGAAAAC	ACGGGAAGAG	GCCAAACAAA	3720
	CATCGATATA	CCCCTTCTAC	AGTGAGCTCA	AGAGCGTCCG	ANACTATACT	TTTCCCTAGA	3840
	CCAGAAAATA	AACATAGAAA	GGGCCCTTAT	GATTCCTTAG	ATTACATGAC	AACCACCAGA	3900
	ACIGITICIC	CATCTTACCC	TAAAGTCCAA	GAGACACTTC	CAGTCACATA	TAAACCCACA	3960
70	TCAGATGGAA	AAGAAATTAA	GGATGATGTT	GCCACAAATC	TTGACAAACA	TAAAAGTGAC	4020
	ATTTTAGTC	CTGGTGAATC	AATTACTAAT	GCCATACCA	CTTCTCGCTC	CTTGGTCTCC	4080
	ACTATGGGAG	AATTTAAGGA	COCTOGGAGG	CTACAGACAG	ACATACCTGT	TACCACCTCT	4200
	GGGGAAAATC	TTACAGACCC	TCCCCTTCTT	AAAGAGCTTC	AGGATGTGGA	TTTCACTTCC	4260
75	GAGTTTTTGT	CCTCTTTGAC	AGTCTCCACA	CCATTTCACC	AGGAAGAAGC	TGGTTCTTCC	4320
	ACAACTCTCT	CAAGCATAAA	AGTGGAGGTG	GCTTCAAGTC	AGGCAGAAAC	CACCACCCTT	4380
	GATCAAGATC	ATCTTGAAAC	CACTGTGGCT	ATTCTCCTT	CTGAAACTAG	CACACAGAAT	4500
	ATGTCTTTT	GACAAACCAC	CACCACTAAG	CCAGCACTTO	CCAGTCCAAG	TOSTRACCITO ACGCCCARC ACGCCCARC ACGCCCARC ACGCCCARC ACGCCTTCT GASTICTCTG GASTICTCTG ACGCCATTCT TTGCTAGA ACCACCAG TAAAAGTGAC CTGGTCTC CACCACCT CACCACCAG TACAACCACA ACCACCAG ACCACCAG ACCACCAG ACCACCAG ACCACCAG ACCACCAG ACCACCAG ACCACCAG ACCACCAG ACCACCACCAG ACCACCACCAC ACCACCACCAC ACCACCACCAC ACCACC	4560
80	GCATCTAGAG	ATTOCAAGGA	AAATGTTTTC	TTGAATTATO	TGGGGAATC	AGAAACAGAA	4620
	GCAACCCCAC	TCAACAATGA	AGGAACACAG	CATATGTCAC	GGCCAAATGA	ATTATCAACA	4680 4740
	CCCTCTTCCC	ACCGGGATGC	ATTTAACTTG	TCTACAAAGC	TGGAATTGG	AMAGUMAGTA	4800
	TITIGGTAGTA		. ACCTOCCCO	B B B CCCCB TOCC	TRACCARCACE.	AACAGTGAGG	4860
85	CTACCTGAA	TGTCCACACA	AAGCGCTTCC	AGATACTTT	TAACTTCCC	GTCACCTCGT AGAGAACAAA CATGTCCAAA	4920
	CACTGGACCI	A ACAAACCGGA	AATAACTACA	TATCCTTCTC	GGGCTTTGCC	AGAGAACAAA	4980
	CAGTTTACA	A CTCCAAGATI	* ATCAAGTACA	ACAATTCCTC	TCCCATTGC	CATGTCCAAA	5040

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	CCCAGCATTC	CTAGTAAGTT	TACTGACCGA	AGAACTGACC	AATTCAATGG	TTACTCCAAA	5100
	GTGTTTGGAA	ATAACAACAT	CCCTGAGGCA	AGAAACCCAG	TTGGAAAGCC	TCCCAGTCCA	5160
	NON AMERICANA	ATTATTCCAA	TOGRAGACTO	COMPTOTTE	CARCARGAC	ACALAL CALANA	5220
	MUMITICAL	ATTATICCAN	TOURNONCIC		OTTOTAL	DOWN DOWN OR	5280
-	CCACAGTTGG	GAGTCACCCG	GAGACCCCAG	ATACCCACTT	Crccracccc	AGTAATGAGA	
5	GAGAGAAAAG	TTATTCCAGG	TTCCTACAAC	AGGATACATT	CCCATAGCAC	CTTCCATCTG	5340
							5400
		***************************************	manconorce	maca ccca ca	COTTOTATOTO	CTTTATAACA	5460
	ACTANCITAC	AGAATATCCC	INIOGICICI	ICCACCCAGA	GIICINICIC	CTTTATAACA TGCAGGAGGA CAAGTCCCCA	
	TCTTCTGTCC	AGTCCTCAGG	AAGCTTCCAC	CAGAGCAGCT	CAAAGTTCTT	TGCAGGAGGA	5520
	CCTCCTGCAT	CCAAATTCTG	GTCTCTTGGG	GAAAAGCCCC	AAATCCTCAC	CAAGTCCCCA	5580
10	CL CL COCCOCC	CCGTCACCGC	MCACACACAC	NOTOTOTTOC	CCTGTGAGGC	AACAGGAAAA	5640
10	CAGACIGIGI	CCGICACCGC	TOMONCAGAC	ACIGIGITEC	CCIGIONOGC	TCCGAATACC	3040
	CCAAAGCCTT	TCGTTACTTG	GACAAAGGTT	TCCACAGGAG	CTCTTATGAC	TCCGAATACC	5700
	AGGATACAAC	GGTTTGAGGT	TCTCAAGAAC	CGTACCTTAG	TGATACGGAA	GGTTCAAGTA	5760
	CERCIMOCING	GCCAGTATAT	CTTCCACCCCC	ACCA ACCTOC	ACCCCCCCCCCCA	CAGGATGGTG	5820
	CAMBATOSAS	GCCAGIAIAI	0.0000000	ACCOUNTED TO	composit ont	ant con coma	5880
1.5	GTCTTGCTTT	CGGTCACCGT TGGGAGACAC	GCAGCAACCT	CARATCCTAG	CCICCCACIA	CCHGGHCGIC	
15	ACTGTCTACC	TGGGAGACAC	CATTGCAATG	GAGTGTCTGG	CCAAAGGGAC	CCCAGCCCCC	5940
	CABATTTOCT	CONTYMENTOR	TORCEGUEGG	GTGTGGCAAA	CTGTGTCCCC	CGTGGAGAGC	6000
	OCCUPATION OCCU	TGCACGAAAA	00001000000	TOCATCARCO	MOCCOTOCTT	CTCAGACAGA	6060
	COCATCACCC	TGCACGAAAA	CCGGMCCCII	ICCAICAAGG	AGGCGTCCTT	CICHORCHOR	0000
	GCCGTCTATA	AGTGCGTGGC	CAGCAATGCA	GCCCGGGGCGG	ACAGCCTGGC	CATCCGCCTG	6120
	CACCITGGGGG	CACTGCCCCC	CGTTATCCAC	CAGGAGAAGC	TGGAGAACAT	CTCGCTGCCC CAGCGTGCGC GAACTTGTTT CGGGCGCTAT	6180
20	0000000000	COLUMNOS ON M	man amagan am	COCKACCCTC	coccerace	Chargrange	6240
20	CCGGGGGCTCA	GCATTCACAT	TCACTGCACT	GCCAMGGC1G	COCCCCIOCC	CHOCOTOCOC	6240
	TGGGTGCTCG	GGGACGGTAC	CCAGATCOGC	CCCTCGCAGT	TCCTCCACGG	GAACTTGTTT	6300
	CITTTTCCCCCA	ACGGGACGCT	CTACATCCCC	AACCTCGCGC	CCAAGGACAG	CGGGCGCTAT	6360
	as amagamaa	GOGGGGA A GGM	COMMOCOMO	COCCCCACCA	COCTOCACCT	GAACGTGCAG	6420
	GMGIGCGIGG	CCGCCAACCI	GOTMOOCICC	GCGCGCAGGA	COGIGCAGCI		6480
	CGTGCAGCAG	CCAACGCGCG	CATCACGGGC	ACCTCCCCGC	GGAGGACGGA	CGTCAGGTAC	6480
25	GGAGGAACCC	TCAAGCTGGA	CTGCAGCGCC	TCGGGGGACC	CCTGGCCGCG	CATCCTCTGG AATCAAGGTG	6540
	*0000000000	CONNCROOR	CATTOCACCCC	CHCTTCACTT	TTCATACCAC	DTCDAGGTG	6600
	MOGCIGCCGI	CCMMONOGNI	GATCGACGCG	CICIICAGII	11041110010		6660
	TTTGCCAATG	GGACCCTGGT	GGTGAAATCA	GTGACGGACA	AAGATGCCGG	AGATTACCTG TGTGGTGATG	
	TGCGTAGCTC	GAAATAAGGT	TGGTGATGAC	TACGTGGTGC	TCAAAGTGGA	TGTGGTGATG	6720
	*********	AGATTGAACA	CARCORGONG	ANOGROCACA	ABGTCTTCTA	CCCCCCCCCCAC	6780
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30	CTGAAAGTGG	ACTGTGTGGC	CACCGGGCTT	CCCAATCCCG	AGATCTCCTG	GAGCCTCCCA	
							6900
	CATCOCCCC	TONACANTOO	CACACTOTAC	TTTTAACCAAC	TOCCCATGAG	GGAGGAAGGA CAGAGTCAAG GGTGCCCTAT	6960
	INIGICUICI	ICANCAATGG	GACACICIAC	22222000000	10000011010	araramarra	7020
	GACTACACCT	GCTTTGCTGA	AAATCAGGTC	GGGAAGGACG	MUNTUMUNUT	CAGAGICANG	7020
	GTGGTGACAG	CGCCCGCCAC	CATCCGGAAC	AAGACTTACT	TGGCGGTTCA	GGTGCCCTAT	7080
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55	GGMGMCG1GG	CONCIDENCE		MOCECACIO	ACTATCACAT	ATACCAAGAT	7200
	TIGICCCCAA	CCANCAGGT	GATCCCCACC	ICCICIONUM	MOINICAGAI	MINCOMMI	
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	ACCRACACCO	CGGGGAGAGGA	TAGGAAGACG	GTGTGGATTC	ACGTCAACGT	CCAGCCACCC CGGGGGCAGT	7320
	**********	00000100000	COCCATIONO	NOOTTO COOK	AGATAGCAGC	POGGGGGGGGG	7380
40	AMGATCAACG	GIMACCCCOOL	CCCCATCACC	ACCGIGCGGG	AGA TAGCAGC		
40	CCGAAACTGA	TTGACTGCAA	AGCTGAAGGC	ATCCCCCACCC	CGAGGGTGTT	ATGGGCTTTT	7440
	CCCGAGGGTG	TRETTTOTOCC	AGCTCCATAC	TATGGAAACC	GGATCACTGT	CCATGGCAAC	7500
			mmmanaana	NO CONTROLOGY	TOTACCTOOT	ATCCATCCCA	7560
	COLLECCION	ACATCAGGAG	IIIanaanaa		amoundance.	COCCAMOCALC	7620
	CGCAACGAGG	GAGGGGAGGC	GAGGTTGATC	GIGCAGCICA	CIGICCIGGA	GCCCATGGAG CCACACCATC CCTTCCCAAT	
	AAACCCATCT	TCCACGACCC	GATCAGCGAG	AAGATCACGG	CCATGGCGGG	CCACACCATC	7680
45	AGCCTCAACT	GCTCTGCCGC	GGGGACCCCG	ACACCCAGCC	TGGTGTGGGT	CCTTCCCAAT	7740
	4000100100	maga as comag	* CINCONCOMO	Chacacatacat	ACCACAAGGC	TGACGGCATG	7800
	GGCACCGATC	IGCAGAGIGG	ACAGCAGCIG	CAGCGCTTCT	ACCACAAGGC	TORCOGCATO	7860
	CTACACATTA	GCGGTCTCTC	CTCGGTGGAC	GCTGGGGCCT	ACCGCTGCGT	GGCCCGCAAT	
	GCCGCTGGCC	ACACGGAGAG	GCTGGTCTCC	CTGAAGGTGG	GACTGAAGCC	AGAAGCAAAC	7920
	*********	NAME OF COMPANY	CACCATCATC	AATGGTGAGA	CCCTGAAGCT	CCCCTGCACC	7980
50	MICHEINIC	MIMICCIGGI	CAGCATCATC	ANIGOTOTO.	doc-manage	GCATCTGGAG	8040
30	CCTCCCGGGG	CTGGGCAGGG	ACGTTTCTCC	TGGACGCTCC	CCAATGGCAT	GCATCIGGAG	8040
	GGCCCCCAAA	CCCTGGGACG	CGTTTCTCTT	CTGGACAATG	GCACCCTCAC	GGTTCGTGAG	8100
	CCCTCCCTCT	TTCACAGGGG	TACCTATOTA	TOCAGGATGG	AGACGGAGTA	CGGCCCTTCG CGAGCCCACC	8160
		######################################	mamanmaaaa	ma moore cooc	CONTCACCAC	CORRECCIONECC	8220
	GICACCAGCA	TCCCCGIGAT	TGTGATCGCC	IMICCICCCC	GGMICACCAG	CONOCCCACC	0220
	CCGGTCATCT	ACACCCGGCC	CGGGAACACC	GTGAAACTGA	ACTGCATGGC	TATGGGGATT AGGGGTTCAG	8280
55	CCCAAAGCTG	ACATCACGTG	GGAGTTACCG	GATAAGTCGC	ATCTGAAGGC	AGGGGTTCAG	8340
-			* mmmcmmc* c	COOCE COCE T	CACTCACCAT	CCROCKTOCC	8400
	GCTCGTCTGT	ATGGAUMCAG	ATTTCTTCAC	CCCCAGGGAI	CACTGACCAT	CCAGCATGCC	0400
	ACACAGAGAG	ATGCCGGCTT	CTACAAGTGC	ATGGCAAAAA	ACATTCTCGG	CCAGCATGCC CAGTGACTCC	8460
	*CARCARROC	CCCCCTTTCTA	ACCCARACCCA	COTTGGGGAA	TAGGAGGTCT	TAAATAATGT	8580
60	ACHACHANGC	GGGGIIIGIA	AUGUANUCCA	99110000001		ACCOUNT CA A DOC	8640
60	GTCACAGTGC	ATGGTGGCCT	CIGGTGGGTT	TCAAGTTGAG	GITGATCITG	ATCTACAATT	0040
	GTTGGGAAAA	GGAAGCAATG	CAGACACGAG	AAGGAGGGCT	CAGCCTTGCT	GAGACACTTT	8700
	CONTRACTOR OF THE PARTY OF THE	TACATCATOC	Chaggggggggg	ATTYCACCOTTC	TOTATACTOR	GACTGCAATT	8760
	CITITIGIGIT	INCATCATOC		************	OMOGOT WAGON	GAGACACTTT GACTGCAATT TATCTGAGGA	8820
	TTTCTTCTTT	TGCAAATGCC	ACTCGACTGC	CITCATANGC	GICCAIAGGA	INICIONOGA	0020
	ACATTCATCA	AAAATAAGCC	ATAGACATGA	ACAACACCTC	ACTACCCCAT	TGAAGACGCA	8880
65							
00	TORCOTAGE	,0100100100		* ODGG TGG	COCCERTANC	Christing	9000
	TCTTTCAGTT	ATTICCICTG	CACTTONAN	ACTUCAGGIT	OCCUPATARO	GATTTAGAAC CAGCTACCAT ATGTTTTATA TTTCTGTCTT	3000
	CAGAGTGACT	GATATATATA	TATATATTTT	AATTCAGAGT	TACATACATA	CAGCTACCAT	9060
	TTTATATCAA	AAAAGAAAAA	CATTTCTTCC	TGGAACTCAC	TTTTTTATATA	ATGTTTTATA	9120
	mhmhmh mann		A TOTAL CO.	CACACTACAA	CONCANAMAC	TTTCTCTCTT	9180
70	INTATATITT	LICCITICAA	M. CHGACGAT	GAUACIAGAA	CONCOUNTIAC		2200
70							
	ATATAATTTT	AAAAAATTTC	TCTCCAACCT	CCTTCAAATT	CAGTCACCAC	· TGTTATATTA	9300
	commonoc: a	Chaccorcas	COCCOCATOC	CONTRACTOR	ACAPTITICATE	GTATGCAAAG	9360
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							9420
	AACTTTACAC	AATTGAATCT	AGAGTCTTCC	CCGAAAAGCC	CAGAAACTTC	TCTGCAGTAT	9480
75	amaa ammana	ar morroconon	*************	COMPONE COCC	ACCCATGAGE	TCTGCAGTAT CAGTTTGTGC	9540
,,	CIGGCIIGIC	CATCIGGICT	NUOGIOCIO		- CCC COAGI	maa.comm	0000
	CCATGAATAA	TACACGACCT	CTTATTTCCA	TGACTGCTTT	ACIGIATITI	TAAGGTCAAT	9600
	ATACTGTACA	TTTGATAATA	AAATAATATT	CTCCCAAAAA	AAAAA		
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80	Protein Ac	cession #:	NP_056234.1				
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	1	11	21	31	41	51	
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	MPKRAHWGAL	SVVLILLWCH	PRVALACPHP	CACYVPSEVH	CTFRSLASVP	AGIARHVERI	60
85	NLGFNSIQAL	SETSFAGLTK	LELLMINGNE	IPSIPDGALR	DLSSLQVFKF	SYNKLRVITG	120
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	DI CTTDUI.VI.	A DAMAUDTI.DA	CMT.DWMDT.T.P	NI.VIAGNPWT	COCEMBUFLE	WDAKSRGILK	240

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	CKKDKAYEGG	QLCAMCFSPK	KTAKHEIHKT	KDMTCLKPSI	BSPLRQNRSR	SIEEEQEQEE	300
	DGGSOLILEK	POLPOWSISL	NMTDEHCNMV	NLVCDIKKPM	DVYKIHLNOT	DPPDIDINAT	360
	VALDFECPMT	RENYEKLWKL	IAYYSEVPVK	LHRELMLSKD	PRVSYQYRQD	ADEEALYYTG	420
	VRACTLARPE	WVMQPSIDIQ	LNRROSTAKK	VLLSYYTOYS	OTISTEDTRO	ARGRSWVMIE	480
5	PSGAVORDOT	VLEGGPCOLS	CNVKASESPS	IFWVLPDGSI	LKAPMDDPDS	KPSILSSGWL	540
-	RIKSMEDSDS	GLYQCIAQVR	DEMORMVYRV	LVOSPSTOPA	BKDTVTIGKN	PGESVTLPCN	600
	ALAT PEAHLS	WILPHRRIIN	DLANTSHVYM	LPNGTLSIPK	VOVSDSGYYR	CVAVNQQGAD	660
	HETVGITVTK	KGSGLPSKRG	RRPGAKALSR	VREDIVEDEG	GSGMGDEENT	SRRLLHPKDO	720
	EVELKTKODA	INGDKKAKKG	RRKLKLWKHS	EKRPETNVAE	GRRVFESRRR	INMANKOINP	780
10	ERWADILAKV	RGKNLPKGTE	VPPLIKTTSP	PSLSLEVTPP	FPAVSPPSAS	PVQTVTSAEE	840
	SSADVPLLGE	EEHVLGTISS	ASMGLEHNIN	GVILVEPEVT	STPLEEVVDD	LSEKTEEITS	900
	TEGOLKGTAA	PTLISEPYEP	SPILHTLDIV	YEKPTHBETA	TEGWSAADVG	SSPEPTSSEY	960
	EPPLDAVSLA	ESEPMOYFDP	DLETKSOPDE	DKMKEDTFAH	LTPTPTIWVN	DSSTSQLFED	1020
	STIGEPGVPG	OSHLOGLTON	IHLVKSSLST	ODTLLIKKGM	KEMSOTLOGG	NMLEGOPTHS	1080
15	RESERVEDORS	KSITLPDSTL	GIMSSMSPVK	KPAETTVGTL	LDKDTTTVTT	TPRQKVAPSS	1140
	TMSTHPSRRR	PNGRRRLRPN	KFRHRHKOTP	PTTPAPSETP	STOPTOAPDI	KISSQVESSL	1200
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	DENKHRNIVT	PSSETILLPR	TVSLKTEGPY	DSLDYMTTTR	KIYSSYPKVQ	ETLPVTYKPT	1320
	SDGKETKDDV	ATNVDKHKSD	ILVIGESITN	AIPTSRSLVS	TMGEFKEESS	PVGFPGTPTW	1380
20	NESSTACEGE	LOTDIPVITS	GENLTDPPLL	KELEDVDFTS	BFLSSLTVST	PPHQEEAGSS	1440
	TTLESIEVEV	ASSOAETTTL	DODHLETTVA	ILLSETRPON	HTPTAARMKE	PASSSPSTIL	1500
	MSLCOTTTTK	PALPSPRISO	ASRDSKENVP	LNYVCNPETE	ATPVNNEGTQ	HMSGPNELST	1560
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25	DSTPSKFTOR	RTDOFNGYSK	VPGNNNI PEA	RNPVGKPPSP	RIPHYSNGRL	PFFTNKTLSF	1740
	POLGVTRRPO	IPTSPAPVMR	ERKVI PGSYN	RIHSHSTPHL	DPGPPAPPLL	HTPQTTGSPS	1800
	TNI ON I PMVS	STOSSISPIT	SSVOSSGSFE	OSSSKFFAGG	PPASKFWSLG	EKPOILTKSP	1860
	OTVEVTARTO	TVFPCRATGK	PKPFVTWTKV	STGALMTPNT	RIORFEVLION	GTLVIRKVQV	1920
	ODRGOYMCTA	SNLHGLDRMV	VLLSVTVQQP	QILASHYQDV	TVYLGDTIAM	ECLAKGTPAP	1980
30	OISWIPPDRR	VWQTVSPVES	RITLHENRTL	SIKRASPSDR	GVYKCVASNA	AGADSLAIRL	2040
	HVAALPPVIH	OEKLENISLP	PGLSIHIHCT	AKAAPLPSVR	WVLGDGTQIR	PSQFLHGNLP	2100
	VFPNGTLYIR	NLAPKDSGRY	ECVAANLVGS	ARRTVQLNVQ	RAAANARITG	TSPRRTDVRY	2160
	GGTLKLDCSA	SGDPWPRILW	RLPSKRMIDA	LFSFDSRIKV	PANGTLVVKS	VTDKDAGDYL	2220
	CVARNKVGDD	AAAPKADAAW	KPAKIEHKEE	NDHKVFYGGD	LKVDCVATGL	PNPEISWSLP	2280
35	DOSLVNSFMQ	SDDSGGRTKR	YVVFNNGTLY	FNEVGMRBEG	DYTCFAENQV	GKDEMRVRVK	2340
	VVTAPATIRN	KTYLAVQVPY	GDVVTVACEA	KGEPMPKVTW	LSPTNKVIPT	SSEKYQIYQD	2400
	GTLLIQKAQR	SDSGNYTCLV	RNSAGEDRKT	AMIHAMAGED	KINGNPNPIT	TVREIAAGGS	2460
	RKLIDCKAEG	IPTPRVLWAP	PEGVVLPAPY	YGNRITVHGN	GSLDIRSLRK	SDSVQLVCMA	2520
	RNEGGEARLI	VOLTVLEPME	KPIPHDPISE	KITAMAGHTI	SLNCSAAGTP	TPSLVWVLPN	2580
40	GTDLQSGQQL	QRPYHKADGM	LHISGLSSVD	AGAYRCVARN	AAGHTERLVS	LKVGLKPEAN	2640
	KQYHNLVSII	NGETLKLPCT	PPGAGQGRPS	WILPNGMHLE	GPQTLGRVSL	LDNGTLTVRE	2700
	ASVFDRGTYV	CRMETEYGPS	VISIPVIVIA	YPPRITSEPT	PVIYTRPGNT	VKLNCMAMGI	2760
		DKSHLKAGVQ	ARLYGNRPLH	PQGSLTIQHA	TORDAGFYKC	MAKWILGSDS	2820
40	KTTYIHVP						
45							

Seq ID NO: 418 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1..5001

	Coding sequ	ience: 15	001				
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55	TCAAGACAGT	ACACCGTGCG	CTATCGAGAG	AAGGGGGAAT	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGGCGTGT	GCTGATTGAG	AACCTGATTC	CAGACACTGT	GTATGAATTT	300
	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAAATGGA	GTACGTCAGT	CTTCCAAAGA	360
	ACACCAGAAT	CTGCCCCTAC	CACAGCTCCT	GANANCTTGA	ACGTCTGGCC	AGTCAATGGC	420
	AAACCTACAG	TTGTCGCTGC	ATCTTGGGAT	GCGCTACCAG	AGACTGAGGG	GAAAGTGAAA	480
60	GTCTGTCTGC	TGGACACAGG	ACTOTTTTCA	GTTTCCTCCT	TCCAACCATC	TGCCAAATCA	540
	TTTCAGAATA	CATTCTTTCA	TACGCCCCGG	CTCTCAAACC	ATTTGGAGCA	AAGTCCCTCA	600
	CCTATCCTGG	AGACACTACT	TCTGCCCTGG	TGGATGGTCT	GCAGCCTGGG	GAACGCTATC	660
	TTTTCAAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATTG	720
	TOGCTATGCC	AACAAGAATG	CAGCTGTACC	CAGAAGGATT	TCAGTTGTCT	AGCTTACCTG	780
65	ATCGATATCC	AAACCAAACA	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTGGA	840
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	GCCAGTAAGG	CGGATGTTCA	GCAGAACACG	GAGGACAATG	GGAAACCCGA	AAAACCTGAG	1020
	CCTTCCTCAC	CTTCTCCCAG	AGCTCCAGCT	TCCTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
70	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAAAAT	ATTGGCTAAT	1140
	GGTGGGGCGC	CCCGAAAACC	CCAGCTTCGC	GCCAAGAAGG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCACTGGGGA	GGAGGAGCTG	GGTTCCCGGG	AGGACTCGCC	CATGTCACCC	1260
	TCAGACACCC	AAGACCAGAA	ACCGACCCTG	AGGCCGCCAA	GTAGACACGG	CCACTCGGTG	1320
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75	GTAGATAAGC	CTGGCTTTTC	CCTGGCCACG	CAGCCCCGCC	CAGGGGGGCCC	CCCCTCGGCT	1440
	TEGGECETETE	CTGCCCACCA	CGCGTCCACC	CAGGGCACCT	CTCATCGTCC	TTCCCTGCCT	1500
	GCCAGCTTGA	ATGACAACGA	CTTGGTGGAC	TCAGACGAAG	ATGAGCGCGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGGCGCCTT	CGCCCAGCCC	CGGCCAGCCC	TGTCCCCCAG	CCGCCAGTCC	1620
~~	CCGTCCAGCG	TTCTCCGCGA	CAGAAGCTCT	GTGCACCCCG	GCGCAAAGCC	AGCCTCGCCG	1680
80	GCGCGGAGGA	CCCCCCATTC	AGGGGCCGCA	GAGGAAGATT	CCAGTGCCTC	AGCCCCACCC	1740
	TCAAGACTTT	CTCCACCCCA	TGGGGGATCA	TCTCGGCTGC	TGCCCACCCA	GCCACACCTG	1800
	AGCTCTCCAC	TTTCCAAGGG	CGGGAAGGAT	GGTGAGGACG	CCCCAGCCAC	CAACTCCAAT	1860
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	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GTGACGGCGA	TAGGGAAGAC	1980
85	GGCGGAAGGC	AGGCGGAGGC	CACGGCCCAG	ACGCTGCGGG	CCCGGCCTGC	CTCTGGACAC	2040
	TTCCATTTGC	TCAGACACAA	ACCCTTTGCT	GCCAACGGGA	GGTCTCCAAG	CAGGTTCAGC	2100
	ATTGGGCGGG	GACCTCGGCT	GCAGCCCTCC	AGCTCCCCAC	AGTCGACTGT	GCCCTCCCGA	2160

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	TCCTCCAGGC GCCAGCCTGC	AGCCCATCTC	CCGGGGCTGG	GAGGACTTAA	AATCCACAGG	GCAGAGAGGG	2340
5	CATCOTOACC	CONCRACTO	CICCAGGGC	TOTALGGETE	AGGATGTTCA	ACAGAGCACA	2460
-	GACGCCGGACA	CGGAGGGTCA	TTCTCCCAAA	GCACAGCCAG	GGTCCACAGA	CCGCCACGCG	2520
	TCCCCTGCTC	GTCCTCCCGC	AGCACGGTCA	CAGCAGCATC	CCAGTGTTCC	CAGAAGGATG	2580 2640
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	ACGGCGAGCT	CCAGAGGGAT	GCTCCCCACG	GCCCTCCAGA	ACCAGGACGA	GGATGCCCAG	2820
	GGCAGCTACG GCCGCGCGCG	ACGACGACAG	CACAGAAGTC	GAGGCCCAGG	ATGIGGGGG	GGAGTCTYCCC	2880
	ACAGGCGCAG	GGGCAGGTGG	CGACCACAGG	TCCCAGCGCG	GACATGOGGC	CTCCCCCGCC	3000
15	MOCCOCNOCC	CACCCCCCCCC	CCCCCAGTCC	CCCCCCCCCC	TCCCCAGCAG	GGCAGCGCCG	3060
	GGGAAGTCGG	AGCCTCCTTC	CAAGCGGCCC	CTGTCCTCCA	AGTCCCAGCA	GTCGGTCTCA	3120 3180
	GCCGAGGACG TCTTCCTCTG	AGGAGGAGGA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TOTACTOCCA	GGGGGGGGAA	AGACCTTCTG	3240
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	CCCTGGCCGC	GACCGCCGCC	TCGCAGCGCT	GCCACCGTGA	GCCCCGTCGC	CCCGATGCTG	3420 3480
	TOTOTOTO	ACACCATCAT.	GCATGCCAGA	TTCCGTAACC	CTCTCTCCCG	ACAGCCTGCC	3540
	AGACCCTCTT	ACAGACAAGG	TTATAATGGC	AGACCAAATG	TAGAAGGGAA	AGTCCTTCCT	3600
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	GTTGTGGACC CATGGAAATC	TTGATCGTGG	TAAACTAGGA	AATGCAGAAG	GAAGGTACCT	AGATCTGGAA	3720
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	CALCACACAC	ATGCCCAAGA	TRACCCAATT	TIGAGICITG	GAGGAAAGCC	GCTGGTGGGC	3900
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	ACGACGCCCC ACCACTACTA	TGCCTACCAC	CCCTACCACT	ACACCCACCA	CCACCACCAC	CACCACCCGC	4080
	COCACCACCA	CCAGGGGTCC	AACAACCACA	GTCCGAACCA	CTACGCGGAC	AACCACCACC	4140
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40	GAATTTGATC	TGGCTGGAAG	GAAACGATTT	GTTGCTCCTT	ACGTGACGTA	CCTAAATAAA	4500 4560
40	GACCCATCAG GATGAAATCA	CCCCGTGCTC	CCTGAAGAAG	ACTUATORGO	CTCCCCAGCA	TGCTCCCCGC	4620
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	TGTCTGCAAG	AATATTGATT	AAAATTGCTA	AATTTGTACT	TGTTCACCAA	ааааааааа	6000
65	АЛАЛАЛА						
	Seq ID NO:	ession #1	n sequence Bos sequenc	e			
	rioccin no		-				
70	1	11	21	31	41	51	
	MDCCCCC CENTRE	A DANYDUTT.K	TEORDETAND	DDTSVRVMSS	OSVLVSWVDP	APSKÖKKAAY	60
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75	PONTFFHTPR	LSNHLEQSPS	PILETLLLPW	DDOLEGOURG	PSKSGPQTGB	MUDITICIPED	240 300
	MCAEUBASSI*	TONGLEGUAA	SKADVOONTE	DNGKPEKPEP	SSPSPRAPAS	SORPSVPASP	360
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80	COUT.DDD CCV	HECKEDASEA	SINDNDLVDS	RDSSASAPPS	RLSPPHGGSS	RLLPTOPHLS	600
	SBI'S KUCKLKI	EDADATNSNA	PSRSTMSSSV	SSHLSSRTOV	SEGARASDGE	SHGDGDREDG	660
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85	HPRVPSHSDS	HPKLSSGIHG	DEEDEKPLPA	TVVNDHVPSS	SKQPISRGWE	DLRRSPQRGA QPGSTDRHAS	780 840
0.5	CODEAGGER	ORDGUDDRMT	PERAPEOOPP	PPVATSOHEP	GPOSRDAGRS	PSQPRLSLTQ	900
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WO 02/086443
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TREVESTORI CORCORNET LANGROFTL SKGKPROM EVEKTRIFT TUMOPITI TE
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                    TROCTICO TECTHAFORG GETTOCCTO TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETOCCT TOGETO
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Seq ID NO: 423 Protein sequence Protein Accession #: NP_003005.1.

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30	ĩ	ī	ī	i	1	1	
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WO 02/086443

CTGTANANA ACCAANACCC ANAAAAAAA AAAAAAAAA

Seq ID No: 425 Protein sequence
Protein Accession #: AAH10423

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	Nucleic Ac:	id Accession	1 #: NM_003	474.2			
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		AAAAAAAAA					

Seq ID NO: 427 Protein sequence Protein Accession #: NP_003465

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	SKNHPEVLNI	RLQRESKELI	INLERNEGLI	ASSFTETHYL	QDGTDVSLAR	NYTVILGHCY	120
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-	ACROSSNSCO	LPEPCTGASP	HCPANVYLHD	GHSCODVDGY	CYNGICOTHE	QQCVTLWGPG	540
	AVDADGICEE	RVNSAGDPYG	NCGKVSKSSF	AKCEMRDAKC	CKIOCOGGAS	RPVIGTNAVS	600
	TREMITOLOGG	GRILCRGTHV	AT-COUNDUDG	LVLAGTKCAD	GKICLNROCO	NISVEGVHEC	660
	MOCHEROVC	NNRKNCHCEA	HWAPPFCDKF	GEGGSTDSGP	IROADNOGLT	IGILVTILCL	720
40	T. S. S. CENTRAL VI. K	RKTLIRLLFT	MEETTTREER	CVRPSRPPRG	POPCOAHLGH	LGKGLMRKPP	780
-10	Deventoring	RLLOCONVDI	CDDINGINUD	OPOSTORVIJE	PLHRAPRAPS	VPARPLPAKP	840
	PAT BOYOGLCK	PNPPQKPLPA	DDLTSTTRLT	HALARTPGOW	BTGLRLAPLR	PAPOYPHOVP	901
	PSTHTAYTE	THE LUNC DE A				-	

45 Seq ID NO: 428 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 135..1043

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	CACTTGGGGG	AAACCTTATA	CCCAGAGGAA	AATACACACC	TGGGGAGTAC	ATTTGACAAA	204
85	TTTCCCTTAG	GATTTCGTTA	TCTCACCTTG	ACCCTCAGCC	AAGATTGGTA	AAGCTGCGTC	210
	CTCCCCATTC	CAGGAGACCC	AGCTGGAAAC	CTGGCTTCTC	CATGTGAGGG	GATGGGAAAG	216
	GAAAGAAGAG	AATGAAGACT	ACTTAGTAAT	TCCCATCAGG	AAATGCTGAC	CTTTTACATA	222

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5		429 Proteir cession #: N					
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10	GDVGCGVFEC ISRKCPAIRE CGEEVKEAIT	TLALVLATFD PENNSCEIRG MVSQLQRECY HSVQVQCEQN	LHGICMTFLH LKHDLCAAAQ WGSLCSILSF	NAGKFDAQGK ENTRVIVEMI CTSAIQKPPT	SFIKDALKCK HPKDLLLHEP APPERQPQVD	AHALRHRFGC YVDLVNLLLT RTKLSRAHHG	60 120 180 240
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	YPLSLSPDDC	RGVQHLYGQP	WPTVTSRTPA	LGPQAGIDTN	EIAPLEPDAP	PDACKASFDA	300 360
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45	LALAIGLGIH	FDCSGKYRCR	SSFKCIELIA	PDADAVAAQI RCDGVSDCKD	LSLLPLKFPP GEDEYRCVRV	GGQNAVLQVF CTDUT.T.DDDV	120 180 240 300
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45 50	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCGGSVITPL LGNDIALMKL VPLISNKICN	PDCSGKYRCR DDWKGHYANV REGCASGHVV WIITAAHCVY AGPLTFNEMI HRDVYGGIIS	SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI QPVCLPNSEB PSMLCAGYLT	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN NFPDGKVCMT GGVDSCQGDS	LSLLPLKFFP GEDEYRCVRV LEGQFREEFV NMSLLSQWPW PAPSHLVEKI SGWGATEDGG	SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300
	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCGGSVITPL LGNDIALMKL VPLISNKICN	PDCSGKYRCR DDWKGHYANV REGCASGHVV WIITAAHCVY AGPLTPNEMI	SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI QPVCLPNSEB PSMLCAGYLT	PDADAVAAQI RCDGVSDCKD VSSDNLRVSS RGYSSRIVGG QVGLVSLLDN NFPDGKVCMT GGVDSCQGDS	LSLLPLKFFP GEDEYRCVRV LEGQFREEFV NMSLLSQWPW PAPSHLVEKI SGWGATEDGG	SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCCGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Sed ID NO:	FDCSGKYRCR DDWEGHYANV REGCASGHVV WIITAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA se	SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI QPVCLPNSEE PSMLCAGYLT DWIHEQMERD	PDADAVAAQI PCDAVSDCKD VSEDNLRVSS RGYSSRIVGG QVGLVSLLDD NFPDCKVCWT GGVDSCQGDS LKT	LSLLPLKFFP GEDEYRCVRV LEGQFREEFV NMSLLSQWPW PAPSHLVEKI SGWGATEDGG	SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
50	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCGGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic Ac:	PDCSGKYRCR DDWKGHYANV REGCASGHVV WIITAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA see id Accessio	SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI QPVCLPNSEE PSMLCAGYLT DWIHEQMERD Quence n #: NM 000	PDADAVAAQI PCDAVSDCKD VSEDNLRVSS RGYSSRIVGG QVGLVSLLDD NFPDCKVCWT GGVDSCQGDS LKT	LSLLPLKFFP GEDEYRCVRV LEGQFREEFV NMSLLSQWPW PAPSHLVEKI SGWGATEDGG	SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCGGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic Ac:	FDCSGKYRCR DDWEGHYANV REGCASGHVV WIITAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA se	SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI QPVCLPNSEE PSMLCAGYLT DWIHEQMERD Quence n #: NM 000	PDADAVAAQI PCDAVSDCKD VSEDNLRVSS RGYSSRIVGG QVGLVSLLDD NFPDCKVCWT GGVDSCQGDS LKT	LSLLPLKFFP GEDEYRCVRV LEGQFREEFV NMSLLSQWPW PAPSHLVEKI SGWGATEDGG	SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
50	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCGGSVITPL LGHDIALMKL VPLISNKICH GIGCAEVNKP Seq ID NO: Nucleic Ac Coding seq	PDCSGKYRCR DDWKGHYANV REGCASGHVV WIITAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA seid Accession Lence: 97	SSFKCIELIA ACAQLGFPSY TIQCTACGHR DLYLPKSWTI OPVCLPNSEE PSMLCAGYLT DWIHEQMERD Quence n #: NM_000	PDADAVAAQI RCDGVSDCKD VSEDNLRVSS RGYSSRIVGG QVGLVSLLDN NFEDGKVCKT GGVDSCQGDS LKT	LSLLPLKFFP GEDEYRCVRV LEGGFREEPV MMSILLSOMPW PAPSHLVEN SGMGATEDGG GGPLVCQERR	GSQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPER DASPVLNHAA LWKLVGATSF	120 180 240 300 360
50	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCGGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic Ac:	PDCSGKYRCR DDWKGHYANV REGCASGHVV WIITAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA see id Accessio	SSFKCIELIA ACAQLGFPSY TLQCTACGHR DLYLPKSWTI QPVCLPNSEE PSMLCAGYLT DWIHEQMERD Quence n #: NM 000	PDADAVAAQI PCDAVSDCKD VSEDNLRVSS RGYSSRIVGG QVGLVSLLDD NFPDCKVCWT GGVDSCQGDS LKT	LSLLPLKFFP GEDEYRCVRV LEGQFREEFV NMSLLSQWPW PAPSHLVEKI SGWGATEDGG	SIDHLLPDDK QASLQFQGYH VYHSKYKPKR DASPVLNHAA	120 180 240 300 360
50	LALAIGLGIH TAASWKTMCS VTALHHSVYV LCGGSVITPL LCHDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic Ac: Coding seq	PDCSGKYRCR DDWEGHYANV REGCASGHVV WIITAAHCVY WIITAAHCVY AGPLIFPNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA secid Accession Lence: 97	SSPKCIELIA ACAQUAGPPSY TLQCTACGHR DLYLPKSWTI DPVCLPNSEB PSMLCAGYLT DWIHEQMERD QUENCE n %: NM_000 2139 21	PDADAVAAQI RCDGVSDCKD VSSDNLRVGS RGYSSRIVGG QVGLVSLLDN NFPDGKVCNT GGVDSCQGDS LKT	LSLLPLKFFP GEDEYRCVRV LBGGFREEPV MMSLLSGWP PAPSHLVEKI SGMGATEDGG GGPLVCQERR	GSQNAVLQVF SIDHLLPDDK QASLQFQGYH VYHSKYKENR DASPVLHHAA LWKLVGATSF	120 180 240 300 360 420
50 55	LALAGIGHE TAASKKTMCS VTALHESVYV LCOGSVITPL LCOMDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic AC Coding seq 1	FDCSGKYRCH DDNKGHYANV REGCASGHVV WIITAAHCVY	SSEKCIELLA ACACLEFEY TLQCTACGHR DLYLIPKSHTI DVYLLENSEE PSMLCAGYLT DWIHEQMEND Quence n #: NM_000 21339 21 i GGGCAGAGG	PADDAVAAQI PEDGYSDCKD VSENNEVSS KGYSSRIVGG QVGLVSLLDM MFPDGKVCKT GGVDSCQGDS LKT 0493.2	LSLLPLKFPP GEDEYRCVRV LBGGFRESPY MNSLLSOPPW PAPSHLVEKI SGNGATEDGG GGPLVCQERR 41	GGGNAVQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPHR DASFVLMHAA LWKLVGATSF	120 180 240 300 360 420
50	LALAGIGHE TAASKKTMCS VTALHESVYV LCOGSVITPL LCOMDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic AC Coding seq 1	FDCSGKYRCH DDNKGHYANV REGCASGHVV WIITAAHCVY	SSEKCIELLA ACACLEFEY TLQCTACGHR DLYLIPKSHTI DVYLLENSEE PSMLCAGYLT DWIHEQMEND Quence n #: NM_000 21339 21 i GGGCAGAGG	PADDAVAAQI PEDGYSDCKD VSENNEVSS KGYSSRIVGG QVGLVSLLDM MFPDGKVCKT GGVDSCQGDS LKT 0493.2	LSLLPLKFPP GEDEYRCVRV LBGGFRESPY MNSLLSOPPW PAPSHLVEKI SGNGATEDGG GGPLVCQERR 41	GGGNAVQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPHR DASFVLMHAA LWKLVGATSF	120 180 240 300 360 420
50 55	LALAGIGHE TAASKKTMCS VTALHESVYV LCOGSVITPL LCOMDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic AC Coding seq 1	FDCSGKYRCH DDNKGHYANV REGCASGHVV WIITAAHCVY	SSEKCIELLA ACACLEFEY TLQCTACGHR DLYLIPKSHTI DVYLLENSEE PSMLCAGYLT DWIHEQMEND Quence n #: NM_000 21339 21 i GGGCAGAGG	PADDAVAAQI PEDGYSDCKD VSENNEVSS KGYSSRIVGG QVGLVSLLDM MFPDGKVCKT GGVDSCQGDS LKT 0493.2	LSLLPLKFPP GEDEYRCVRV LBGGFRESPY MNSLLSOPPW PAPSHLVEKI SGNGATEDGG GGPLVCQERR 41	GGGNAVQVF SIDHLLPDDK QASLQFQGYH VYHSKYKPHR DASFVLMHAA LWKLVGATSF	120 180 240 300 360 420
50 55	LALATGLEIH TAASKKTMCS VTALHESVYV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucleic Ac. Coding seq CACCTICINGC CCAGGAACTC CTGCTAGTATAAA AGGGTATAAA	FDCSGKYRCE DDNKGHYANV REGCASGRVV WIITAAHCVY AGPLTFNEMI HRDVYGGIIS GVYTRVTSFL 434 DNA se- id Accession mence: 97 11 ACTGCTCATC CCAGCAGGCA CCTTGAACTT AAGGCCCCT	SSPRCIELLA ACACLGPBY TLQCTACGHR DLYLPKSHCAGTLT OPVCLPNSEB PSMLCAGTLT DWHHEGMEND TURENCE 1 H: NM_000 2139 21 1 TGGGCAGAGG GAATCCATCT GGTTCATGGA ACCCACACACA ACACAGACACA	PDADAVAAQI RCDGVSDCKD VSSDNLRVS RGYSSRIVGG QVGLVSLIVG GGVDSCQGDS LKT 31 AAGCTTCAGA AAGACACAGT CAAGGACACAGT	LSLLPLKSPP GEDEYRCVRV LEGGFREEFY MNSILSGMFW PAPSHLVENI SGNGATEDG GGPLVCQERR 41 AAGCTGCCAA TGCCACAAAT TCTGATCG TGGACGATA	SIDHLLPDDK QASLQPGOYH VYISKYKPKR DASPVLMHAA LWKLVGATSF 51	120 180 240 360 420 60 120 180 240
50 55 60	LALATGLGIH TAASHKTMCS VTALHESVYV. LCOGSVITPL LCHDIALMKL VPLISNRICH Seq ID NO: Nucleic Ac Coding seq CACCTICTGC CCAGGAACTC CTGCTAGTAT ACAGGCATAA AAGAGTAAGA	FDCSGKYRCE DDMEGHYANV REGCASGHVV WIITAAHCVY AGPLIFNEMI HRDVYGGIIS GVYTRVISFL 434 DNA sei id Accession Lence: 97 1 1 ACTGCTCATC CCAGCACGCA CCTTGAACTT AAGGCCCACT GTATAGCAGT	SSPKCIELLA ACACLGPPSY TLQCTACCHR TLYLPKSWTI OPVCLPNSEB PSMLCAGYLT DWIHECMEND Quence n #: NM_000 2139 TGGGCAGAGG GAATCCATCT GGTTCATGAG ACCCAACACA AAAAGAGAAGA	PDADAVAAQI RCDGVSDCKD VSSDNLRVS RGYSSRIVGG QVGLVSLLDN MFPDGKVCNT GGVDSCQGDS LKT 1 AAGCTTCAGA AAGCACATTTTACG GAGAATATGC GTGTTTTTACG AAGCACAGT CAAGCACAGT CACCAGGTACCA	LSLLPLIGPP GEDEYRCVRV LEGGFREEPV MISILISGNFW PAPSHLVEKI SGNGATEROI GGPLVCQERR 41 	SIDELLIPDOK QASLOPGOYN VYBSKYRPK VYBSKYRPK DASPVLMRAA LWKLVGATSF 51 GGCACCATCT ACCCTITTIG CCAAATGCCC CTACACCATA AGGCCCTGCT AGGCCCTGCT CTACACCATA AGGCCCTGCT CCGAAGTCCT CCCCAACTCT CCCCAACTCT CCCCAACTCT CCCCAACTCT CCCCAACTCT CCCCAACTCT CCCCAACTCT CCCCAACTCT CCCCAACTCT CCCCACCT CCCCCCCC	120 180 240 300 360 420 60 120 180 240 300 360
50 55	LALATGLGIH TAASHKTMCS VTALHESVYV. LCOGSVITPL LCHDIALMKL VPLISNRICH Seq ID NO: Nucleic Ac Coding seq CACCTICTGC CCAGGAACTC CTGCTAGTAT ACAGGCATAA AAGAGTAAGA	FDCSGKYRCE DDMEGHYANV REGCASGHVV WIITAAHCVY AGPLIFNEMI HRDVYGGIIS GVYTRVISFL 434 DNA sei id Accession Lence: 97 1 1 ACTGCTCATC CCAGCACGCA CCTTGAACTT AAGGCCCACT GTATAGCAGT	SSPKCIELLA ACACLGPPSY TLQCTACCHR TLYLPKSWTI OPVCLPNSEB PSMLCAGYLT DWIHECMEND Quence n #: NM_000 2139 TGGGCAGAGG GAATCCATCT GGTTCATGAG ACCCAACACA AAAAGAGAAGA	PDADAVAAQI RCDGVSDCKD VSSDNLRVS RGYSSRIVGG QVGLVSLLDN MFPDGKVCNT GGVDSCQGDS LKT 1 AAGCTTCAGA AAGCACATTTTACG GAGAATATGC GTGTTTTTACG AAGCACAGT CAAGCACAGT CACCAGGTACCA	LSLLPLIGPP GEDEYRCVRV LEGGFREEPV MISILISGNFW PAPSHLVEKI SGNGATEROI GGPLVCQERR 41 	SIDELLIPDOK QASLOPGOYN VYBSKYRPK VYBSKYRPK DASPVLMRAA LWKLVGATSF 51 GGCACCATCT ACCCTITTIG CCAAATGCCC CTACACCATA AGGCCCTGCT AGGCCCTGCT CTACACCATA AGGCCCTGCT CTACACCATA AGGCCCTGCT CTACACCATA AGGCCCTGCT CTACACCATA AGGCCCTGCT CTACACCATA AGGCCCTGCT CTACACCATA AGGCCCTGCT CTACACCATA AGGCCCTGCT CTACACCATA AGGCCCTGCT CTACACCATA AGGCCCTGCT CTACACCCATA CCGAAGTCCT CTACACCCATA CCCATACACCCATA ACCCATA CCCATACACCCATACACCCATA CCCATACACCCATACACCCATA CCCATACACCCATACACCCATA CCCATACACCCATACACCCATA CCCATACACACACACACACACACACACACACACACACACACACAC	120 180 240 360 420 60 120 180 240 300 360 420
50 55 60	LALAGGEH TAASKKTKCS VTALHESVYV LCOGSVITPL LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: CCOding seq CCACGACTCTCTGC CCACGACTCTCTGC CCACGACTCTCTGC CCAGGAACTC CTGCTAGTATA AAGAGTATAA AAGAGTATAA AGGACTCCAAG GGACTCCAAG GGACTCAAG GGACTCCAAG GGACTCCAAG GGACTCAAG GGACT	PDCSGKYRCE DDMKGHYANV REGCASGHVV WIITAAHCVY AGPLITFNEMI GWITTRVTSFL 434 DNA sei did Accession Lence: 97 11 ACTGCTCATC CCAGGACGCA CCTTGAACTT AAGGCCCACT GGCACCAGG GGCACCCAGG	SSPRCIELLA ACACLGPSY TIQCTACHEN DIYLPKSHTI OPVCLPNSEN PSMLCAGYLD DWIHEGMERD Quence n #: NM_000 2139 21 TGGGCAGAGG GAATCCATCT GGTTCATGGA ACCCAACACC AAGAGGAGAG GTTGCCAGGA GTTGCCAGGA AAAACCAGGA AAAACCAGGA	PDADAVAAQI RCDGVSDCKD VSSDNLRVS RGYSSRIVGG QVGLVSLLDN NFPDCKVCNT GGVDSCQGDS LKT 493.2 AAGCTTCAGA AAGACACAGT CAACAGGTACC CCACCAGGAA CCACCGGGAA CCACCGGGAA CCACCGGGAA CGAGAGGAAGGA	LSLLPLKSPP GEDEYRCVRV LEGGPREEPV MNSLLSQMPW PAPSHLVSIC SGNGATEDGG GGPLVCQERR 41	SIDHLLPDDK OASLOPGOYN VIHSKYNDRR DASPULMHAA LWKLVGATSF 51	120 180 240 360 420 60 120 180 360 420
50 55 60	LALATGLEIH TAASKKTMCS VTALHESVTV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucloic ac Coding seq CACCTICTGC CCAGGAACTC CTGGTAGTAT ACAGGCATAA GGACCTCAAG GGACCTCAAG GGACCTCAAG GTTGCACCAG GTTGACCAG GTTGACCAG	PDCSGKYRCE PDCSGKYRCE PDMSGHYANV RSGCASGHVV WIITAAHCVY AGPLITPNEMI GUYTRVTSFL 434 DNA sei did Accession Lence: 97 11 ACTGCTCATC CCAGCAGCAC CCTGGACTAC GGCACCCCAGG GGCACCCCAGG GGCACCCCAGG GGAGGCCAGG GAGGCCAGG GAGGCCAGG CTGGGCTACC CTGGCTACC CCGCTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGCCTACC CTGCCTACC CTGCTACC CTG	SSPKCIELLA ACALGPPSY TLQCTACHER TLYLPKSWTI DVYLPKSWTI DWYLLPNSEB PSMLCAGTLT DWHHEQMERD TURNEO THE NM_000 2139 21 TGGGCAGAGG GARTCARTCT GGTTCATGGA ACCCACACAC ACGAGAGG TCCTTCTGGA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCACGAGAA AAAACCAGGAA AAAACCAGGAA AAAACCACGAGAA ACCACGAGAAAAACCACGAGAAAAACCACGAGAAAAAA	PDADAVAAQI RCDGVSDCKU RCDGVSDCKU RCDGVSDCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RFDCKVCH GGVDSCKGDS LKT 1 AGCTTCAGA AGGAATATGC CGACCAGGAA CAAGGACACAGT CCACCGGGAC GAGAGAGGGAC GGCCCACCAG GGCCCACCAG GGCCCACCAG AGGACACCAG	LEGLELKFEP GENETRCVAV LEGOGPREEP MNSLLSOWEN PAPSHLVEST SONGATEDGG GGPLVCQERR 41 AAGCTGCCAAAT TCTCACATAT TCTTCATTCC CTGSTCCAC AACCAGGCTA CATTCAGGCTA	SIDHLLPDDK QASLQPGGYH VYHSKYKPKR DASFYLMHAA LWKLYGATSF 51	120 180 240 360 420 60 120 180 240 360 420 420
50 55 60	LALATGLEIH TAASKKTMCS VTALHESVTV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucloic ac Coding seq CACCTICTGC CCAGGAACTC CTGGTAGTAT ACAGGCATAA GGACCTCAAG GGACCTCAAG GGACCTCAAG GTTGCACCAG GTTGACCAG GTTGACCAG	PDCSGKYRCE PDCSGKYRCE PDMSGHYANV RSGCASGHVV WIITAAHCVY AGPLITPNEMI GUYTRVTSFL 434 DNA sei did Accession Lence: 97 11 ACTGCTCATC CCAGCAGCAC CCTGGACTAC GGCACCCCAGG GGCACCCCAGG GGCACCCCAGG GGAGGCCAGG GAGGCCAGG GAGGCCAGG CTGGGCTACC CTGGCTACC CCGCTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGCCTACC CTGCCTACC CTGCTACC CTG	SSPKCIELLA ACALGPPSY TLQCTACHER TLYLPKSWTI DVYLPKSWTI DWYLLPNSEB PSMLCAGTLT DWHHEQMERD TURNEO THE NM_000 2139 21 TGGGCAGAGG GARTCARTCT GGTTCATGGA ACCCACACAC ACGAGAGG TCCTTCTGGA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCACGAGAA AAAACCAGGAA AAAACCAGGAA AAAACCACGAGAA ACCACGAGAAAAACCACGAGAAAAACCACGAGAAAAAA	PDADAVAAQI RCDGVSDCKU RCDGVSDCKU RCDGVSDCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RFDCKVCH GGVDSCKGDS LKT 1 AGCTTCAGA AGGAATATGC CGACCAGGAA CAAGGACACAGT CCACCGGGAC GAGAGAGGGAC GGCCCACCAG GGCCCACCAG GGCCCACCAG AGGACACCAG	LEGLELKFEP GENETRCVAV LEGOGPREEP MNSLLSOWEN PAPSHLVEST SONGATEDGG GGPLVCQERR 41 AAGCTGCCAAAT TCTCACATAT TCTTCATTCC CTGSTCCAC AACCAGGCTA CATTCAGGCTA	SIDHLLPDDK QASLQPGGYH VYHSKYKPKR DASFYLMHAA LWKLYGATSF 51	120 180 240 360 420 60 120 180 240 360 420 420
50 55 60	LALATGLEIH TAASKKTMCS VTALHESVTV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucloic ac Coding seq CACCTICTGC CCAGGAACTC CTGGTAGTAT ACAGGCATAA GGACCTCAAG GGACCTCAAG GGACCTCAAG GTTGCACCAG GTTGACCAG GTTGACCAG	PDCSGKYRCE PDCSGKYRCE PDMSGHYANV RSGCASGHVV WIITAAHCVY AGPLITPNEMI GUYTRVTSFL 434 DNA sei did Accession Lence: 97 11 ACTGCTCATC CCAGCAGCAC CCTGGACTAC GGCACCCCAGG GGCACCCCAGG GGCACCCCAGG GGAGGCCAGG GAGGCCAGG GAGGCCAGG CTGGGCTACC CTGGCTACC CCGCTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGCCTACC CTGCCTACC CTGCTACC CTG	SSPKCIELLA ACALGPPSY TLQCTACHER TLYLPKSWTI DVYLPKSWTI DWYLLPNSEB PSMLCAGYLT DWHHEGMERD TURNEG TURNEG THE NM_000 2139 21 TGGGCAGAGG GARTCARTCT GGTTCATGGA ACCCACACAC ACGAGGAGG TCCTTCTGGA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCACGAGAA AAAACCACGAGAA AAAACCAGGAA AAAACCACGAGA AAAACCACGAGA AAAACCACGAGA AAAACCACGAA AAAACCACGAGA AAAACCACCACCCCCCCC	PDADAVAAQI RCDGVSDCKU RCDGVSDCKU RCDGVSDCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RFDCKVCH GGVDSCKGDS LKT 1 AGCTTCAGA AGGAATATGC CGACCAGGAA CAAGGACACAGT CCACCGGGAC GAGAGAGGGAC GGCCCACCAG GGCCCACCAG GGCCCACCAG AGGACACCAG	LEGLELKFEP GENETRCVAV LEGOGPREEP MNSLLSOWEN PAPSHLVEST SONGATEDGG GGPLVCQERR 41 AAGCTGCCAAAT TCTCACATAT TCTTCATTCC CTGSTCCAC AACCAGGCTA CATTCAGGCTA	SIDHLLPDDK QASLQPGGYH VYHSKYKPKR DASFYLMHAA LWKLYGATSF 51	120 180 240 360 420 60 120 180 240 360 420 420
50 55 60 65	LALATGLEIH TAASKKTMCS VTALHESVTV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucloic ac Coding seq CACCTICTGC CCAGGAACTC CTGGTAGTAT ACAGGCATAA GGACCTCAAG GGACCTCAAG GGACCTCAAG GTTGCACCAG GTTGACCAG GTTGACCAG	PDCSGKYRCE PDCSGKYRCE PDMSGHYANV RSGCASGHVV WIITAAHCVY AGPLITPNEMI GUYTRVTSFL 434 DNA sei did Accession Lence: 97 11 ACTGCTCATC CCAGCAGCAC CCTGGACTAC GGCACCCCAGG GGCACCCCAGG GGCACCCCAGG GGAGGCCAGG GAGGCCAGG GAGGCCAGG CTGGGCTACC CTGGCTACC CCGCTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGCCTACC CTGCCTACC CTGCTACC CTG	SSPKCIELLA ACALGPPSY TLQCTACHER TLYLPKSWTI DVYLPKSWTI DWYLLPNSEB PSMLCAGYLT DWHHEGMERD TURNEG TURNEG THE NM_000 2139 21 TGGGCAGAGG GARTCARTCT GGTTCATGGA ACCCACACAC ACGAGGAGG TCCTTCTGGA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCACGAGAA AAAACCACGAGAA AAAACCAGGAA AAAACCACGAGA AAAACCACGAGA AAAACCACGAGA AAAACCACGAA AAAACCACGAGA AAAACCACCACCCCCCCC	PDADAVAAQI RCDGVSDCKU RCDGVSDCKU RCDGVSDCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RFDCKVCH GGVDSCKGDS LKT 1 AGCTTCAGA AGGAATATGC CGACCAGGAA CAAGGACACAGT CCACCGGGAC GAGAGAGGGAC GGCCCACCAG GGCCCACCAG GGCCCACCAG AGGACACCAG	LEGLELKFEP GENETRCVAV LEGOGPREEP MNSLLSOWEN PAPSHLVEST SONGATEDGG GGPLVCQERR 41 AAGCTGCCAAAT TCTCACATAT TCTTCATTCC CTGSTCCAC AACCAGGCTA CATTCAGGCTA	SIDHLLPDDK QASLQPGGYH VYHSKYKPKR DASFYLMHAA LWKLYGATSF 51	120 180 240 360 420 60 120 180 240 360 420 420
50 55 60 65	LALATGLEIH TAASKKTMCS VTALHESVTV LCOGSVITPL LGNDIALMKL VPLISNKICN GIGCAEVNKP Seq ID NO: Nucloic ac Coding seq CACCTICTGC CCAGGAACTC CTGGTAGTAT ACAGGCATAA GGACCTCAAG GGACCTCAAG GGACCTCAAG GTTGCACCAG GTTGACCAG GTTGACCAG	PDCSGKYRCE PDCSGKYRCE PDMSGHYANV RSGCASGHVV WIITAAHCVY AGPLITPNEMI GUYTRVTSFL 434 DNA sei did Accession Lence: 97 11 ACTGCTCATC CCAGCAGCAC CCTGGACTAC GGCACCCCAGG GGCACCCCAGG GGCACCCCAGG GGAGGCCAGG GAGGCCAGG GAGGCCAGG CTGGGCTACC CTGGCTACC CCGCTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGACTACC CTGGCCTACC CTGCCTACC CTGCTACC CTG	SSPKCIELLA ACALGPPSY TLQCTACHER TLYLPKSWTI DVYLPKSWTI DWYLLPNSEB PSMLCAGYLT DWHHEGMERD TURNEG TURNEG THE NM_000 2139 21 TGGGCAGAGG GARTCARTCT GGTTCATGGA ACCCACACAC ACGAGGAGG TCCTTCTGGA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCAGGAA AAAACCACGAGAA AAAACCACGAGAA AAAACCAGGAA AAAACCACGAGA AAAACCACGAGA AAAACCACGAGA AAAACCACGAA AAAACCACGAGA AAAACCACCACCCCCCCC	PDADAVAAQI RCDGVSDCKU RCDGVSDCKU RCDGVSDCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RCDGVSCKU RFDCKVCH GGVDSCKGDS LKT 1 AGCTTCAGA AGGAATATGC CGACCAGGAA CAAGGACACAGT CCACCGGGAC GAGAGAGGGAC GGCCCACCAG GGCCCACCAG GGCCCACCAG AGGACACCAG	LEGLELKFEP GENETRCVAV LEGOGPREEP MNSLLSOWEN PAPSHLVEST SONGATEDGG GGPLVCQERR 41 AAGCTGCCAAAT TCTCACATAT TCTTCATTCC CTGSTCCAC AACCAGGCTA CATTCAGGCTA	SIDHLLPDDK QASLQPGGYH VYHSKYKPKR DASFYLMHAA LWKLYGATSF 51	120 180 240 360 420 60 120 180 240 360 420 420
50 55 60 65	LALATGISTH TAASHKTMES TAASHKTMES TAASHKTMES TAASHKTMES TAASHKTMES TOOGNYTTHE TOOGNYTTHE TOOGNYTTHE TOOGNYTH TOO	FDCSGXYRCR DDMRGHYANY RSGCASGRVY RSGCASGRVY RSGCASGRVY RSGCASGRVY RSGCASGRVY RSGCASGRVY RSGCASGRVY RSGCASGRVY RSGCASGRVY RSGCASGRCAG RGGAGCCAGG RGGAGCAGG RGGAGC RGGAGC RGGAGG RGGAGG RGGAGCAGG RGGAGG RGGAGG RGGAGG RGGAGG RGGAGG RGGAGG RGGAGG RGGAGG RGGAG	SSENCIELIA ACQUIERE LA CACCALGREE LA CACCALG	PRADAVAAQI RCOGVSDCTD VSSDMLRVSS RGYSSRITVOG GOVDSCDD LKT 31 AGCTTCAGA AGAGAGGTC CCACCAGGGA CCACCAGGGA GGCCCACAG GGCCCACAG	LEGLEPLETPE GENERACYAN LEGOGREEPE MISSILSGMEN PAPERILMENT SONGATEDOS GOPATOCICA A LI LI LI LI LI LI LI LI LI LI LI LI LI	STIDILIAPOUR STIDI	120 180 300 420 120 180 240 360 480 540 660 720 680 780 840
5055606570	LALATGIGHT TAASHKTME TAASHKTME TAASHKTME TAASHKTME LOUDILAMIL LOUD	FDCSGKYRCE DDMGGHYANY RGGCAGGHYW RGGCAGGHYW RGGCAGGHYW RGGCAGGHYW RGGCAGGHYW AADILTRIBHIN HEDWYGGIIS GYTKRYTSFL 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SSPRCIBLIA ACOQUEPSE TIQCTACGHR DIVIDENSHI	PENDAVAAGI RCDGVSDCED VSSDNIEWS RCDGSDCED VSSDNIEWS RCDGSDCED VSSDNIEWS RCDGSDCED LKT GVUDSCQGDS LKT 31 31 AAGCTTCAGA GAGAARATGC GTGTTTTAGG AAGACAGG CCACAGGAG GAGAARATGC CCACGGGGAG GAGACAGG CCACGGGGAG GAGACAGG GGCCCACGGAG TTTCCCCAGGGGT CCACGGGGAT TTCCCGGGGG	LEGLEPLATPE GENEYRCVEV INSELLSQUENE INSELLSQ	SIL AND AND AND AND AND AND AND AND AND AND	120 180 240 300 360 420 120 120 120 300 420 480 600 600 600 600 720 780 900
50 55 60 65	LALATGIGHT TAASHKTME TAASHKTME TAASHKTME TAASHKTME LOUDILAMIL LOUD	FDCSGKYRCE DDMGGHYANY RGGCAGGHYW RGGCAGGHYW RGGCAGGHYW RGGCAGGHYW RGGCAGGHYW AADILTRIBHIN HEDWYGGIIS GYTKRYTSFL 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SSPRCIBLIA ACOQUEPSE TIQCTACGHR DIVIDENSHI	PENDAVAAGI RCDGVSDCED VSSDNIEWS RCDGSDCED VSSDNIEWS RCDGSDCED VSSDNIEWS RCDGSDCED LKT GVUDSCQGDS LKT 31 31 AAGCTTCAGA GAGAARATGC GTGTTTTAGG AAGACAGG CCACAGGAG GAGAARATGC CCACGGGGAG GAGACAGG CCACGGGGAG GAGACAGG GGCCCACGGAG TTTCCCCAGGGGT CCACGGGGAT TTCCCGGGGG	LEGLEPLATPE GENEYRCVEV INSELLSQUENE INSELLSQ	SIL AND AND AND AND AND AND AND AND AND AND	120 180 240 300 360 420 120 120 120 300 420 480 600 600 600 600 720 780 900
5055606570	LALATGISTH TAASHEMEN TAASHEMEN TAASHEMEN TAASHEMEN LOOP LOOP LOOP LOOP LOOP LOOP LOOP LOOP	FDCSSKYRCE DDMKGHYAMY RBGCASGRYWCE RBGCASGRYWCE RBGCASGRYWCE AAADILTMBHH HBDYYGGIIS GYTRETSEIL 434 DNA sei dAccessidie CCMGCAGGC CCTTGAACTT AAGGCCACCT CCMGCAGGC GAGAGCCAGG GATTCATGGC CCTTGAGCT CTTCTTGAGGA GATTCATGGC CCTTGAGCAG GATTCATGGC CCCAGGGCC CCCAGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGCCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGCCC CCCAGGCCC CCCCAGGCCC CCCCCAGGCCC CCCCCAGGCC CCCCCAGGCC CCCCCAGGCC CCCCCAGGCC CCCCCAGGCC CCCCCCC CCCCCC CCCCCC CCCCCCC CCCCCC	SSPRCIBLIA ACQUIRERS OF THE CONTROL	STATE OF THE STATE	LEGLEPLATPE GENETACVEV INSELLEGATE INSELLE	SUBMILLIANT SUBMICATION SUBMIC	120 180 240 360 420 60 120 180 180 180 420 360 420 420 780 840 960 960 960 960
5055606570	LALATGISTH TAASHEMEN TAASHEMEN TAASHEMEN TAASHEMEN LOOP LOOP LOOP LOOP LOOP LOOP LOOP LOOP	FDCSSKYRCE DDMKGHYAMY RBGCASGRYWCE RBGCASGRYWCE RBGCASGRYWCE AAADILTMBHH HBDYYGGIIS GYTRETSEIL 434 DNA sei dAccessidie CCMGCAGGC CCTTGAACTT AAGGCCACCT CCMGCAGGC GAGAGCCAGG GATTCATGGC CCTTGAGCT CTTCTTGAGGA GATTCATGGC CCTTGAGCAG GATTCATGGC CCCAGGGCC CCCAGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGCCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGCCC CCCAGGCCC CCCCAGGCCC CCCCCAGGCCC CCCCCAGGCC CCCCCAGGCC CCCCCAGGCC CCCCCAGGCC CCCCCAGGCC CCCCCCC CCCCCC CCCCCC CCCCCCC CCCCCC	SSPRCIBLIA ACQUIRERS OF THE CONTROL	STATE OF THE STATE	LEGLEPLATPE GENETACVEV INSELLEGATE INSELLE	SUBMILLIANT SUBMICATION SUBMIC	120 180 240 360 420 60 120 180 180 180 420 360 420 420 780 840 960 960 960 960
50 55 60 65 70 75	LALATGISTH TAASHEMEN TAASHEMEN TAASHEMEN TAASHEMEN LOOP LOOP LOOP LOOP LOOP LOOP LOOP LOOP	FDCSSKYRCE DDMKGHYAMY RBGCASGRYWCE RBGCASGRYWCE RBGCASGRYWCE AAADILTMBHH HBDYYGGIIS GYTRETSEIL 434 DNA sei dAccessidie CCMGCAGGC CCTTGAACTT AAGGCCACCT CCMGCAGGC GAGAGCCAGG GATTCATGGC CCTTGAGCT CTTCTTGAGGA GATTCATGGC CCTTGAGCAG GATTCATGGC CCCAGGGCC CCCAGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGCCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGGCC CCCAGGGCCC CCCAGGCCC CCCCAGGCCC CCCCCAGGCCC CCCCCAGGCC CCCCCAGGCC CCCCCAGGCC CCCCCAGGCC CCCCCAGGCC CCCCCCC CCCCCC CCCCCC CCCCCCC CCCCCC	SSPRCIBLIA ACQUIRERS OF THE CONTROL	STATE OF THE STATE	LEGLEPLATPE GENETACVEV INSELLEGATE INSELLE	SUBMILLIANT SUBMICATION SUBMIC	120 180 240 360 420 60 120 180 180 180 420 360 420 420 780 840 960 960 960 960
5055606570	LALAGIGHT TAASHKYNE TAASHKYNE TAASHKYNE LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSST LOOSS	FDCSGKYRCE DDMGGFYAND DDMGGFYAND DDMGGFYAND DDMGGFYAND HARD HARD HARD HARD HARD HARD HARD HAR	SSPRCIELIA ACQUERES PSMLCAGYLT DIALDESETI OVICLIANSE PSMLCAGYLT DIALDESETI OVICLIANSE PSMLCAGYLT IN 8 NM_001 2139 TOMOCCAGAGAG ACCCAGAGAG ACCCAGAGAG ACCCAGAGAG TCCTTCTGGA TCTGCCAGAG TCCTTCTGGA TCTGCCAGAG ACCCAGAGAG ACCCAGAGAG TCCTTCTGGA TCTGCCAGAG ACCCAGAGG TCCTTCTGGA TCTGCCAGAG TCCTTCTGGA TCTGCCCTGGA TCTGCCCGGA TCCTGGAGAG TCCTTCTGGA TCCTGGAGAG TCCTTCTGGA TCCTGGAGAG TCCTTCTGGA TCCTGGAGAG TCCTTCTGGAG TCCTGGAGAG TCCTTCTGGAG TCCTGGAGAG TCCTTGGAGAG TCCTGGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAG TCCTGAG TCCTGAGAG TCCTGAGAG TCCTGAGAG TCCTGAG TCCTGAGAG TCCTGAG TCCT	CONTINUENCE	LEST. LEST.	SOURCE VIEW CONTROL OF THE CONTROL O	120 240 300 360 420 600 120 180 300 340 420 480 960 1140 1140 1120 1120 1120 1120 1120 112
50 55 60 65 70 75	LALAGIGHT TAASHKYNE TAASHKYNE TAASHKYNE LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSST LOOSS	FDCSGKYRCE DDMGGFYAND DDMGGFYAND DDMGGFYAND DDMGGFYAND HARD HARD HARD HARD HARD HARD HARD HAR	SSPRCIELIA ACQUERES PSMLCAGYLT DIALDESETI OVICLIANSE PSMLCAGYLT DIALDESETI OVICLIANSE PSMLCAGYLT IN 8 NM_001 2139 TOMOCCAGAGAG ACCCAGAGAG ACCCAGAGAG ACCCAGAGAG TCCTTCTGGA TCTGCCAGAG TCCTTCTGGA TCTGCCAGAG ACCCAGAGAG ACCCAGAGAG TCCTTCTGGA TCTGCCAGAG ACCCAGAGG TCCTTCTGGA TCTGCCAGAG TCCTTCTGGA TCTGCCCTGGA TCTGCCCGGA TCCTGGAGAG TCCTTCTGGA TCCTGGAGAG TCCTTCTGGA TCCTGGAGAG TCCTTCTGGA TCCTGGAGAG TCCTTCTGGAG TCCTGGAGAG TCCTTCTGGAG TCCTGGAGAG TCCTTGGAGAG TCCTGGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAG TCCTGAG TCCTGAGAG TCCTGAGAG TCCTGAGAG TCCTGAG TCCTGAGAG TCCTGAG TCCT	CONTINUENCE	LEST. LEST.	SOURCE VIEW CONTROL OF THE CONTROL O	120 240 360 360 420 60 120 240 300 660 780 900 900 900 910 1200 1080 1200 1140 1200 1380
50 55 60 65 70 75	LALAGIGHT TAASHKYNE TAASHKYNE TAASHKYNE LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSSYTTPL LOOSST LOOSS	FDCSGKYRCE DDMGGFYAND DDMGGFYAND DDMGGFYAND DDMGGFYAND HARD HARD HARD HARD HARD HARD HARD HAR	SSPRCIELIA ACQUERES PSMLCAGYLT DIALDESETI OVICLIANSE PSMLCAGYLT DIALDESETI OVICLIANSE PSMLCAGYLT IN 8 NM_001 2139 TOMOCCAGAGAG ACCCAGAGAG ACCCAGAGAG ACCCAGAGAG TCCTTCTGGA TCTGCCAGAG TCCTTCTGGA TCTGCCAGAG ACCCAGAGAG ACCCAGAGAG TCCTTCTGGA TCTGCCAGAG ACCCAGAGG TCCTTCTGGA TCTGCCAGAG TCCTTCTGGA TCTGCCCTGGA TCTGCCCGGA TCCTGGAGAG TCCTTCTGGA TCCTGGAGAG TCCTTCTGGA TCCTGGAGAG TCCTTCTGGA TCCTGGAGAG TCCTTCTGGAG TCCTGGAGAG TCCTTCTGGAG TCCTGGAGAG TCCTTGGAGAG TCCTGGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAGAG TCCTGAGAG TCCTGAG TCCTGAGAG TCCTGAGAG TCCTGAGAG TCCTGAG TCCTGAGAG TCCTGAG TCCT	CONTINUENCE	LEST. LEST.	SOURCE VIEW CONTROL OF THE CONTROL O	120 180 300 300 300 300 300 300 180 240 300 540 480 600 600 600 600 720 780 900 1260 1260 1270 1280 1290 1290 1290 1290 1290 1290 1290 129
50 55 60 65 70 75	LALAGUSTH TAASHKTUS TAASHKTUS TAASHKTUS LOOSSYTTPL LOOS	FDCSGNYRGE BDCSGNYRGE	SSENCIELLY TECHNOLOGY	DUDLYMACT	LEST. LEST.	STEMPLY OF THE PROPERTY OF THE	120 240 300 300 300 300 420 180 240 300 660 780 840 900 900 900 901 1200 1200 1200 1200 12
50 55 60 65 70 75	LALAGUSTH TAASHKYNES TAASHKYNES TAASHKYNES LAGDIZHMIL LOGGSVITPL L	FDCSGKYKCK DDMGGMTANN DDMGGMTANN HITAAHCYY HITAAHCY	SSENCIELLY TOTAL CAPACITY TO	CONTINUENCE CONTINUENCE	LELLELICEPEP GENERACONE GENERACONE HISTORIA AGCTGCCAA TOCCACAA TOCCACAA TOCCACAA TOCCACAA TOCCACAA TOCCACAA AACAGGCTA CATCAGGTA GACCACCTG GACCACCAG GACCACCAC GACCACCAC GACCACCAC GACCACCACCAC GACCACCAC GACCACAC GACCACCAC GACCAC	SOURCH VIEW CONTROL OF THE CONTROL O	120 240 360 420 60 120 240 360 420 480 600 720 960 1080 840 1200 960 1200 1260 1320 1380 1440 1260 1360 1360 1360 1360 1360 1360 1360 13
50 55 60 65 70 75	LALAGUSTH TAASHKYNES TAASHKYNES TAASHKYNES LAGDIZHMIL LOGGSVITPL L	FDCSGKYKCK DDMGGMTANN DDMGGMTANN HITAAHCYY HITAAHCY	SSENCIELLY TOTAL CAPACITY TO	CONTINUENCE CONTINUENCE	LELLELICEPEP GENERACONE GENERACONE HISTORIA AGCTGCCAA TOCCACAA TOCCACAA TOCCACAA TOCCACAA AGCTGCCAA AGCTGCCAA AGCTGCCAA AGCAGCCAC CTGGTCCACC AGCACAC GACCACCAC GACCACCAC GACCACCAC GACCACCAC GACCACCAC GACCACCAC GACCACCAC GCATTGGAA GACCACCTCC TOGGTCACC TOCCTCTGGGTC TOCCTCTGGGTC TOCCTCTGGTC TOCCTCTGGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTGGTC TOCCTGTC TOCCTGGTC TOCCTGGTC TOCCTGGTC TOCCTGGTC TOCCTGGTC TOCCTGGTC TO	SOURCH VIEW CONTROL OF THE CONTROL O	120 240 360 420 60 120 240 360 420 480 600 720 960 1080 840 1200 960 1200 1260 1320 1380 1440 1260 1360 1360 1360 1360 1360 1360 1360 13
50 55 60 65 70 75	LALAGUSTH TAASHKYNES TAASHKYNES TAASHKYNES LAGDIZHMIL LOGGSVITPL L	FDCSGKYKCK DDMGGMTANN DDMGGMTANN HITAAHCYY HITAAHCY	SSENCIELLY TOTAL CAPACITY TO	CONTINUENCE CONTINUENCE	LELLELICEPEP GENERACONE GENERACONE HISTORIA AGCTGCCAA TOCCACAA TOCCACAA TOCCACAA TOCCACAA AGCTGCCAA AGCTGCCAA AGCTGCCAA AGCAGCCAC CTGGTCCACC AGCACAC GACCACCAC GACCACCAC GACCACCAC GACCACCAC GACCACCAC GACCACCAC GACCACCAC GCATTGGAA GACCACCTCC TOGGTCACC TOCCTCTGGGTC TOCCTCTGGGTC TOCCTCTGGTC TOCCTCTGGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTCTGGTC TOCCTGGTC TOCCTGTC TOCCTGGTC TOCCTGGTC TOCCTGGTC TOCCTGGTC TOCCTGGTC TOCCTGGTC TO	STEMPLY OF THE PROPERTY OF THE	120 240 360 420 60 120 240 360 420 480 600 720 960 1080 840 1200 960 1200 1260 1320 1380 1440 1260 1360 1360 1360 1360 1360 1360 1360 13

	WO 02/0)86443			* COO * CO * T	*CCA ACTCCC	1800
	ATGCCTGTGT ATACCATTTG TTTACTTGTC	CIGCITITAC	CTATALICIC	CARCAGCATT	ATGACCCAGG	CACTGGAATC	1860
	TTTACTTCTC	AGATACCAGG	AATATACTAT	TTTTCATACC	ACGTGCATGT	GAAAGGGACT	1920
							1980
5	ACCARAGGCT	ACCTGGATCA	GGCTTCAGGG	AGTGCCATCA	TCGATCTCAC	AGAAAATGAC	2040
	ACCAAAGGCT CAGGTGTGGC	TCCAGCTTCC	CAATGCCGAG	TCAAATGGCC	TATACTCCTC	TGAGTATGTC	2100
							2220
	TAAATCTTGT	GCTAGAAAAA	GCATTCTCTA	TECTOTALCCCC	CACATTTGAG	CTATCAGACC	2280
10	AACAAACCTT	AAAAGAATGT	NATTITITATI	AACCTABABA	CCTATCTCAA	CONTENENCE	2340
10	AATTTCTAGT	TAGCAATCTT	ARGGCTCTTT	AAGGTTTTCT	CCAATATTAA	AAAATATCAC	2400
							2460
							2520
	ATTTCCTTTT	TAAAAAAGCC	TGTTTCTAAC	TATGAATATG	AGAACTTCTA	GGAAACATCC	2580
15	ATTTCCTTTT AGGAGGTATC TGTATCCCCT CAATATCTAT	ATATAACTTT	GTAGAACTTA	AATACTTGAA	TATTCAAATT	TAAAAGACAC	2640 2700
	TGTATCCCCT	AAAATATTTC	TGATGGTGCA	CTACTCTGAG	GCCTGTATGG	CCCCTTTCAT	2760
	CAATATCTAT	TCAAATATAC	AGGTGCATAT	ATACTIGITA	ARGUIUTTAT	CTTTTCAAAA	2820
	CCCAAAATAT	TGAAGTTCAT	ACCEPTEDATE	ATACCCACCA	TARCTTOCAL	ACAGGTATCT	2880
20							2940
20	AATCTTATCT	CATATCATT	TCTGGATTTA	CAGAACATTA	GCACATGTAC	CTTGTGCCTC	3000
	CCATTCAAGT	GAAGTTATAA	TTTACACTGA	GGGTTTCAAA	ATTCGACTAG	AAGTGGAGAT	3060
	AATCTTATGT CCATTCAAGT ATATTATTA	TTTATGCACT	GTACTGTATT	TTTATATTGC	TGTTTAAAAC	TTTTAAGCTG	3120
							3180
25	AACATCAATA	GATTTTTAGG	CTGAATTAAT	TTGAAAGCAG	CAATTIGCIG	TTCTCAACCA	3240
	TTCTTTCAAG	GCTTTTCATT	CGACACAATA	AAATAACATC	AATAG		
	a 70 110						
	Sed in Moi	435 Proteir ession #: 1	D OOOASA.2				
30	Procein Acc	Session #1 1	1.000404.5				
50	1	11	21	31	41	51	
	ī	ī	1	1.	1	1	
	WIRGIPFILL	VSLNLVHGVP	YAERYOMPTG	IKGPLPNTKT	OFFIRALIKS	KGIAVRGEQG	60
25	TPGPPGPAGP	RGHPGPSGPP	GKPGYGSPGL	QGEPGLPGPP	GPSAVGKPGV	PGLPGKPGER	120 180
35	GPYGPKGDVG	PAGLPGPRGP MGYGAPGRPG	PGPPGIPGPA	GISVPGKPGQ	QGPTGAPGPR	CEPGERGAPG	240
							300
	GEMGPIGPPG	GPAGLPGGPG GYPGAKGERG	PREBUGBACI.	DCKDCI TCDD	GNMGPOGPKG	TPGSHGLPGP	360
	KORTGRAGRA	GYPGAKGERG	SPGSDGKPGY	PGKPGLDGPK	GNPGLPGPKG	DPGVGGPPGL	420
40							480
	ATKGLNGPTG	PPGPPGPRGH VSAFTVILSK	SGEPGLPGPP	GPPGPPGQAV	MPEGPI KAGQ	RPSLSGTPLV	540
	SANOGVTGMP	VSAFTVILSK	AYPAIGTP1P	PDKILYNRQQ	HYDPRTGIFT	CQIPGIYYFS	600
	YHVHVKGTHV	WVGLYKNGTP	VMYTYDEYTK	GYLDOASGSA	IIDLTENDQV	MİQLPNAESN	660
45	GLYSSEYVHS	SFSGFLVAPM					
45	GLYSSEYVHS	SFSGFLVAPM					
45	GLYSSEYVHS Sea ID NO:	SFSGFLVAPM	nuence .				
45	GLYSSEYVHS Seq ID NO: Nucleic Ac	SFSGFLVAPM 436 DNA sec d Accession	quence				
	GLYSSEYVHS Seq ID NO: Nucleic Ac:	SFSGFLVAPM	quence				
45 50	GLYSSEYVHS Seq ID NO: Nucleic Ac:	SFSGFLVAPM 436 DNA sec d Accession	quence		41	51	
	GLYSSEYVHS Seq ID NO: Nucleic Ac: Coding sequ	SFSGFLVAPM 436 DNA sectid Accession sence: 18	quence 1 #: XM_062 98 21	811 31	41 	1	
	GLYSSEYVHS Seq ID NO: Nucleic Act Coding sequents	SFSGFLVAPM 436 DNA sec 1d Accession sence: 18	quence #: XM_062 8 21	31 	41 	1	60
	GLYSSEYVHS Seq ID NO: Nucleic Act Coding sequents	SFSGFLVAPM 436 DNA sec 1d Accession sence: 18	quence #: XM_062 8 21	31 	41 	1	120
50	GLYSSEYVHS Seq ID NO: Nucleic Act Coding sequent	SFSGFLVAPM 436 DNA sec 1d Accession sence: 18	quence #: XM_062 8 21	31 	41 	1	120 180
	GLYSSEYVHS Seq ID NO: Nucleic Ac: Coding sequ ATTGGGGGGG CTGCTGGTGGACG GGCGACGCCA	SFSGPLVAPM 436 DNA sec 1d Accession sence: 180 11	guence a #: XM_062 98 21 GTCCGTCTCC GGCGGCGGGG CTGGCGCATC CGGCAGCTGC	31 TCATCCTGGA GCGAGGGCCA GGCTTGCGGT	41 ACGCCGCTTC GCGGCGAGTA GTCCCGAGCG ACTGCTGCTC	GCTCCTGCAG CTGCCACGGC CTTCGACGGC CAGCGCCGAG	120
50	GLYSSEYVHS Seq ID NO: Nucleic Ac: Coding sequ ATTGGGGGGG CTGCTGGTGGACG GGCGACGCCA	SFSGPLVAPM 436 DNA sec 1d Accession sence: 180 11	guence a #: XM_062 98 21 GTCCGTCTCC GGCGGCGGGG CTGGCGCATC CGGCAGCTGC	31 TCATCCTGGA GCGAGGGCCA GGCTTGCGGT	41 ACGCCGCTTC GCGGCGAGTA GTCCCGAGCG ACTGCTGCTC	GCTCCTGCAG CTGCCACGGC CTTCGACGGC CAGCGCCGAG	120 180 240
50	GLYSSEYVHS Seq ID NO: Nucleic Ac: Coding sequ ATTGGGGGG TGGTGGTGG TGGTGGAGG GGGGAGGCG GGGGGGAGCCA ATTGGGGGGG	SFSGFLVAPM 436 DNA see 1d Accession sence: 18 11 CTCGGGGCTC CTGGGGTGCT CGCAGGGGGT CCATCTGCTA ACCAGGGGGA AGAGGGCGT ACCAGGGGGA AGAGGGCGC ACCAGGGGGGA AGAGGGCGG ACGAGGGGGGGA AGAGGGCGGA AGAGGGCGGA AGAGGGCGGA AGAGGGCGGA	quence 1 #: XM_062 88 21 GTCGTCTCC GGCGCGGG CTGGCGCATC CTGCGACAAT CGACGGCTGC CTTTATATCATC	31 TCATCCTGGA GCGAGGGCCA GCGTTGCGCT GACCGCCAGC GCATGCCCA	41 	GCTCCTGCAG CTGCCACGGC CTTCGACGGC CAGCGCCAG CGAGCCTGGC GTTCCTCATT CTGTTGCTGC	120 180 240 300 360 420
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50 55	GLYSSEYVHS Seq ID NO: Nucleic Aci Coding sequ 1 ATGTGGGGGG CTGCTGCTGG GGGGAGGCA GGGGAGCA GGGGAGCA GTGGCTGGG AGATTCTCC ATGGAGACCA	SFSGFLVAPM 436 DNA sected accession 11 CTCGCGCGTC CTCGCGGTC CCACTGCT CCACTGCT ACCAGGGGGT ACCAGGGGGT TGTTGTGGC GGCCTAGGCGG TGTTTGTGGC TGCCCATGAT	guence a #: XM_062 88 21 grecorerce ggeaceass cracecearce craceacaac craceacaac craceacaac craceacaac craceacaac craceacaac craceacaac craceacaac craceacaacaac craceacaacaac craceacaacaac craceacaacaac craceacaacaac craceacaacaac	31 TCATCCTGGA GCGAGGGCCA GCGTTGCGCT GACCGCCAGC GACGCCCAC CAGAGCCCAC CAGAGCCGAG AGCACCTCCC	41 ACGCCGCTTC GCGGCGAGTA GTCCCGAGCG ACTGCTGCTC TGGTGGCAGC CCCCAGGGGG GGGGTCGTC GGGCCGGGGGGGTCGTC GGGCCGGGGGGGGTCGTC	GCTCCTGCAG GCTCCTGCAG CTTCGACGGC CTTCGACGGC CAGCGCCGAG GTTCCTCATT CTGTTGCTGC TAACGGCTTG CTCACGCCAG GCCCCAACA	120 180 240 300 360 420 480 540
50 55	GLYSSEYVHS Seq ID NO: Nucleic Ac: Coding sequence Total Action of the Coding sequence GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	SFSGFLVAPM 436 DNA sed d Accession sence: 18 11	quence a #: XM_062 88 21 GTCCGTCTCC GGCGCGCGGG CTGCGCATA CGACGGTGC CTTTATCATC GGATCCCAG CCCCAGTGCC CAGCTCCAGC CAGCTCCAGC CAGCTCCAGC CAGCTCCAGC CAGCTCCAGC	31. TCATCCTGGA GCGAGGGCCA GCGTTCCAGT GCGTTGCGCT GACCGCAGC GCATGCCCA AGCACTCCC GCGAACTCCAG GCACTCCC GCCAACTCAG	41 ACGCCGCTTC GCGGGGAOTA GTCCGAGGG ACTGCTGCTC AGGGGCTGG TCTACGTGCC CCCCAGGGG GGGGTCGTC GGGCCCGGC ACACCTTCA	GCTCCTGCAG CTGCCACGGC CTTCGACGGC CAGCGCCGAG CAGCCTGGC GTTCCTCATT CTGTTGCTGC TAACCGCTTG CTCACGCCAG GCCCCAACATA	120 180 240 300 360 420 480 540 600 660
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50 55 60	GLYSSEYVHS Seg ID NO: Nucleic Acc. Coding sequity I ATGTGGGGCG TGGCTGGTGG GGCGACGCCAG GGCGACGCCAG GGCGGCTGC AGATGTCCCAG AGATGTCCCAG AGATGTCCAG TGGGGGCACAG TCGAGCACAG ACCAGAACAC TCCAGCACAG TCGAGCACAG TCCAGCACAG TCGAGCACAG CAC TCCAGCACAG TCGAGCACACACACAC TCCAGCACACACAC TCCAGCACACACACAC TCCAGCACACACAC TCCAGCACACACAC TCCAGCACACACACAC TCCAGCACACACACACACAC TCCAGCACACACACACACACACACACACACACACACACAC	SFSGFLVAPM 436 DNA sec tence: 18i 11 CTCGCCGCTC CTCGCCTCC CGCAGGGCT CCATCTGCTG ACCAGGGGGAAGACGCCC TGTTTGTCGC GGCTAACAT CTCCCATACAT CTCCCATACAT CTCCCATTCT CTCATCTTTCTCTCTC	puence 1 #: XM_062 98 21 TCCGTCTCC GGCGGCGGGG CTGGCGCATC CGCGACAAT CGACGCTCC GGATCCCAG CCTTTATCATC GGATCCCAG CCTTGCGGAAA GACTCCAG AGTCCAGA GACTCCAGA GACTCCAGGA GACTCCAGGA GACTGCAGGA GACTGTCAGGA GACTGCAGGA GACTCAGA GACTCACAGA GACTCAGA GACTCACAGA GACTCACAC GACTCACAC GACTCACAC GACTCACA	31 TCATCCTIGA GCGAGGGCA GCGTTGCAGT GACCGCAGG GACCGCAGG CAGAGCCAGG AGCACCTCCC GCCAACTCAG GGGACCATGA AGGGCCACGA	41 	GCTCCTGCAG GCTCCTGCAGGC CTTGCACGGC CTTGCACGGC CAGCGCCGGG GTTCCTCATT CTGTTGCTGC TAACCGCTTG CCCCAGCCAGG GCCCCCAACA TGTCAACATG ACATCAAGGCA GGCCCCATGACA GGCCCCATGACA	120 180 240 300 360 420 480 540 600 660
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50 55 60	GLYSSEYVHS Seq ID NO: Nucleic Ac. Coding sequ I I ATGGGGGG GTGGTGGGGG GGGGGGGGGGGGGG	SFSGFLVAPM 436 DNA see 436 Accession sence: 18 11 TCGGCGCTC CTGGGCTGCT CCAGGGGGGGT ACCAGGGGGGG TGTTTGTCGCT ACCAGGGGCGC TGTTTGTCGCT ACCAGGGGGGG TGCCAAGAC TCGCCATGAT CTGCCAGTT CCAACTGTTG ATCCCCATGAT ATCCCCCATGAT ATCCCCCATGAT ATCCCCCATGAT ATCCCCCATGAT ATCCCCCATGAT ATCCCCCATGAT ATCCCCCATGAT ATCCCCCATGAT ACCAGGTGAACA	RUENCE 2 H: XM_062 98 21 1 GEOGRAPH GEOGRAPH GEOGRAPH GEOGRAPH GEOGRAPH GEOGRAPH GEOGRAPH CHAPTER GEOGRAPH CHAPTER GEOGRAPH GEOGRAPH CHAPTER GEOGRAPH GEOGRA	31 TCATCCTGGA GCGAGGGCCA GCGTTCCAGT GCGTTGCGCT GACCGCCAGG GCACCTCCC CAGAGCCGAG GCAACTCAG GCGACCTCCA GCGACCTCCA CGGGCACCC ACGGTGCAGC	41 ACGCCGCTTC GCGGCGAGCO ACTGCTGCTC GGGGCCTGG TCTACOTGCC TCGTGCGCG GCGCCGGGC ACAACGTCTA AGATTGTGC ACGACTCTG GGCACTCTG GGCACTCTG GGCACTCTG GGCACTCTG GGCACTCTG	GCTCCTGCAG GCTCCTGCAGGC CTTGCACGGC CTTGCACGGC CAGCGCCGGG GTTCCTCATT CTGTTGCTGC TAACCGCTTG CCCCAGCCAGG GCCCCCAACA TGTCAACATG ACATCAAGGCA GGCCCCATGACA GGCCCCATGACA	120 180 240 300 360 420 480 540 660 720 780
50 55 60 65	GLYSSEYVHS Seq ID NO: Nucleic Aci Coding sequ 1 ATGTGGGGGG GCTGCTGGCGG GGGGAGGCA GGGGGAGGCA GGGGAAGCA GGGGAAGCA TCAGCACAG AGGTGACAG CCTAGCACAG AGGTCACACCA Seq ID NO: Seq ID NO:	SFSGFLVAPM 436 DNA sected accession Lence: 18 11	quence 3 #: XM_062 88 21 dTCCGTCTCC GGCGGCGGGG CTGGCCCATC GGAGGCGCGGG CTTTATCATC GGATCCCCAT GGATCCCCA CCCCATCATC CACCTCCATC CACCTCATC CACCTCCATC CACCTCCATC CACCTCCATC CACCTCATC CACC	31 TCATCCTGGA GCGAGGGCCA GCGTTCCAGT GCGTTGCGCT GACCGCCAGG GCACCTCCC CAGAGCCGAG GCAACTCAG GCGACCTCCA GCGACCTCCA CGGGCACCC ACGGTGCAGC	41 ACGCCGCTTC GCGGCGAGCO ACTGCTGCTC GGGGCCTGG TCTACOTGCC TCGTGCGCG GCGCCGGGC ACAACGTCTA AGATTGTGC ACGACTCTG GGCACTCTG GGCACTCTG GGCACTCTG GGCACTCTG GGCACTCTG	GCTCCTGCAG GCTCCTGCAGGC CTTGCACGGC CTTGCACGGC CAGCGCCGGG GTTCCTCATT CTGTTGCTGC TAACCGCTTG CCCCAGCCAGG GCCCCCAACA TGTCAACATG ACATCAAGGCA GGCCCCATGACA GGCCCCATGACA	120 180 240 300 360 420 480 540 660 720 780
50 55 60	GLYSSEYVHS Seq ID NO: Nucleic Aci Coding sequ 1 ATGTGGGGGG GCTGCTGGCGG GGGGAGGCA GGGGGAGGCA GGGGAAGCA GGGGAAGCA TCAGCACAG AGGTGACAG CCTAGCACAG AGGTCACACCA Seq ID NO: Seq ID NO:	SYSGETUVAPM 416 DNA seed dd Accession ence: 18i 11 CTOSCOSTIC CONTINUES	quence 1 % XM_062 88 21 1 GROSSICIONE GROS	31 TOATCCTGGA GGGARGGCCA GGCTTCOART GGGARGGCCA GGCTTCOART GGGARCCTACA GGARCCTACA GGARCCTACA GGGARCCTACA AGGGCCACCA AGGGCCACCA AGGGCCACCA AGGGCCACCA CCAGGGGGTGA CCAGGGGGTGA	41 AGGCGGCTTC GGGGGGAGTA GTCCCGGGGGGGGGGGGG	GOTCCTGCAG GGCCCAGGG CTTCGACGGC CAGCGCCGAG CGAGCCCGAG GGACCCGGG GTTCCTCATT CTGTTGCTGC TAACCGCTTG CTCAGCCAG GCCCCAACA TGTCAACATG ACATCAACATG ACATCAACATG GCCCCATGACA GTCCCCCTTC	120 180 240 300 360 420 480 540 660 720 780
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50 55 60 65	GLYSSETVHS Seq ID NO: Nuclaic Aci Coding seq: 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SISSETUADM A16 DNA sec dd Accession Lence: 18i L CTOGGCGCTC CTGGCCTTGCTC CACCTTGCTC CACCTTGCTC CACCTGCTAAGCA GCCTAAGCA GCCTAAGCA CTGCTGCTC CACCTGCTC CACCTGCTC CACCTGCTC CACCTGCTC CACCTGCTC CACCTGCTC CACCTGCTC CACCTGCTC CACCTGTTC CACC	TUENCE TO SERVICE TO S	31 TCATCCTGGA GCGAGGGCA GCGTCCART GCGTTCCART GCGTTCART GCGTTCART GCGTCCART GCGACCACA GCACCTCAR GCCACCTCA GCGACCACA ACGCCACCA ACGCCACCA CCTGGCTAA CCTGGCTGAC CCTGGCTAA CCTGGCTGAC	41 AGGCGGTTC GCGGGGGAGTA GCGCGGAGGA GCCGGAGGA GCCGGAGGA GCGCGGGGG GCGGGGGGGG	GCCCATGAG GGCCCAGGG GAGCCTGGC GAGCCTGGC GAGCCTGGC GTTCCACATG CTGTTGGTGC TACCGCTTG TCCACATGAGC GCCCCAACA GCCCCCAACA GCCCCCAACA GCCCCCAACA GCCCCCTTC 51	120 180 240 360 420 480 660 720 780 840
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50 55 60 65 70	GUYSETVHES Seq ID NO. Nucleic Ac. Coding seq 1 1 1 ACCOMMINGATION	SISSETUVAPM 415 ENA see dd Accession 18 11 11 11 11 11 11 11 11 11 11 11 11 11	RUESCE 3 8 1 MM_062 21 1 CONTINUE CO	31 I I I I I I I I I	41 AGGCGGTTC GGGGGAMTA GGCGGAMGTA GTCCCGARGO ACTGCTGCTC AGGGGCTGC CCCCAGGGGG CCCCAGGGGG ACAGCTGTC ACAGCTCTC ACAGCTCTC ACAGCTCTC ACAGCTCTC ACAGCTCTCT ACAGCTCTTA ACAGCTCTTA 41	GCCCATGAG GCCCCAGGG GAGCCTGGC GAGCCTGGC GAGCCTGGC GTTCCACATGC CTGTTGCTGC TAACCGCTTG TCACACCAG GCCCCAACA GCCCCCAACA GTCCCCCTTC 51	120 180 240 300 360 480 540 600 720 780 840
50 55 60 65 70	GUYSSETVHS SEQ ID NO. Nuclaic Act Coding seq coding seq	ASSETUTATE 436 DNA sected Accession 11 CONTROL OF ACCESSION ACCASSION	NUMBER 1 B. XM.062 2 1 I I XM.062 2 1 I I XM.062 2 1 I I XM.062 2 1 I I XM.062 CTOSCOCCHTC GROGOGOGOC CTOSCOCCHTC GROGOCOCC CAGCTCCAGC CAGCTCCAGC GACTCCAGC GACTCCAGC GACTGCAGC GACTGCA	31 I I I I I I I I I	41 AGGCGGTTC GGGGGAMTA GGCGGAMGTA GTCCCGARGO ACTGCTGCTC AGGGGCTGC CCCCAGGGGG CCCCAGGGGG ACAGCTGTC ACAGCTCTC ACAGCTCTC ACAGCTCTC ACAGCTCTC ACAGCTCTCT ACAGCTCTTA ACAGCTCTTA 41	GCCCATGAG GCCCCAGGG GAGCCTGGC GAGCCTGGC GAGCCTGGC GTTCCACATGC CTGTTGCTGC TAACCGCTTG TCACACCAG GCCCCAACA GCCCCCAACA GTCCCCCTTC 51	120 180 240 300 360 480 540 600 720 780 840
50 55 60 65 70	GUYSSETVHS SEQ ID NO. Nuclaic Act Coding seq coding seq	A 15 DIA se control de la cont	NUMBER 3 B: XM4_062 3 B: XM4_062 3 B: XM4_062 3 B: XM4_062 3 B: XM4_062 4 GOOGGOOGGOOGGOOGGOOGGOOGGOOGGOOGGOOGGO	1811 TCATCCTGGA GGGAGGGCOA GGGAGGGCOA GGGAGGGCOA GGCAGTGCCA GGCAGTGCCA GGCAGTGCCA GGCAGTGCCA GGGAGTGCCA GGGAGTGCCA GGGAGTGCCA GGGAGTGCCA GGGAGTGCA GGGGGTGA ARASGGGGGGG GGRAGTGCA GGGAGTGCA 4884 489	41 OCCUPATION GOSGIGARION GOSGIGARION GOSGIGARION ACTOCTUCE GOSGIGATION GOSGIGATION GOSGIGATION ACTACTUCTUC GOSGIGATION ACTACTUCT ACTACTUC GOSGIGATION GOSGIGATI	GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCCCAG GCCCCCAG GCCCCCAG GCCCCCAG GCCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCAG AG GCCCCCAG GCCCCCCAG GCCCCCCAG GCCCCCCCAG GCCCCCCCAG GCCCCCCCC	120 180 240 300 360 480 540 600 720 780 840
50 55 60 65 70	GUYSEFVHS Seq ID NO. Nuclaic Act Coding seq 1 1 ARTHOGOGICA ARTHO	ASSENTATION AND ASSESSED ASSES	NUMBERS 1 81 XM_0628 2 11 2 11 3 FORWARD AND AND AND AND AND AND AND AND AND AN	31 TOATCCTGGA GGCTACGACGACGACGACGACGACGACGACGACGACGACGACGA	41 I ACCCCCCTTC GEOGRAPHO GEOGRAPHO GEOGRAPHO TOTACOPICC ACAGCTCTO GEOGRAPHO ACAGCTCTO ACA	GCTCCTUGAR GTTCCTAGAR GTTCCTAGAR GARGACCAGAR GARGACCAGAR GARGACCAGAR GTTCCTCATT CTGTTAGCTAC TAGCACCTTA GCCCCACAA ACATCAAGG GCCCCAACAA GTCCCCCTTC 51 GTCCCCTTC 51 GTCCCCCTTC 51 GTCCCCTTC 51 GTCCCCTTC 51 GTCCCCCTTC 51 GTCCCCTTC 51 GTCCCTTC 51 GTCCCTTC 51 GTCCCCTTC 51 GTCCC	120 180 240 300 360 480 540 600 720 780 840
50 55 60 65 70 75 80	GUYSEFVHS Seq ID NO. Nuclaic Act Coding seq 1 1 ARTHOGOGICA ARTHO	ASSENTATION AND ASSESSED ASSES	NUMBERS 1 81 XM_0628 2 11 2 11 3 FORWARD AND AND AND AND AND AND AND AND AND AN	31 TOATCCTGGA GGCTACGACGACGACGACGACGACGACGACGACGACGACGACGA	41 I ACCCCCCTTC GEOGRAPHO GEOGRAPHO GEOGRAPHO TOTACOPICC ACAGCTCTO GEOGRAPHO ACAGCTCTO ACA	GCTCCTUGAR GTTCCTAGAR GTTCCTAGAR GARGACCAGAR GARGACCAGAR GARGACCAGAR GTTCCTCATT CTGTTAGCTAC TAGCACCTTA GCCCCACAA ACATCAAGG GCCCCAACAA GTCCCCCTTC 51 GTCCCCTTC 51 GTCCCCCTTC 51 GTCCCCTTC 51 GTCCCCTTC 51 GTCCCCCTTC 51 GTCCCCTTC 51 GTCCCTTC 51 GTCCCTTC 51 GTCCCCTTC 51 GTCCC	120 180 240 300 420 420 540 660 720 840
50 55 60 65 70	Seq ID NO. Nucleic Acic Coding seq 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	416 DNA se tid Accession tid Consense tid Accession tid Consense tid Consense tid Consense tid Consense tid Consense tid Consense tid Accession 8: 11 12 13 15 15 16 17 17 17 18 18 19 19 19 19 19 19 19 19 19 19	NUMBER OF THE PROPERTY OF THE	SENTI TONTICCTORDA GONZOLO CONTROLO CON	41	GETECTIGUAG GETECT	120 180 240 300 360 480 540 600 720 780 840
50 55 60 65 70 75 80	Seq ID NO. Nucleic Acic Coding seq 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	416 DNA se tid Accession tid Consense tid Accession tid Consense tid Consense tid Consense tid Consense tid Consense tid Consense tid Accession 8: 11 12 13 15 15 16 17 17 17 18 18 19 19 19 19 19 19 19 19 19 19	NUMBER OF THE PROPERTY OF THE	SENTI TONTICCTORDA GONZOLO CONTROLO CON	41	GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCTGCAG GCTCCCCAG GCCCCCAG GCCCCCAG GCCCCCAG GCCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCCAG GCCCAG AG GCCCCCAG GCCCCCCAG GCCCCCCAG GCCCCCCCAG GCCCCCCCAG GCCCCCCCC	120 180 300 360 420 420 420 660 720 720 720 720 180 240

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	CTGATCTTCG	TGTCCAGCCC .	AGCGCTCCTA	ATA A AGRGTO	ACTIGGCCIA	CATCGAGGAG	360
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10	Seq ID NO:	439 Protein	sequence				
	Protein Acc	ession #: N	P_003995.1				
		11	21	31	41	51	
15	î	ī	1	1	1	Ĭ.	
13	MONGTLOTTE	GGVNKHSTSI	GKIWLTVLFI	PRIMILVVAA	KEVWGDEQAD	FVCNTLQPGC	60
	MINOVINUVED	OTAWATOTHOT	LIFVSSPALL	VAMHVAYRRH	EKKRKFIKGE	IKSEFKDIEE	120
						AWPCPNTVDC	180
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20							
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	Nucleic Aci	d Accession	#: XM 061	.091.1			
25	Coding sequ	ence: 124	81				
23	1	11	21	31	41	51	
	i	ī.	ī	ī	Ī	1	
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20	CACCGAGCGC	TGGTCGCCGC	TCTCCTTCCG	GTGAGTCCCA	GCCCCGAGTT	GGCTCTGGCG	120
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	ATTTCAGCTG	CCAGCAAAAT ACAGCGTCGG	GATGTGGTGC	TCGGCTGCAG	TGGACATCAT	GTTTCTGTTA	360
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35		GTCTGGACAT ATCTGGAATT					540
	TCCACTCCTC	GGATGGTTTT	COCCUTTGGAT	CCACCGAGA	CGGAACTTGC	TCTGAAATAC	600
	CHIMCHOCO'S C'S	anacomicco.	TYGORGGCAGA	AATGCTTCTG	TGCCCCAGAT	CCTCATCATC	660
	CTCS CTCS TG	CCDACTOCCA	REGERGATETE	GCACTGCCAT	CCAAGCAGCT	DUARADUAAD	720
40	COTTOTOLOTO	different Contraction	GGGGGTCAGG	TTTCCCAGGT	GGGAGGAGCT	GCATGCACTG	780 840
	GCCAGCGAGC	CTAGAGGGCA GCACCCTCAG	GCACGTGCTG	TTGGCTGAGC	AGGTGGAGGA	AGCTGGGAGC	900
	COCCACCETO	TOTTCATGGA	COCCUTANTS	GGCATCTCTC	TGATAGGCCC	CTGTGACTCG	960
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		TCGTGAAGCG CCACATACAG					1260
	Chromocom	ACCTYCCTCTC	CAGCCTCGAT	GGCATTCCCT	TCCGTGGTGG	CCCCACCCTG	1320
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55	COCCONGGGT	GCCCGGACACA	AGCCCTGGAC	CTCGTCTTCA	TGTTGGACAC	CICIGCUICA	1680
							1740 1800
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05							2340
							2400
	ACCCCTCCCA	GCAACTACAG	AGAAGGCCTG	GGCACTGAA	TGGTGCCTAC	CTTCTGGAAT	2460
70	GTCTGTGCCC	CAGGTCCTTA	G				
/0	Com TD MO.	441 Protei	n semience				
	Protein Ac	cession #:	XP_061091.1				
75	1	11	21	31	41	51 I	
13	I	BYMT TOPPOS	I DATABATT	USPSPELAT.	PGYPPVPAA	DRFTLPMIGG	60
							120
							180
	DAMMINA	OTETETALEY	T.T.LIDGIT.DGGT	NASVPOILI	t VTDGKSOGD	ALPSKOLKER	240 300
80	GVTVFAVGVE	FPRWEELHAL	ASEPRGQHVI	LAEQVEDATI	CDLANGCER	I CSSATPAGS	360
						CALKLSLECR LVAVPVGEYQ	420
	DVPDLVWSt.r	GIPPRGGPTI	TGSALROAN	RGFGSATRT	QDRPRRVVV	LTESHSEDEV ELOGRICSRQ	480
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85							600
	APGLDTKPTI	AAMLRAISO	PYLGGVGSA	J TALLHIYDK	PRIVOKGARP	VPKAVVVLTG ADLRYHQDVL	720
	GRGAEDAAVI	AUKLKNNGIS	APAAGAGBA	O DEGLIARANG			0

IEWLCGEAKQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ 780
GWILETDIRH MAPVDEGSSR TPPSNYREGL GTENVPTFMN VCAPGP

Seg ID NO: 442 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1..2424

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	TCTCTCCCTC	TCCAGGAAGT	CCATGTAAGC	AAAGAAACCA	TCGGGAAGAT	TTCAGCTGCC	120
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	AGCGTCGGGA	AAGGGAGCTT	TGAAAGGTCC	AAGCACTTTG	CCATCACAGT	CTGTGACGGT	240
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	ATGGTTTTCA	AAGGAGGGCG	CACGGAGACG	GAACTTGCTC	TGAAATACCT	TCTGCACAGA	420
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	AAGTCCCAGG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACTGTG	540
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	ACCCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
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	CGGGCCAAAG	TCTTCGTGAA	GCGGTTTGTG	CGGGCCGTGC	TGAGCGAGGA	CTCTCGGGCC	1140
	CGAGTGGGTG	TGGCCACATA	CAGCAGGGAG	CTGCTGGTGG	CGGTGCCTGT	GGGGGAGTAC	1200
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	TCAGTAGGGC	CCGAGAATTT	TGCTCAGATG	CAGAGCTTTG	TGAGAAGCTG	TGCCCTCCAG	1680
	TTTGAGGTGA	ACCCTGACGT	GACACAGGTC	GGCCTGGTGG	TGTATGGCAG	CCAGGTGCAG	1740
	ACTGCCTTCG	GGCTGGACAC	CAAACCCACC	CGGGCTGCGA	TGCTGCGGGC	CATTAGCCAG	1800
40	GCCCCCTACC	TAGGTGGGGT	GGGCTCAGCC	GGCACCGCCC	TGĊTGCACAT	CTATGACAAA	1860
	GTGATGACCG	TCCAGAGGGG	TGCCCGGCCT	GGTGTCCCCA	AAGCTGTGGT	GGTGCTCACA	1920
	GGCGGGAGAG	GCGCAGAGGA	TGCAGCCGTT	CCTGCCCAGA	AGCTGAGGAA	CAATGGCATC	1980
	TCTGTCTTGG	TOGTGGGGGT	GGGGCCTGTC	CTAAGTGAGG	GTCTGCGGAG	GCTTGCAGGT	2040
	CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCCGACC	TGCGGTACCA	CCAGGACGTG	2100
45	CTCATTGAGT	GGCTGTGTGG	AGAAGCCAAG	CAGCCAGTCA	ACCTCTGCAA	ACCCAGCCCG	2160
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	GGCTGGGAGG	GCCCCCACTG	CGAGAACCGT	GAGTGGAGCT	CTTGCTCTGT	ATGTGTGAGC	2280
	CAGGGATGGA	TTCTTGAGAC	GCCCCTGAGG	CACATGGCTC	CCGTGCAGGA	GGGCAGCAGC	2340
		CCAGCAACTA		CTGGGCACTG	AAATGGTGCC	TACCTTCTGG	2400
50	AATGTCTGTG	CCCCAGGTCC	TTAG				

Seq ID NO: 443 Protein sequence Protein Accession #: Eos sequence

VEPELLEBNY CVEPESSUPP SLELGEVIN'S (STICKISA SOMMICSAN DISPLICIOS SYMBOSESSES MERITYCOS LOS PERSENVO GAPPESTH LEPPLOSTO COSYNACTION OF SYMBOSESSES MERITYCOS LOS PERSENVO GAPPESTH LEPPLOSTO COSYNACTION OF SYMBOSES COSYNACTIO

Nucleic Acid Accession #: Eos sequence Coding sequence: 89..2356

PEDDENVERG LOTEMVETEN NVCAPGE

GOOCCOTTAGE COGAGECTOR COCCGGGTCTG TGAGTAGAGE CGCCCGGGCA CCGAGCGCTG GTCGCCGCTC TCCTTCCGTT ATATCAACAT GCCCCCTTTC CTGTTGCTGG AAGCCGTCTG GEOGRACIE TOCTICOGTI ATATOANATI GEOCOCTTIC CIPTRICTOS AMGOSTICTI OTTITTICCI TITTICCAGAI TOCCOCCATA (TECCOCTCI CAGAMATICA TATOTACAA AGAMACIAC) GORMANTIT CAGCIGOGO CAMANTATO TOTTICCOGO CITCATOGA AGAMACIAC CONTRACTO CON

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	GCAGCTGAAG	GAAAGGGGTG GCACTGGCCA	TCACTGTGTT	TGCTGTGGGG	GTCAGGTTTC	CCAGGTGGGA	660 720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TCGGCCATCT	GCTCCAGCGC	780
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	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
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	TGAGCTGCAG	ATGTTGGACA	CCTCTGCCTC	ACTAGGGCCC	GAGAATTTTG	CTCAGATGCA	1740
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	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCACCCAC	2580
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40		445 Protein		_			
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	1	11	21	31	41	51	
				7-			
	MODELLLEAV	CVPI.PSPVDP	PLPI OEVHVS	KETIGKISAA	SKMMWCSAAV	DIMPLLDGSN	60
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45	SVGKGSFERS	KHPAITVCDG	LDISPERVRV	GAFQF9STPH POILIIVTDG	LEFPLDSFST KSQGDVALPS	QQEVKARIKR KQLKERGVTV	120 180
45	SVGRGSPERS MVPKGGRTET FAVGVRPPRW	KHPAITVCDG ELALKYLLHR EELHALASEP	LDISPERVRV GLPGGRNASV RGQHVLLAEQ	GAFQFSSTPH PQILIIVTDG VEDATNGLFS	LEFPLDSFST KSQGDVALPS TLSSSAICSS	QQEVKARIKR KQLKERGVTV ATPDCRVEAH	120
	SVGKGSPERS MVPKGGRTET FAVGVRPPRW PCEHRTLEMV SOPCONGGTC	KHPAITVCDG ELALKYLLHR EELHALASEP REPAGNAPCW VPEGLDGYOC	LDISPERVRV GLPGGRNASV RGQHVLLAEQ RGSRRTLAVL LCPLAFGGEA	GAFQFSSTPH PQILIIVIDG VEDATNGLFS AAHCPFYSWK NCALKLSLEC	LEFPLDSFST KSQGDVALPS TLSSSAICSS RVPLTHPATC RVDLLPLLDS	QQEVKARIKR KQLKERGVTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL	120 180 240 300 360
45 50	SVGKGSPERS MVPKGGRTET FAVGVRPPRW PCEHRTLEMV SOPCONGGTC	KHPAITVCDG ELALKYLLHR EELHALASEP REPAGNAPCW VPEGLDGYOC	LDISPERVRV GLPGGRNASV RGQHVLLAEQ RGSRRTLAVL LCPLAFGGEA	GAFQFSSTPH PQILIIVIDG VEDATNGLFS AAHCPFYSWK NCALKLSLEC	LEFPLDSFST KSQGDVALPS TLSSSAICSS RVPLTHPATC RVDLLPLLDS	QQEVKARIKR KQLKERGVTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL	120 180 240 300 360 420
	SVGRGSFERS MVFKGGRTET FAVGVRFPRW PCEHRTLEMV SQPCQNGGTC RAKVFVKRFV LTGSALROAA	KHPAITVCDG ELALKYLLHR EELHALASEP REFAGNAPCW VPEGLDGYQC RAVLSEDSRA ERGFGSATRT	LDISPERVRV GLPGGRNASV RGQHVLLAEQ RGSRRTLAVL LCPLAPGGEA RVGVATYSRE GODRPRRVVV	GAFQFSTPH PQILIIVTDG VEDATNGLFS AAHCPFYSWK NCALKLSLEC LLVAVPVGEY LLTESHSEDE	LEFPLDSFST KSQGEVALPS TLSSSAICSS RVFLTHPATC RVDLLFLLDS QDVPDLVWSL VAGPARHARA	QQEVKARIKR KQLKERGVTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL DGIPFRGGPT RELLLLGVGS	120 180 240 300 360 420 480
	SVGRGSFERS MVPRGGRTET FAVGVRFPRW PCEHRTLEMV SQPCQNGGTC RAKVFVKRFV LTGSALRQAA BAVRAELEEI	KHPAITVCDG ELALKYLLHR EELHALASEP REFAGNAPCW VPEGLDGYQC RAVLSEDSRA ERGFGSATRT TGSPKHVMYY	LDISPERVRV GLPGGRNASV RGQHVLLAEQ RGSRRTLAVL LCPLAFGGEA RVGVATYSRE GQDRPRRVVV SDPQDLPRQI	GAFQFSSTPH PQILIIVTDG VEDATNGLFS AAHCPFYSWK NCALKLSLEC LLVAVPVGEY LLTESHSEDE PELQGKLCSR	LEFPLDSFST KSQGDVALPS TLSSSAICSS RVFLTHPATC RVDLLFLLDS QDVPDLVMSL VAGPARHARA QRPGCRTQAL	QQEVKARIKR KQLKERGVTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL DGIPFRGGPT RELLLLGVGS DLVFMLDTSA DAMMLDAIGO	120 180 240 300 360 420 480 540
50	SVGEGSFERS MVPKGGRTET FAVGVRPPRW PCEHRTLEMV SQPCONGGTC RAKVFVKRPV LTGSALRQAA EAVRAELEEI SVGPENFAG APYLGGVGSA	KHPAITVCDG ELALKYLLHR EELHALASEP REFAGNAPCW VPEGLDGYQC RAVLSEDSRA ERGFGSATRT TGSPKHVMVY QSFVRSCALQ GTALLHIYDK	LDI SPERVRV GLPGGRNASV RGQHVLLAEQ RGSRRTLAVL LCPLAFGGEA RVGVATYSRE GQDRPRRVVV SDPQDLFNQI FEVNPDVTQV VMTVQRGARP	GAPQFSSTPH PQILIIVTDG VEDATNGLTS AAHCPPYSWK NCALKLSLEC LLVAVPVGEY LLTESHSEDE PELQGKLCSR GLVVYGSQVQ GYPKAVVVLT	LEFPLDSFST KSQGIVALPS TLSSSAICSS RVFLTHPATC RVFLTHLDS QDVPDLVWSL VAGPARHARA QRPGCRTQAL TAFGLDTKPT GGRGAEDAAV	QQEVKARIKR KQLKERGYTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL DGIPFRGGPT REILLLGYGS DLVFMLDTSA RAMLRAISQ PAQKLRINGI	120 180 240 300 360 420 480 540 600 660
	SVGRGSFERS MVFRGGRTET FAVGVRFPRW PCEHRTLEMV SQPCQNGGTC RAKVFVKFR LTGSALRQAA EAVRAELEEI SVGPENFAQM APYLGGVGSA SVLVVGVGPP	KHPAITVCDG ELALKYLLHE EELHALASEP REFAGNAPCW VPEGLDGYQC RAVLSEDSEN ERGFGSATRT TGSPKHVMVY QSFVRSCALQ GTALLHIYDK LSEGLERLAG	LDI SPERVRV GLPGGRNASV RGQHVLLAEQ RGSRTLAVL LCPLAFGGEA RVGVATYSR GQDRPRVVV SDPQDLFNQI FEVNPDVTQV VMTVQRGARP PRDSLIHVAA	GAPQFSSTPH PQILIIVIDG VEDATNGLFS AAHCPFYSWK NCALKLSLEC LLVAVPVGEY LLTESHSEDE PELQGKLCSR GLVYYGSOVQ GVPKAVVVLT YADLRYHQDV	LEFPLDSFST KSQGIVALPS TLSSSAICSS RVFLTHPATC RVFLTHLDS QDVPDLVWSL VAGPARHARA QRPGCRTQAL TAFGLDTKPT GGRGAEDAAV	QQEVKARIKR KQLKERGYTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL DGIPFRGGPT REILLLGYGS DLVFMLDTSA RAMLRAISQ PAQKLRINGI	120 180 240 300 360 420 480 540
50	SVGRGSPERS MVPRGGRTET FAVGVAPPRM PCEHRTLEMV SQPCONGGTC RAKVFVKRPV LTGSALRQAA EAVRAELEEI SVGPENFAQM APYLGGVGSA SVLVVGVGPV CMREGSCVLQ	KHPAITVCDG ELALKYLLHE EELHALASEP REFAGNAPCW VPEGLDGYQC RAVIJSEDSRA ERGFGSATRT TGSPKHVMVY QSFVRSCALQ GTALLHIYDK LSEGLRRLAG MGSYRCKCRD	LDISPERVRV GLPGGRNASV RGQHVLLAEQ RGSRRTLAVL LCPLAFGGEA RVGVATYSRE GQDRPRRVVV SDPQDLFMQI FEVNPDVTQV VMTVQRGARP PRDSLIHVAA GWEGPHCENR	GAPQFSSTPH PQILIIVIDG VEDATNGLFS AAHCPFYSWK NCALKLSLEC LLVAVPVGEY LLTESHSEDE PELQGKLCSR GLVYYGSOVQ GVPKAVVVLT YADLRYHQDV	LEFPLDSFST KSQGIVALPS TLSSSAICSS RVFLTHPATC RVFLTHLDS QDVPDLVWSL VAGPARHARA QRPGCRTQAL TAFGLDTKPT GGRGAEDAAV	QQEVKARIKR KQLKERGYTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL DGIPFRGGPT REILLLGYGS DLVFMLDTSA RAMLRAISQ PAQKLRINGI	120 180 240 300 360 420 480 540 600 660
50	SVERGSFERS MVFEGRTET FAVGVRFPRN PCEHRTLEMV SQPCQNGGTC RAKVFVKRFV LTGSALRQAA EAVRAELEEI SVGPENFAQM APYLGGVGSA SVLVVQGVGVC CMREGSCVLQ Seq ID NO:	KHPALTVCDG ELALKYLLHR EELHALASEP REFAGNAPCW VPEGLDGYQC RAVLSEDSRA ERGFGSATRT TGSPKHVMVY QSFVRSCALQ GTALLHIYDK LSEBLRRLAG MGSYRCKCRD 446 DNA Bec	LDISPERVRY GLPGGRNASV RGQHVLLAEQ RGSRRTLAVL LCPLAFGGEA RVGVATYSRE GQDRPRRVVV SDPODLFNQI FEVNPDVTQV VMTVQRGARP PRDSLIHVAA GWEGPHCENR	GAPQFSSTPH PQILIIVTDG VEDATNGLFS AARCPPYSWK NCALKLSLEC LLVAVPVGEY LLTESHSEDE PBLQGKLCSR GLVYYGSQVQ GVPKAVVVLT YADLRYHQDV FLRRP	LEFPLDSFST KSQGIVALPS TLSSSAICSS RVFLTHPATC RVFLTHLDS QDVPDLVWSL VAGPARHARA QRPGCRTQAL TAFGLDTKPT GGRGAEDAAV	QQEVKARIKR KQLKERGYTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL DGIPFRGGPT REILLLGYGS DLVFMLDTSA RAMLRAISQ PAQKLRINGI	120 180 240 300 360 420 480 540 600 660
50 55	SVERGSFERS MVFKGRTET FAVGVRFPRN PCEHRTLEMV SQPCONGSTC RAKVFVKRFV LTGSALRQAA EAVRAELEEI SVGPENFAQM APYLEGGGSA SVLVVGVGPV CMEGSCVLQ Seq ID NO: Nucleic Ac	KHPAITVCDG ELALKYLLHR ELHALASEP REFAGNAPCW VPEGLDGYQC RAVLSEDSRA ERGFGSATRT TGSPKHVMVY QSFVRSCALQ GTALLHIYDK LSEGLRRLAG MGSYRCKCRD 446 DNA Sec id Accession	LDISPERVRV GLPGGRNASV RGGNVLLAEQ RGSRRTLAVL LCPLAFGEEA RVGVATYSRE GQDRPRRVVV SDPQDLFNQI FEVNPDVTQV VMTUQRGRP PRDSLIHVAA GWEGPHCENR QUEDRE LIEL NM 033	GAPQFSSTPH PQILIIVTDG VEDATNGLFS AARCPPYSWK NCALKLSLEC LLVAVPVGEY LLTESHSEDE PBLQGKLCSR GLVYYGSQVQ GVPKAVVVLT YADLRYHQDV FLRRP	LEFPLDSFST KSQGIVALPS TLSSSAICSS RVFLTHPATC RVFLTHLDS QDVPDLVWSL VAGPARHARA QRPGCRTQAL TAFGLDTKPT GGRGAEDAAV	QQEVKARIKR KQLKERGYTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL DGIPFRGGPT REILLLGYGS DLVFMLDTSA RAMLRAISQ PAQKLRINGI	120 180 240 300 360 420 480 540 600 660
50	SVERGSFERS MVFKGRTET FAVGVRFPRN PCEHRTLEMV SQPCONGSTC RAKVFVKRFV LTGSALRQAA EAVRAELEEI SVGPENFAQM APYLEGGGSA SVLVVGVGPV CMEGSCVLQ Seq ID NO: Nucleic Ac	KHPAITVCDE ELALKYLLHR EELALASEP REFAGNAPCW VPEGLDGYQC RAVLSEDSRA REGFGSATRT TGSPKHWAYY QSFWRSCALQ GTALLHIYDK LSEGLRELAG MGSYRCKCRD 446 DNA sec id Accession uence: 145.	LDISPERVRV GLPGGRNASV RGQHVLLAEQ RGSRRTLAVL LCPLAFGGEA RVGVATYSRE GQDEPRRVVV SDPODLFMOI FEVNPDVTQV VMTVQRGARP PROBLIHVAA GWEGPHCENR RUEICE 1 NM_031	GAPGPSTPH POILLIVIDG VEDATNGLFS AAHCPFYSWK MCALKLSLEC LLVAVPVGEY LLTESHSEDE PELQCKLCSR GLVVYGSQVQ GVPKAVVVLIT YADLRYHQDV FLRRP	LEFPLDSFST KSQGUVALPS TLSSSAICSS RVFUTHPATC RVDLLPFLLDS QDVPDLVMSL VAGPAREAR QROGCRTQAL TAFGLDTKPT TAFGLDTKPT TAFGLDTKPT TAFGLDTKPT TAFGLDTKPT TAFGLDTKPT TAFGLDTKPT	QQEVKARIKR KQLERRGVTV ATPDCRVEAH YRTTCROPCD SAGTTLDGFL DGIPFRGEPT EELLLLGVGS DLVPALDTSA RAMLRAISQ PAGKLERINGI QPVNLCKPSP	120 180 240 300 360 420 480 540 600 660
50 55	SVERGSFERS MVFKGRTET FAVGVRFPRN PCEHRTLEMV SQPCONGSTC RAKVFVKRFV LTGSALRQAA EAVRAELEEI SVGPENFAQM APYLEGGGSA SVLVVGVGPV CMEGSCVLQ Seq ID NO: Nucleic Ac	KHPAITVCDG ELALKYLLHR ELHALASEP REFAGNAPCW VPEGLDGYQC RAVLSEDSRA ERGFGSATRT TGSPKHVMVY QSFVRSCALQ GTALLHIYDK LSEGLRRLAG MGSYRCKCRD 446 DNA Sec id Accession	LDISPERVRV GLPGGRNASV RGGNVLLAEQ RGSRRTLAVL LCPLAFGEEA RVGVATYSRE GQDRPRRVVV SDPQDLFNQI FEVNPDVTQV VMTUQRGRP PRDSLIHVAA GWEGPHCENR QUEDRE LIEL NM 033	GAPQFSSTPH PQILIIVTDG VEDATNGLFS AARCPPYSWK NCALKLSLEC LLVAVPVGEY LLTESHSEDE PBLQGKLCSR GLVYYGSQVQ GVPKAVVVLT YADLRYHQDV FLRRP	LEFPLDSFST KSQGIVALPS TLSSSAICSS RVFLTHPATC RVFLTHLDS QDVPDLVWSL VAGPARHARA QRPGCRTQAL TAFGLDTKPT GGRGAEDAAV	QQEVKARIKR KQLKERGYTV ATPDCRVEAH YRTTCPGPCD SAGTTLDGFL DGIPFRGGPT REILLLGYGS DLVFMLDTSA RAMLRAISQ PAQKLRINGI	120 180 240 300 360 420 480 540 600 660
50 55 60	SUGKOSPERS MYPKGGTTET FAVOVAPPRH PCEHRTLBAV SOPCONGGTC RAKVEYMCREV LTGSALRQAA BAVRAELEEI SVOPENFAQM APYLGGVGSA SVLVVQVGEV GMIEGSCVLQ Seq ID NO: Nucleic Ac Coding seq	KHPAITVCDE ELALKYLLHR EELHALASEP REFAGNAPCW VPECLDGYQC RAVLSEDSRA ERGFGSATRT TGSPKHVMVY QSFVRSCALQ GTALLHIYDK LSGELRELAG MGSYRCKCRD 446 DNA secial Accession uence: 145	LDISPERVRV GLPGGRNASV RGGIVLLAEO RGSRRTLAVL LCPLAFGGEA RVGVATYSRE GQDEPRRVVV SDPQDLPNGI FEVNPDVTQV VMTVQRGRRP PROBLINA GWEGPHCENR QUEDPRCSNR 1260 21 6000000000000000000000000000000	GAPGPSTPH PQILLIVIDG VEDATNGLPS AAHCPPYSWK NCALKLSLEC LLVAVPVGBY LLTESHSEDE PELQOKLCSR GLVVYGSQV GUPKAVVVLT YADLRYHQDV FLRRP 1942.1 31	LEFPLDSFST TLSSSAICSS RVFUTHPATC RVDLLFFLDS GDVPDLVWSL RVGDAFRARA QRGCGTQAL TAFGLDTKPT GGRGABDAAV LIEWLCGRAK	QQEVKARIKR KQLKERGYV ATDDGRVEAH YRTTCPQPC SAGTTLDGPL DGIPFRGGPT RELLLLGVGS DLVPRLDTSA RAMILRI QPVNLCKPSP	120 180 240 360 420 480 540 600 660 720
50 55	SUGROFERS MVPKGGTET FAVQUEPPH PCEHRTLENV SOPCINGTO RAKYPYKEV SOPCI	MHPAITVCDE ELALKYLLHER EELHALASEP REPAGNAPCW VPEGLDGYGC RAVI,SEDSICA RTGSPKINWYY QSFVRSCALQ GTALLHYDK LSECLERLAG MGSYRCKCRD 446 DNA sec id Accessiou uence: 145. 11	LDISPERVAV GLOGGRNASV RGQHVLLAEQ RGSRRTLAL LCPLAFGGEA RVGVATYSE GUDBERRVAVI SPODLENAV SPODLENAV SPODLENAV SPODLENAV SPODLENAV MITVQRGARP ROBLINVAA GWEGHCENR QUBBER 1 #: NM_03; 1260 21 GCCCGGGGTCG GCCCGGGGTCG	GARGPSSTPH PQILLIVIDG VEDATNGLPS VEDATNGLPS AAHCPPYSNK NCALKLSLEC LLVAPVPGL LLTESHSEDE PELOCKLCSR GLVVVGSOVO GVPKAVVVLT PADLRYHQDV FLRRP 942.1 31	LEFPLDSFST TLSSSAICSS TLSSSAICSS TVPUTHRATC RVDLLFLLDS QUPPDLVML AGRAGARA AGRAGARA LIEWLCGBAK 41	QGEVKARIKR KQLKERGYUTV ATDDCRVEAH YRTTCEGPCD SAGTILOGFL DGIPFROGFT RELLLLCVGS DLVFMLDITSA RAMMLRAISQ PAQKLRINGI QPVNLCCPSP	120 180 240 300 360 420 540 600 600 720
50 55 60	SUGRISTERS MVPKGGTTET FAVGVEPPRM PCEHRTLENV SQPCONGGTC RAKVPYRGE LTGSALRQAA AVYLAGLESI SUGPENFAGM APYLGGVGV MEGSCVLQ OMICSCOLIN Nucleic Ac Coding seq 1 1 1 CCCGAGCCCC TOCTCCTCCT	MHPAITVCDE ELALKYLLHER ESLIALASEP REFAGNASEP REFAGNASEP RAVISEDSRA RRGFGSATRT TGSPKRYWAY OSFWRSCALQ GTALLH TGSPKRYWAY AGENERALAG MGSYRCKCRD 446 DNA sectid Accession usence: 145 1.1 1.1 1.2 1.1 1.1 1.1 1.1 1.1 1.1	LDISPERVRV GLPGGRNASV RGGIVLLAEQ RGGIVLLAEQ RGSRRTLAVL LCPLAFGGEA RVGVATYSRE GQDEPRRVVV SDPQDLFNGI FEVNPDVTQV VMTVQRGRRP PROBLINA GWEGPHCENR QUECE 1 NM_03; 1260 21	GARGESTERH POILLIVIDG VEDATNGLES AAHCPPYSWK MCALKLSLEC LLVAVPVGEY LLTESHSEDE PELOGKLCSR GLVVYGSGVO GVPKAVVVLT VADLRYHGDV FLRRP 1942.1 31 GGGGGGCGCAG GGGGGTGCTC GCGGGGGGCGCAG GGGGGGGGCGCAG GGGGGGGGCGCAG GGGGGGGCGCAG	LEFPLDSFST TLSSSAICSS KSQGUVALPS TLSSSAICSS RYFLTHPATC RYDLLFPLDS GDVPDLVWSL AGRARBAA REGCETQAL LIEWLCGEAK 41 CCTGCCAGGC GCTTCTCCCC GCTTCTCCCCAGGA	QQEWKARIKR KQLKERGYUTV ATPDCRVEAH YRTTCEGPCD SAGTILDGFI REILLLGVGS BLYFMLDTSA RAMMLRAISQ PAOKLENIG QPVNLCKPSP	120 180 240 300 360 480 540 660 720
50 55 60	SUGRISTERS MVPKGGTTET FAVGVEPPRM PCEHRTLENV SQPCONGGTC RAKVPYRGE LTGSALRQAA AVYLAGLESI SUGPENFAGM APYLGGVGV MEGSCVLQ OMICSCOLIN Nucleic Ac Coding seq 1 1 1 CCCGAGCCCC TOCTCCTCCT	MHPAITVCDE ELALKYLLHER ESLIALASEP REFAGNASEP REFAGNASEP RAVISEDSRA RRGFGSATRT TGSPKRYWAY OSFWRSCALQ GTALLH TGSPKRYWAY AGENERALAG MGSYRCKCRD 446 DNA sectid Accession usence: 145 1.1 1.1 1.2 1.1 1.1 1.1 1.1 1.1 1.1	LDISPERVRV GLPGGRNASV RGGIVLLAEQ RGGIVLLAEQ RGSRRTLAVL LCPLAFGGEA RVGVATYSRE GQDEPRRVVV SDPQDLFNGI FEVNPDVTQV VMTVQRGRRP PROBLINA GWEGPHCENR QUECE 1 NM_03; 1260 21	GARGESTERH POILLIVIDG VEDATNGLES AAHCPPYSWK MCALKLSLEC LLVAVPVGEY LLTESHSEDE PELOGKLCSR GLVVYGSGVO GVPKAVVVLT VADLRYHGDV FLRRP 1942.1 31 GGGGGGCGCAG GGGGGTGCTC GCGGGGGGCGCAG GGGGGGGGCGCAG GGGGGGGGCGCAG GGGGGGGCGCAG	LEFPLDSFST TLSSSAICSS KSQGUVALPS TLSSSAICSS RYFLTHPATC RYDLLFPLDS GDVPDLVWSL AGRARBAA REGCETQAL LIEWLCGEAK 41 CCTGCCAGGC GCTTCTCCCC GCTTCTCCCCAGGA	QQEWKARIKR KQLKERGYUTV ATPDCRVEAH YRTTCEGPCD SAGTILDGFI REILLLGVGS BLYFMLDTSA RAMMLRAISQ PAOKLENIG QPVNLCKPSP	120 180 240 300 360 420 540 600 720
50 55 60 65	SUGRISTERS MYPKGGRTET FAVOURPEN PCEHRTLENV SOPCONGGTC RAKVFVKRPV LTGSALROAN ANYRAELEEI SUGPENFAQM MAPYLGGVGSA SVLVVVVGVGPV GREGSCVLQ Seq ID NO: Nucleic Ac Coding seq CCGGAGCCCC TUGTCCTCCT CGAACTCCC GTAAACAAA TCCTCGATG TCAGTTCCIGGT TCAGTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGTTCCIGGT TCAGT TCAGTTCCIGGT TCAGTT TCAGTTCCIGGT TCAGTT TCAGTTCCIGGT TCAGTT TCAGTT TCAGTT TCAGTT TCAGTT TCAGTT	MHPAITVCDE ELALKYLLHR EELSHALSEB REPAGNAPCW VPEGLDGYQC RAVISEDSRA REGEGSATRT TGSPRHYWNY QSFVRSCALQ GTALLHIQA LSEGLRLLAG MGSYRCKCRD 446 DNA Sec Ld Accessio Lonce: 145. 11 CCCCCCCCGG GCCCTCCGG GCCCTCCGGG GCCTCTCGGG GCCTCTCGGG ACTOTAGAAA ACAGTTGTGAA ACAGTTGTGAA ACAGTTGTGAA	LDISPERVAV GUIPGERNASV ROGINILADE GLEGGRANASV ROGINILADE GUIPGERNASV ROSSRILAVI LCPLAFGGER GUIPGERNAV SIPPOLIPGER GUIPGERNAV VINTYQRGARP PROBLINVAN GUIPGERNAV TURCAGA TURCAGA GUICGGGTTG GUICGGGTTG GUIPGERNACCIG CAGCATGGAC ATTCAGAT CAGCTTGGT CAGCCTTGGT CACCGGGTTG GACCGGGTTG GACCGGGCGGG	GARGESTEN POLILIVIDG VEDATNGLES AAHCEPTSMK NCALKLSLEC LLVANPVGES LLVANPVGES GUVYGSGVO GVPRAVVVLT YADLRYHGDV FLRRP 11 10 60G00CCCAG 60GGCCCCAG 60GGCGCCCCAG 60GGCGCCCAG 60GGCGCCAG 60GGCGCCCAG 60GGCGCCAG 60GGCGCCCAG 60GGCGCCAG 60GGCGCCCAG 60GGCGCCAG 60GGCGCCAG 60GGCGCCAG 60GGCGCCAG 60GGCGCCCAG 60GGCGCCCAG 60GGCGCCCAG 60GGCGCCAG 60GGCGCCCAG 60GGCGCCCAG 60GGCGCCAG 60GGCGCCCAG 60GGCGCCCAG 60GGCGCCAG 60GGCGCCAG 60GGCGCCAG 60GGCGCCAG 60GCGCCAG 60GGCGCCAG 60GGCGC	LEFPLDSPST TLSSAICSS RVPLTHPATC RVDLLFLLDS ONPOLVMSL VAGPARHARA CRECKTOAL TAFGLDTICPT GGRGABDAV LIEWLCGBAK 41	QGEVKARIKR KQLKERGYTV ATPDCRVEAH FRITCEGPCD SAGTILDGFL	120 180 300 360 420 480 660 720 60 120 240 300 360
50 55 60	SUGRISPERS MVPRIGATET FAVOURPERM PCEHRTLEAV SOPCONGGTC RAVEFVERE LIGISALROAN SULVIVATION SULVIVATION SEQ ID NO: 1 1 CCOGGAGCCCC TGCTCCTCCC CCGARCTCCCC CGARCTCCCC CGARCTCCCC CCGARCTCCCC CCGARCTCCCC CCGARCTCCC CCGARCTCCCC CCGARCTCCC CCGARCTCCCC CCGARCTCCC CCGARCTCCCC CCGARCTCCCC CCGARCTCCC CCGARCTCCCC CCCARCTCCCC C CCCCCCCCCC	KHPALTVCOS ELALKYLLHR EELSALASEB REPAGNAPCW VPEGLOGYQC TGSPERIVMYZ TGSPERIVMZ	LDISPERVING GLIPGGRIASS ROGIPULLASS ROGIPULLASS ROGIPULLASS ROSERTIAUL LCPLAFOGEA ROGIPULLASS ROGIPULL	GAPGPSSTPH POPLILITING POPLILITING NEARINGLES ANCEPTSME NCALKLELEC LLUTAPPOPEST LLUTAPPOPEST LLUTAPPOPEST LLUTAPPOPEST GUPVANOVIL 31 GGGGGGCCCAG GGGGGCGCC GTGAAATTGA TCAGTGCAGCA	LEPPLDSPST KROGUNALPS TIASSANICSS RYPUTHPATC	QQEVKARIKR KQLKERGYTV ATPDCRVEAN YRTTCEGPCD SAGTTLDGFL SAGTTLDGFL BELLLOVGE RELLLOVGE RELLLOVGE RELLLOVGE RELLLOVGE RELLOVGE SAGTCTCGC GCTCCAGGCT GCTCCAGGGT GAGGCTCCAGGGT GAGGCTCCAGGGT TCTCAGGGT TCTCAGGGT TCTCAGGGT TCTCAGGGT TCTCAGGGT TCTCAGGGT TCTCAGGTCC	120 180 240 360 420 480 540 660 720 60 120 180 360 360 360 420
50 55 60 65	SVERISSERS WYERGESTEE FAVOURPERS TO FORESTEE	KEPATYCOG ELAMCTLAIRE EELAMCTLAIRE EELAMCTL	LDISPERVING GLIPGGINASO, ROGIVILIADO ROSSRITATIVA LCPLAPOGEA ROSTRITATIVA LCPLAPOGEA ROWATYSES SPODLEMGI PEVMEDVITO VANTURGGARE QUERERVIVA SPODLEMGI PEVMEDVITO VANTURGGARE QUERERVIVA SPODLEMGI PEVMEDVITO VANTURGGARE QUE	GAPGPSSTPH POILLIVING POILLIVING POILLIVING POILLIVING POILLIVING POILLIVING POILLIVING POILLIVING POILLIVING POILLIVING POILCIVING	LEPPLOSPST KSQGUNALPS TLGSSATCSS TLGSSATCSS TVDLIPLLDS QUPPLIVMSI VAGPAERARA QUPPLIVMSI TAPGLITKIT COTOCCAGCC TOCCCCAGCC TCCCCCAGAACACA ACTCTGAGCA ACCAAAAAAC CAGAAAAAAC CAGAAAAAAC	QGEVKARIKE KQLEERGYTY ATPICKUVENH TYTTCKREZ DI BELLLIZAVE BELLLIZAVE BELLLIZAVE BELLLIZAVE BELLLIZAVE BELLLIZAVE BELLLIZAVE BELLLIZAVE BELLLIZAVE BELLLIZAVE PAQKLERNOI QPVHLCKDSP GCGCTGCTGC GCTCCAAGG AACTCCAGG AACTCAGG AACTCCA	120 180 240 300 420 480 540 660 720 60 120 120 240 360 420 420
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50 55 60 65 70 75 80	SVERISSERS WYREGISTERS OF THE PROPERTY OF THE	MEPATYCOS EFALATTALES EFALATATES	LDISPERVING LDISPE	GAPGPSTPH POPLLIVING AND CONTROL OF CONTROL	LESPLISSES KAGGUNALES KAGGUNALES RYPLIBEATE REPLIBEATE REPLIB	GOEVERALIER GOLIEROTY STORMAN	120 180 240 420 420 420 660 660 672 180 300 240 300 420 420 780 600 600 600 600 600 600 600 600 600 6

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	PCTATTTCCA .	ATGCTCCTCT TATTTTATTT	CCAACCGCTT .	AGTTTCTGAA	TTTCTTTTAA	ATTACAGTTT	1560 1620
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5	GAAACACAAT .	AATAGTATTA CAAAAACGAG	ACTAACTAGA	CACTONTACT	ACTICAGAGAAG	TTTANTAGAA	1740
	TCARGGCACA	AAACTCTTAA	AACCATGTGG	AAAAATTAGG	TAATTATTGC	AGATTGATGT	1800
	CTCTCTATCC	CATGTATTGC	CCTTATCTTA	CAAGTTGTTG	TCACAGTTGA	GACTTAATTT	1860
	TTTTAATTT	CTTCTGCCCG	AAGGGTAAGT	GGTGCGTCCA	GCTTACACGA	TCATAATTCA	1920
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	TIGATATTAA	AAACTAGTCT GTTTAGATTT	GTGGTTCTTT	GCAGTTTCTT	ATANGTOCCT	TTTTTCCAGGAT	2220
							2280
15	CTGTGTCAGT	ATTCCCCCTC ATGTCCAATT	CTCTTTGCAT	TAATCAAGGT	ATTTGGTAGA	GGTGGAATCT	2340
10	AAGTGTTTGT	ATGTCCAATT	TACTTGCATA	TGTAAACCAT	TGCTGTGCCA	TTCAATGTTT	2400
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25	MDARRVPQKD	LRVKKNLKKP	RYVKLISMET	SSSSDDSCDS	FASDNPANTR	LOSVREGCRT	60
	PROCERRECEL.	RVAMKEPARS	TRGATNKKAB	SROPSENSVT	DSNSDSEDES	GMNFLERRAL	120
							180 240
	TREESRILGS	LDALPMEEEE ENVCSNSREK	EEDKYMLVRK	RKTVDGYMNE	DDLPRSRRSR	SSALTERITE	300
30	PVEEITEEEL	DALLDPWHIC	PROPERTY	BCBCBCBCBCA	MINCKNIPCA	HOROGREGAL	360
30	KSLKQEFEMQ		PPCRGICAGO	PCRQIADACA		1101 011111111	
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40	AAACCCCCTA	TOTOTOATOGA	GACCTTCAGA	AAGGTGGGGA	TCCCCATCAT	CATAGCACTA	120
							180
	TACTTOTT	GCGGGCAGCC	TCTCCACTTC	ATCCCGAGGA	AGCAGCTGTG	TGACGGAGAG	240
	CTGGACTGTC	CCTTGGGGGA	GGACGAGGAG	CACTGTGTCA	AGAGCTTCCC	CGAAGGGCCT	300 360
45	GCAGTGGCAG	TCCGCCTCTC TCTCTGCCTG	CAAGGACCGA	TCCACACTGC	AGGTGCTGGA	CTCGGCCACA	420
45	GGGAACTGGT	CTACAGCAG	TTTCGACAAC	TTCACAGAAG	TOTOTOGOTOGO	CCCACACCAG	480
	AGGCAGATGG	GCTACAGCAG	CACACCCACT	ACCCAGGAGCIG	TTYGCATGG	GAACTCAAGT	540
	GCCCCCTGTC	TTGTTGAAAT TCTCAGGCTC	CCTGGTCTCC	CTGCACTGTC	TTGCCTGTGG	GAAGAGCCTG	600
							660
50	AGCATCCAGT	ACGACAAACA	GCACGTCTGT	GGAGGGAGCA	TCCTGGACCC	CCACTGGGTC GGTGCGGGCA	720
	CTCACGGCAG	CCCACTGCTT	CAGGAAACAT	ACCGATGTGT	TCAACTGGAA	GGTGCGGGCA	780
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	TTCAACCCCA	TGTACCCCAA	AGACAATGAC	ATCGCCCTCA	TGAAGCTGCA	GTTCCCACTC GCTCACTCCA	960
55	ACTITCTCAG	TCTGGATCAT	#CCCATCIGI	TTTACCAACC	MODATGGAGG	GAAGATGTCT	1020
33	CACCACCCCAC	TGCAGGCGTC	AGTCCAGGTC	ATTGACAGCA	CACGGTGCAA	TGCAGACGAT	1080
	COGTACCAGG	GGGAAGTCAC	CGAGAAGATG	ATGTGTGCAG	GCATCCCGGA	AGGGGGTGTG	1140
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	GTGGGCATCG	TTAGCTGGGG	CTATGGCTGC	GGGGGCCCGA	GCACCCCAGG	AGTATACACC GTAA	1260
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	YPLCGQPLHF	IPRKQLCDGE	POCATGEORE	HCVKSFPEGP	DIDUNCTION	STLQVLDSAT SQELRMRNSS	180
70							240
70	GPCLEGELVS	TOURNAMENTO	KIPKVVGGEE	LAVAKTITTE	PNPMYPKDND	IALMKLOFPL	300
	TESGTVRPIC	LPFFDEELTP	ATPLNIIGNO	PTKQNGGKMS	DILLQASVQV	IALMKLQFPL IDSTRCNADD GGPSTPGVYT	360
	AYOGEVTERM	MCAGIPEGGV	DTCQGDSGGP	LMYQSDQWHV	VGIVSWGYGC	GGPSTPGVYT	420
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	GCTCACCCAG	GAAAAATATG	CAATCGTCCC	ATTGATATAC	AGGCCACTAC	AATGGATGGA	60
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85	CCCAAACTCA	CAGTCACCAT	TGACACCAAT	GTGAACAGC	CCATTCTGAR	CTTGGAGGAT	300
	AATGTACAGT	CATGGAAACC	1 GGAGATACC	TOCAGATO	GOGGGGGGGG	CCAGGTCAAA	360
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GGCTCGCCA TGTTTCTGGT GAGCCAATTT GGCTGATCTT GGGTGTCTGA ACAGCTATTG
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ATAGAGAGCC CAAAGAGCTC CTGTAAGAGG GAGAACTCTA TCTGTGGTTT ATAATCTTGC

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	ACCCTCCTCT	GAAATGCTTG	TCTTTTTTCT	GTTGCCGAAA	TAGCTGGTCC	TTTTTCGGGA	5640
	GTTAGATGTA	TAGAGTGTTT	GTATGTAAAC	ATTTCTTGTA	GGCATCACCA	TGAACAAAGA AGAAATAAAG	5700
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Seq ID NO: 457 Protein sequence Protein Accession #: NP_001191.1

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5	MVAGTRCLLA PGLKQRPTPS LPETSGKTTR	RDAVVPPYML RPFFNLSSIP	DLYRRHSGQP	GSPAPDHRLE	RAASRANTVR	SEPELRLLSM SFHHEESLEE INIYEIIKPA	60 120 180

Seq ID NO: 458 DNA sequence
Nucleic Acid Accession #: NM_001999.2

10	Nucleic Act	ld Accession mence: 187	#: NM_001	999.2			
	1	11	21	31	41	51	
15	1	GACGGAGGCT	CTCTCCTCC	CTC TATELOC	TOTACCTAGA	CTROTROTROGTO	60
13	CTCTCGGGGGG	ACCCCACCCC	COGCCAGCCT	CAGCCTCCTC	CGCCCAAGCC	GCCCCGGCCCC	120
	CNCCCCCCCCC	COCABCAGGT	TOTAL	ACAGCAGGCT	CTGAAGGCGG	CTTTCTAGCG	180
	CCCGAGTATC	GCGAGGAGGG	TGCCGCAGTG	GCCAGCCGCG	TCCGCCGGCG	AGGACAGCAG	240
	GACGTGCTCC	GAGGGCCCAA	CGTGTGCGGC	TCCAGATTCC	ACTOCTACTG	CTGCCCTGGA	300 360
20	TGGAAGACGC	TCCCTGGAGG	AAACCAGTGC	ATTGTCCCGA	TTTGTAGAAA	TAGTTGTGGA	420
	GATGGATTTT	GTTCCCGTCC AATCAATTCA	CONCECNO	ACTIGITCCA CTGACATGCA	TYPE	GACCTGTGCA	480
	CARROL COLOR	COCK CTCCCC	CARACCATAT	ATTYCK ACTT	ATTOTOTOTACA	ACCTGTCTGT	540
	GAAAATGGAT	GTCAGAATGG CACAGTGTGA	TGGACGTTGC	ATCGCCCAAC	COTOTOCTTG	TGTTTATGGG	600
25	TTCACTGGTC	CACAGTGTGA	AAGAGATTAC	AGGACAGGCC	CGTGTTTCAC	TCAGGTCAAC	660
							720
	ACCACTGGAC	GGGCGTGGGG	CCATCCCTGT	GAGATGTGTC	CAGCCCAGCC	TCAGCCCTGC	780 840
	CGACGGGGTT	TCATCCCCAA	CATCCGCACT	GGAGCTTGCC	CACTOCCCTC	TTTTGAATGC	900
30	GCTATCCCAG	COCCOCACA	ACACACTCAA	ACTACTORGA	AATGTGAAGA	TTTTGAATGC CATTGATGAG	960
50							
	AGAACAGGCA	TGTGTTTCTC	GGGCCTGGTG	AATGGCCGCT	GTGCACAAGA	GCTCCCGGGG CGGAACCATT GGATGGACTT GGGAAATGGC	1140
25	AGAATGACGA	AAATGCAGTG	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	CGGAACCATT	1200
35	CCTGAAGCCT	GTCCTGTCAG	AGGTTCTGAG	GAATATCGCA	GACTITICAT	CCCNNATCCC	1320
	CONGREGO	ATGGCTTTTC	TOCTGGCGTT	GGGGGAGCCG	GTGTGGGGGC	CGGGGGACAG TAAGCATCAT ATGTGAATGC	1440
	GGACCTATCA	TCACTGGACT	AACAATTCTG	AACCAGACAA	TAGATATCTG	TAAGCATCAT	1500
40	GCTAACCTTT	GTTTAAATGG	ACGCTGTATA	CCAACTGTCT	CAAGCTACCG	ATGTGAATGC	1560
	AATCCCTGCA	CTAATGGAGA	TTGTGTTAAC	ACACCTGGTT	CCTATTATTG	TAAATGTCAT GTGCATCCAG	1740
	GCTGGATTCC	AGAGGACTCC	TACCAAGCAA	GENTGENTIG	ATATIONION	CCAGTGCATT	1800
45	MATUGUGTTC	COTTOTALA	AACTACAGAT	GGAAAAAACT	GTGTTGATCA	TGATGAATGT	1860
73	A CA A CT A CCA	ACATC:TCTTT	CAATCCAATC	TGCATCAATG	AAGATGGCAG	CTTCAAGTGC	1920
	ATCTCCABAC	CAGGATTTGT	CTTGGCTCCA	AATGGGCGTT	ACTGTACTGA	TGTTGATGAA	1980
	TOCCAGACCC	CAGGAATCTG	CATGAATGGG	CACTGCATCA	ACAGTGAAGG	GTCCTTCCGC	2040 2100
50	TGTGACTGTC	CCCCAGGCCT	GGCTGTGGGC	ATGGATGGAC	GTGTGTGTGT	TGATACTCAC	2100
30	ATGCGCAGTA	CCTGCTATGG	AGGAATCAAG	AAAGGAGIGI	ATGGTTTTTGG	TTTCCCCGGT AGAACCCTGC TGGAGTAGGT ATGTGCCAAT	2220
	CAGTGACCA	CTGCAAAAA	TTCAGCTGAA	TTCCACGGCC	TTTGTAGTAG	TGGAGTAGGT	2280
	ATCACTGTGG	ATGGAAGAGA	TATCAATGAA	TGTGCTTTGG	ATCCTGATAT	ATGTGCCAAT	2340
55							
	GATAACGGAT	TGTGCCGAAA	CACGCCAGGA	AGTTACAGCT	GTACGTGCCC	ACCAGGGTAT CAACCCATGT GCCCGGCAGC	2520
	GTGTTCAGGA	CTGAGACAGA	GACCIGIGAA	TOTAL MARKET	CTYCALATOTTC	GCCCGGCAGC	2640
	BARCECACCE	CCIGCIGADA	CARCCITOGA	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC	2700
60	ATCCAGGACA	GCCGCTGTGA	GGTGAATATT	AATGGAGCCA	CTCTGAAATC	TIGGCICAAC TGAATGCTGT TACAGCTTGC GTGTGAGGTG TCATTGCGAG TCGCATGGAG	2760
•••	GCCACCCTCG	GAGCCGCCTG	GGGGAGCCCC	TOTGAGCGGT	GTGAACTAGA	TACAGCTTGC	2820
	CCAAGAGGG	TTGCCAGGAT	TAAAGGTGTT	ACGTGTGAAG	ATGTTAATGA	GTGTGAGGTG	2880
	TTCCCTGGCG	TTTGTCCAAA	TGGACGCTGT	GTCAACAGTA	AGGGATCTTT	TCGCATGGAG	3000
65	TGCCCTGAAG	GCCTTACGTT	GGATGGGACT	GGCCGTGTAT	COTTCCTC	AAAGTTCCGC	3060
05	ATTICATION	CONCORRE	TOTOGGGGGG	GCTTGGGGGCA	COGAGTOTGA	GGAGTGCCCC	3120
	AAACCTYGGCA	CCAAGGAATA	CGAGACACTG	TGCCCCCGCG	GGGCTGGCTT	AAAGTTCCGC GGAGTGCCCC TGCTAACCGA AGCATTTCCT CCGTTGCAAT	3180
	GGGGATGTTC	TTACTGGGCG	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCATTTCCT	3240
	GGGATGTGCA	CTTATGGGAA	GTGCAGAAAT	ACAATCGGAA	GCTTCAAATG	CCGTTGCAAT	3300
70	AGTGGCTTTG	CTCTAGACAT	GGAGGAAAGA	AACTGCACGG	ACATCGACGA	GTGCAGGATT TGAGTGCGAG	3360
	TCTCCTGACC	TCTGTGGCAG	TGGAATCTGC	GTCAATACAC	CGGGCAGCTT	CATTGACGGA	3420
	TGTGAACGTA	ACCOLUTECT	ACACCARGCTC	TCACCATCC	GTGAGGACTG	GGGCAGCTTT TGTGGATATT	3600
75							
,,,	ACCTATCACT	COTOTTOCAN	TCCTGGATAT	CAGGCTACGC	CAGACCGCCA	GGGCTGTACA	3720
	GATATTGATG	AATGTATGAT	AATGAACGG	GGCTGTGACA	CCCAGIGCAC	AAATTCAGAG	3 / 80
90	GCAGACATTO	ATGAATGTGA	AAACAATCCT	GATATCTGTG	ATGGCGGCCA	GTGTACCAAC GGACATGAAA	3900
80	ATTCCTGGAC	AGTATCGCTG	CCTCTGCTAT	GATGGCTTCA	TURCTTCCAT	TOTAL	3960
	ACATGCATTO	ATGTCAATGA	ATGTGACCTA	AATICAAATA	CTTACTCACT	TGGGGAATGT	4080
	AGGRACACA	CTACACATCCT	CCATCACTC	GAAATTGGTG	CTCATAACTG	CGACATGCAT	4140
	GCCTCATGT	TGAATATCCC	AGGAAGCTTC	AAGTGTAGCT	GCAGAGAAGG	GAAGAAGGG GCGACATGCAT CTGGATTGGA	4200
85							
	AARCCTCACT	CTOTABATAC	CCCCCCCCCCCC	TACCGCTGTG	CCTGCTCCG	AGGTTTCACT	4320
	GGTGATGGCT	TTACCTGCTC	AGATGTTGAT	GAGTGTGCAG	AAAACATAAA	CCTCTGTGAG	4380

	AACGGACAGT	GCCTTAATGT	CCCGGGTGCA	TATCGCTGCG	AGTGTGAGAT	GGGCTTCACT	4440
							4500
							4560
_	GAATTGGACA	GAACAGGAGG GCCTATGTGT	GAACTGTACA	GATATTGATG	AGTGTGCAGA	TCCTATAAAC	4620
5	TGTGTCAATG	GCCTATGTGT	CAACACGCCT	GGTCGCTATG	AGTGTAACTG	CCCACCCGAT	4680
	TTTCAGTTGA	ACCCAACTGG	TGTGGGTTGT	GTTGACAACC	GTGTGGGCAA	CTGCTACCTG	4740
	AAGTTTGGAC	CTCGAGGAGA	TGGGAGTCTG	TCTTGCAACA	CCGAGATCGG	GGTGGGCGTC	4800
	AGTOGCTCTT	ACCCAACTGG CTCGAGGAGA CATGCTGCTG ATAGCACTGA	CTCTCTGGGA	AAGGCCTGGG	GAAACCCCTG	TGAGACATGC	4860
10	CCCCCTGTCA	ATAGCACTGA	ATATTACACC	CTGTGTCCCG	GAGGTGAAGG	CTTCAGACCT	4920
10	AACCCCATCA	CAATCATTTT	AGAAGACATT	GACGAATGCC	AGGAGTTACC	AGGTCTCTGC	4980
	CAGGGTGGAA	ACTGCATCAA	CACTTTTGGG	AGCTTCCAGT	GTGAGTGCCC	ACAAGGCTAC	5040
	TACCTCAGCG	AGGATACCCG	CATCTGTGAG	GATATTGATG	AGTGTTTTGC	ACATCCTGGT	5100
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15	GAGTACATGC	AGGTCAATGG	AGGCCACAAC	TGCATGGACA	TOAGAAAAAA	DEPENDENCE	6280
13	CGAAGCTATA	ATGGAACCAC	TTGTGAGAAT	GAGTIGCCTT	CONTIGUE	AUCCOCARCE	5240
	TGCTGCTGCA	CATATAATGT	DOGCAMAGET	CONNEMANC	CTCGATTCAC	CTTTCACATT	5400
	CCAGGAACAG	CIGACITIAA	CATTOTATOT	TOTA A A CACA	TTCCACCCAT	TTGTGCABAT	5460
	CACACAGGAA	MAGCIGITIGA	TOCCACTOR	COCTOTOLA	GCCCTACAGG	ATTCACTTAC	5520
20	GGTGTGTGCA	TIMECAGAI	TOTALCATATA	CATCACTCCA	GCAATGGTGA	TAATCTCTGC	5580
20	CACCOCAADO	CACACTCCAT	CAATACTCCT	CCTACTTACC	GCTGTGAATG	TGCCGCGGGT	5640
	THE CAR A COMME	CACCCAATGG	CCCCTCTCTA	GATCGCAATG	AATGTTTAGA	AATTCCTAAC	5700
	COMPACTO	ATCCCTTCTC	TOTTGATCTG	CAAGGAAGTT	ACCAGTGCAT	CTGCCACAAT	5760
	COCTTTANCO	CTTCTCAGGA	CCAGACCATG	TGCATGGATG	TTGATGAGTG	CGAGCGGCAC	5820
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	GGGTTTGAAC	TCACTCATAA	TAATGATTGC	CTGGACATAG	ATGAGTGCAG	TTCCTTTTTT	5940
	GGTCAGGTGT	GCAGAAATGG	ACGITGITIT	AATGAAATTG	GTTCTTTCAA	GTGTCTATGT	6000
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	GAAGATCCCA	ACATTTGTCT	TTTTGGTTCC	TGTACTAATA	CTCCAGGGGG	CTTCCAGTGC	6240
	CTCTGCCCCC	CTGGCTTTGT	ACTATCTGAT	AATGGACGGA	GATGCTTTGA	TACTCGCCAG	6300
	AGCTTCTGCT	TCACAAATTT	TGAAAATGGA	AAGTGTTCTG	TACCCAAAGC	TTTCAACACC	6360
	ACAAAAGCAA	AATGCTGCTG	TAGTAAGATG	CCAGGAGAGG	GCTGGGGGGA	CCCCTGTGAG	6420
35	CTGTGCCCCA	AAGACGATGA	AGTTGCATTT	CAGGATTTGT	GTCCATATGG	CCATGGAACT	6480
	GTCCCTAGTC	TTCATGATAC	ACGTGAAGAT	GTCAATGAGT	GTCTTGAGAG	CCCAGGCATT	6540 6600
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	TACAACCTTG	ACTACACTGG	AGTACGCTGT	GTGGATACTG	ATGAGTGTTC	AATCGGCAAT	6660
40	CCCTGTGGAA	ATGGTACATG	CACCAATGTT	ATTGGGAGTT	TTGAATGCAA	CECGRACIAT TECANTIGUE TATIONATURA TATIONATURA TATIONATURA TATIONATURA TATIONATURA TATIONATURA TATIONATURA TATIONATURA TATIONATURA TATIONATURA TATIONATURA TORTIONATURA TORTION	6720
40	GGCTTTGAGC	CAGGGCCCAT	GATGAATTGT	GAAGATATCA	ACGAATGTGC	CCAGAACCCA	6780
	CTGCTGTGTG	CTTTACGCTG	CATGAACACT	TTTGGGTCCT	ATGAATGCAC	GTGCCCGATT	6840
	GGCTATGCCC	TCAGGGAAGA	TCAAAAGATG	TGCAAAGATC	TGGATGAATG	TGCTGAAGGG	6900
	TTACACGACT	GTGAATCTAG	GGGCATGATG	TGTAAGAATC	TAATCGGCAC	CTTCATGTGC	6960
45	ATCTGCCCTC	CTGGAATGGC	CCGAAGGCCC	GATGGAGAAG	GCTGTGTAGA	TORMANIGAN	7020
43	TGCAGGACCA	AGCCAGGAAT	CTGTGAAAAT	GGACGITGIG	COLORGENER	COTTOACAAT	7140
	AGATGTGAGI	GTAATGAAGG	ATTCCAGTCA	CACTOTICAG	CTCARATOCC	ATCCACTACT	7200
	CGACAGGGTC	TCTGCTTTGC	AGAGGIACIG	TOTAL TOTAL	CCCCACCCC	GGGCCACCAG	7260
	CUCAATCTCC	COCCACTARGIC	TOTAL COLOC	CACTACAAA	AGATATGTCC	TCATGGCCCA	7320
50	COLUMN	CTCATCCAAC	AGRACIGCO	CARTCTARGO	TANTGCCARA	CCTCTGCACC	7380
30	AATTCCTCACT	CONTONNAC	CATGGGCTCA	TTCCGATGCT	TCTGCAAGGT	TGGCTACACC	7440
	ACTORCAMO	CONTENTACE	TTGTATAGAC	CTTGATGAAT	GCTCCCAGTC	CCCGAAACCA	7500
	INCOME ACTACA	TCTCCAAGAA	CACTGAGGGG	AGTTATCAGT	GTTCATGTCC	GAGGGGGTAT	7560
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55	AACTGCCAGT	TOCTOTOTOT	CAACACCCTG	GGGGGGTTTA	CCTGTAAATG	TCCACCTGGT	7680
•	TTCACACAGO	ATCACACTGC	TTGTATCGAC	AACAACGAAT	GTGGGTCTCA	ACCTTTGCTT	7740
	TGTGGAGGAA	AGGGAATCTG	TCAAAACACT	CCAGGCAGTT	TCAGCTGTGA	ATGCCAAAGA	7800
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60	GGCTACATCC	AGCACTACCA	GTGGAATCAG	TGTGTCGATG	AGAATGAATG	CTCCAATCCC	7980
•••	AATGCCTGTC	GCTCTGCTTC	CTGCTACAAC	ACCCTGGGGA	GTTACAAGTG	CGCCTGCCCC	8040
	TCGGGGTTC1	CCTTCGACCA	GTTCTCCAGT	GCCTGCCACG	ACCTGAATGA	GTGCTCGTCC	8100
	TCCAAGAACC	CCTGCAATTA	CGGCTGCTCT	AACACGGAGG	GGGGCTACCT	CTGTGGCTGC	8160
	CCCCCTGGGT	ATTACAGAGT	GGGACAAGGC	CACTGTGTCT	CAGGAATGGG	ATTTAACAAG	8220
65	GGGCAGTACO	TGTCACTGGA	TACAGAGGTC	GATGAGGAAA	ATGCTCTGTC	CCCAGAAGCA	8280
	TGCTACGAGT	GCAAAATCAA	CGGCTATCCT	AAGAAAGACA	GCAGGCAGAA	GAGAAGTATT	8340
	CATGAACCTC	ATCCCACTGC	TGTTGAACAG	ATCAGCCTAG	AGAGTGTCGA	CATGGACAGC	8400
	CCCGTCAACA	TGAAGTTCAA	CCTCTCCCAC	CTCGGCTCTA	AGGAGCACAT	CCTGGAACTA	8460
-	AGGCCCGCC	TCCAGCCCCT	CAACAACCAC	ATCCGTTATG	TCATCTCTCA	AGGGAACGAT	8520
70	GACAGCGTCT	TCCGCATCCA	CCAAAGGAAT	GGGCTCAGCT	ACTTGCACAC	GGCCAAGAAG	8580
	AAGCTCATG	COGGCACATA	CACACTGGAA	ATCACTAGCA	TCCCTCTCTA	CAAGAAGAAG	8640
	GAGCTTAAG	A AACTGGAAGA	GAGCAATGAG	GATGACTACC	TCCTAGGGGG	GCTTGGGGGAG	8700
	GCTCTCAGA	TGAGGCTGCA	GATTCAGCTC	TATTAACCGI	TCACAGACTT	GGGCCCAGGC	8760
75	TCAAATCCT	GCACAGCCAG	TCTGCAGAAG	CATTIGAAAA	GICAAGGACT	PARTITIANA	8820
75	AGGAAAAATA	ATAATAACTC	TIGITICITY	PERCOCAL	ATTENDACTOR	ANTOTTUACC	8886
	CTCACAGGGI	GGGATAATIT	AGACTCTGGT	MIGGCUARAG	ATTIGNOCTO	ACCUPATATOR	9000
	GTGGTTACT	TATTTTTAT	ATAACTICAT	CARAAATAI	CTCACCTTTT	- WCCIMMIGI	9050
	TCAAGATAT	AGCATATGGC	ACTAAATGCA	CHARACTAAT	TOTOLITT	BEREARDETT	9176
80	CCTGTTAGC	GICTGTAACA	CITIGGGTAT	ATTOCIATAL	CANCANATIA	CATGGACAGC CCTGGAACTA AGGGAACGAT GGCCAAGAAG GCTTGGGGAG GGGCCCAGGAC AATTTTAAAG AATGTTGAAC AAAGGCAAC ACCTAAATGT TTTTTTTTTT	9120
οU	GATGTTTAT	TATTTTTAAT	GCAGTAATAT	TATALATOR	ACCTATOTA	TTTAGAGGT	9240
	AAGGGAAAC	CACTIGITITI	TACARGACAT	CTTTCCTTTC	CTTTTCTCCC	AGTCATCCAG	9300
	CTTTTTAAA	ACCCAATAGA	IACAAGAGAT	CCCACACACAC	CONTRACTOR	GCAGTGCTAA	9360
	CTGATACAC	A CCTUATOGAT	AATOTCATTA	CATCCTTTAT	AACGTAGATC	CAAGCCAAAG	9420
85	CAATAATT	n coch con Car	TTCATATCAC	CAGACACAC	AGGCAACAGA	AGTTGAAGCA	9480
0.0	CAGCTCATT	D ACCARDAGE	CTTCACTCAC	TGTGAGACC	TTAGCATTG	TTTAGAGGTG AGTCATCCAG GCAGTGCTAA GAAGCCAAAG AGTTGAAGCA AGGCCAAACC ACACCTCATT	9540
	CTACTOTT	r recovered	AACCTCAACC	AACCATATO	GCTACCCACA	ACACCTCATT	9600
	JINC. GIAI						-

	WO 02/0	086443	m.ecena	. amam. aaa	acman nana	accommode.	9660
	TTGAAAGGGA	ACACCTRICCA	TECTGTGGTG	TTTCGTGCTG	TCTTAAATAA	TGGTGCATTT	9720
	ATTATGTTCA A	AGTTATTTCA	GGATTGCCAT	ATUTUCAAAC	ARATCATUCA	AIGCAGCCAA	9780
-	GGAATATATG '		TGTTTTAAAC	CCATTTTTTT	TTTAGAATTT TGTGTATGAA	TCATTAATAC	9840 9900
5	TGTAGTTATA (CACCATATGC	CTCATTTAT	CATAGCCTAT	GATATTGTAC	CAGGATGTTGC	9960
	TATTANCACC	TATOTATOOA	TATTCTCC	AACCCAAGAA	CCTGTTTCCT	GGACCAGTGA	10020
	CCANACCTCA S	TATGTGAAAT	GGCCAAAGCA	CATGCAGGCT	CCTGGTTGTT	CCTCTCAAAC	10080
	CTGTGCTGAC	CAAAGATTAG	TAACCAGTTA	TACCCAGTAT	TTTGAGGTTT	TATTGTTTTT	10140
10	TTAATAACTA	AAAAAAAACT	CGTGCC				
	Seq ID NO:	459 Protein	sequence				
	Protein Acc	ession #: N	P_001990.1				
15	1	11	21	31	41	51	
13	î	i ·	ī	ī	Í .	1	
	MGRRRRLCLQ	LYPLWLGCVV	LWAQGTAGQP	QPPPPRPPRP		TAGSEGGPLA	60 120
	PEYREEGAAV	ASRVRRRGQQ	DVLRGPNVCG	SRPHSYCCPG	WKTLPGGNQC	IVPICRNSCG IGTYCGOPVC	180
20	DGPCSRPNMC ENGCQNGGRC	TCSSGQISST	CGSKSIQQCS	DIVIDOPTOUN	MUNICOCOLITIC	TUCTETLCCA	240
20	THERMOURE	EMCPAOPOPC	REGFIENIET	GACODVDECO	AIPGICOGGN	CINTVGSPEC	300
	BCBYCHKUGE.	TTOKCEDIDE	CSTIPGICET	GECSNTVGSY	FCVCPRGYVT	STDGSRCIDQ	360
	RTGMCPSGLV	NGRCAQELPG	RMTKMQCCCB	PGRCWGIGTI	PEACPVRGSE	BYRRLCMDGL	420
05	DMOCTDGGAG	SECTORORS	FARSCNICKCY	GPGGTGFIPI	PGGNGFSPGV	GGAGVGAGGQ	480 540
25	GPIITGLTIL NPCTNGDCVN	NOTIDICKHH	ANLCLNGRCI	PTVSSYRCEC	MACH CANGES	VNSDGSFOCI	600
	CHACDELTTO	CIONCADHDEC	TTTNMCLNGM	CINEDGSFKC	ICKPGFVLAP	NGRYCTOVDE	660
	COTPGICMNG	HCINSEGSFR	CDCPPGLAVG	MDGRVCVDTH	MRSTCYGGIK	KGVCVRPFPG	720
	NUMBERCOCK	MUDDAGEGERG	ODCDAKUSAE	PHOLCSSGVO	TTVDGRDINE	CALDPDICAN	780
30	GICENLRGSY	RCNCNSGYEP	DASGRNCIDI	DECLVNRLLC	DNGLCRNTPG	SYSCICPPGY	840 900
	VFRTETETCE	DINECESNIC	VNGACRNNLG	CERCELDTAC	PRGLARIKGV	TCEDVNECEV	960
	PROVEDNODE	VMSKGSFHCE	CPECLTLDGT	GRYCLDIRME	OCYLKWDEDE	CIHPVPGKPR	1020
	MDACCCAVGA	AWGTECEECP	KPGTKEYETL	CPRGAGFANR	GDVLTGRPFY	KDINECKAPP	1080
35	ORGENORGEN	TICEDYCECN	SCHALDMERR	NCTDIDECRI	SPDLCGSGIC	VNTPGSFECE	1140
	CPEGYESGPM	MMKNCMDIDG	CERNPLLCRG	GTCVNTEGSF	DIDECMINNG	SPSREDCVDI	1200
	NECSLSDNLC	RNGKCVNMIG	TYQCSCNPGY	DICEGGGGGGG	IPGEYRCLCY	DEFMASKONK	1320
	GSYECSCSEG	YALMPDGRSC NEWY CMPGRC	ENTKGSFICH	COLGYSVKKG	TTGCTDVDEC	EIGAHNCOMH	1380
40	ASCLNIPGSF	KCSCREGWIG	NGIKCIDLDE	CSNGTHQCSI	NAQCVNTPGS	YRCACSEGFT	1440
		ECAENINLCE		YRCECEMGPT	PASDSRSCQD	IDECSFQNIC	1500
	VSGTCNNLPG	MPHCICDDGY	ELDRTGGNCT	DIDECADPIN	CVNGLCVNTP	GRYECNCPPD	1560 1620
	FQLNPTGVGC	VENRVGNCYL	KFGPRGDGSL NPITIILEDI	DECORPORA	OGGNCINTEG	SPOCECPOGY	1680
45	VI.CPDTPICE	DIDECEMBE	VCGPGTCYNT	LCMYTCICPP	EYMOVNGGHN	CMDMRKSFCI	1740
75	DOVECTOUR	PT.DUNUTKOM	CCCTYNUGKA	CNEPCEPCPT	PGTADFKTIC	GNIPGFTFDI	1800
	HTGKAVDIDE	CKEIPGICAN	GVCINQIGSP	RCECPTGFSY	NDLLLVCEDI	DECSNGUNLC	1860
	QRNADCINSP	GSYRCECAAG	PKLSPNGACV	DRNECLEIPN	GPELTHNNDC	TOTOPCECER	1980
50	GFKASQDQTM	CMDADECEKH	PCGNGTCKNT NEGYELTPDG	MUCIDINECA	ALPGSCSPGT	CONLEGSPRO	2040
50	TODDOVEVE	ENCYDINECD	EDPNICLEGS	CTNTPGGFOC	LCPPGFVLSD	NGRRCFDTRQ	
	COCPUNDENC	VCCUDE'S EMT	TKAKCCCSKM	PGEGWGDPCE			2100
					PCTKDDRAW	ODDICATOROT	2160
55	VPSLHDTRED	WIRCLESDAT	CSNGOCINTD	GSFRCECPMG	YNLDYTGVRC	VDTDECSIGN	2160 2220
	POGNICITOTIV	VNECLESPGI	CSNGQCINTD	GSFRCECPMG	LLCALRCMNT	FGSYECTCPI	2160 2220 2280
33	PCGNGTCTNV GYALREDQKM	VNECLESPGI IGSPECNONE CKDLDECAEG	GPEPGPMANC LHDCESRGMM	GSFRCECPMG EDINECAQNP CKNLIGTFMC SSSGTECLON	LLCALRCMNT LCPPGMARRP ROGLCPABVL	FGSYECTCPI DGEGCVDENE OTICONASSS	2160 2220 2280 2340 2400
33	PCGNGTCTNV GYALREDQKM CRTKPGICEN BNIJTKSECC	VNECLESPGI IGSFECNCNE CKOLDECAEG GRCVNIIGSY CDGGRGWGHO	CSNGQCINTD GPEPGPMMC LHDCESRGMM RCECNEGFQS CELCPLPGTA	GSFRCECPMG EDINECAQNP CKNLIGTFMC SSSGTECLDN QYKKICPHGP	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCFABVL GYTTDGRDID	PGSYECTCPI DGEGCVDENE QTICQNASSS ECKVMPNLCT	2160 2220 2280 2340 2400 2460
33	PCGNGTCTNV GYALREDQKM CRTKPGICEN RNLVTKSECC NGOCINTMGS	VNECLESPGI IGSFECNCNE CKOLDECAEG GRCVNIIGSY CDGGRGWGHQ FRCFCKVGYT	CSNGQCINTD GPEPGPMMIC LHDCESRGMM RCECNEGFQS CELCPLPGTA TDISGTSCID	GSFRCECPMG EDINECAQNP CKNLIGTFMC SSSGTECLDN QYKKICPHGP LDECSQSPKP	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG	PGSYECTCPI DGEGCVDENE QTICQNASSS ECKVMPNLCT SYQCSCPRGY	2160 2220 2280 2340 2400 2460 2520
	PCGNGTCTNV GYALREDQKM CRTKPGICEN RNLVTKSECC NGQCINTMGS VLQEDGKTCK	VNECLESPGI IGSFECNCNE CKDLDECAEG GRCVNIIGSY CDGGRGWGHQ FRCFCKVGYT DLDECQTKQH	CSNGQCINTD GPEPGPMMNC LHDCESRGMM RCECNEGFQS CELCPLPGTA TDISGTSCID NCQFLCVNTL	GSFRCECPMG EDINECAQNP CKNLIGTFMC SSSGTECLDN QYKKICPHGP LDECSQSPKP GGFTCKCPPG	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCFAEVL GYTTDGRDID CNYICKNTEG FTQHHTACID	FGSYECTCPI DGEGCVDENE QTICQMASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL	2160 2220 2280 2340 2400 2460 2520 2580
60	PCGNGTCTNV GYALREDQKM CRTKPGICEN RNLVTKSECC NGQCINTMGS VLQEDGKTCK CGGKGICONT	VNECLESPGI IGSFECNCNE CKOLDECAEG GRCVNIIGSY CDGGRGWGHQ FRCFCKVGYT DLDECQTKQH PGSPSCECOR	CSNGQCINTD GPEPGPMENC LHDCESRGMM RCECNEGFQS CELCPLPGTA TDISGTSCID NCQFLCVNTL GFSLDATGLN	GSFRCECPMG EDINECAQNP CKNLIGTFMC SSSGTECLDN QYKKICPHGP LDECSQSPKP GGFTCKCPPG CEDVDECDGN	YNLDYTGVRC LLCALRCHNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG FTQHHTACID HRCQHGCQNI	FGSYECTCPI DGBGCVDENE QTICQMASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL LGGYRCGCPQ	2160 2220 2280 2340 2400 2460 2520 2580 2640
	PCGNGTCTNV GYALREDQKM CRTKPGICEN RNLVKSECC NGQCINTMGS VLQEDGKTCK CGGKGICQNT GYIQHYQNNQ	VNECLESPGI IGSFECNCNE CKOLDECAEG GRCVNIIGSY CDGGRGWGHQ FRCPCKVGYT DLDECQTKQH PGSPSCECQR CVDENECSP	CSNGQCINTD GPEROPMONC LHDCESRGMM RCECNEGFQS CELCPLPGTA TDISGTSCID NCQFLCVNTL GFSLDATGLM NACGSASCYN PRGYYRVGOG	GSFRCECPMG EDINECAQNP CKNLIGTFMC SSSGTECLDN QYKKICPHGP LDECSQSPKP GGFTCKCPPG CEDVDECDGN TLGSYKCACP HCVSGMGPNK	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG FTQHITACID HRCQHGCQNI SGPSPDQPSS GOYLSLDTEV	FGSYECTCPI DGEGCVDENE QTICQNASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL LGGYRCGCPL ACHDVNECSS DBENALSPEA	2160 2220 2280 2340 2400 2460 2520 2580 2640 2700 2760
	PCGNGTCTNV GYALREDQKM CRTKPGICEN RNLVTKSECC NGQCINTMGS VIQEDGKTCK CGGKGICQNT GYIQHYQNNQ SKNPCNYGCS	VNECLESPGI IGSPECNCUM CXDLDECAEG GRCVNIIGSY CDGGRGWGHQ FRCFCKVGYT DLDECQTKQH PGSPSCECQR CVDENECSNP NTEGGYLCGC	CSNGQCINTD GPEPGPMMNC LHDCESRGMM RCECNEGFQS CELCPLPGTA TDISGTSCII HCQFLCVNTL GFSLDATGLM NACGSASCYN PPGYYRVQQG HEPDPTAVEO	GSFRCECPMG EDINECAQNP CKNLIGTFMC SSSGTECLDN QYKKICPHGP LDBCSQSPK GGFTCKCPPG CEDVDECDGN TLGSYKCACP HCVSGMGFMD	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG FTQHHTACID HRCQHGCQNI GGPSPDQPSS GQYLSLDTEV PVMMENLSH	VOTDECSIGN FGSYECTCPI DGEGCYDENE QTICQMASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL LGGYRCGCPQ ACHDVNECSS DEENALSPEA LGSKEHTLEL	2160 2220 2280 2340 2400 2520 2580 2580 2700 2760 2820
60	PCGNGTCTNV GYALREDQKM CRTKPGICEN RNLVTKSECC NGQCINTMGS VLQEDGKTCK CCGKGICQNT GYIQHYGNNQ SKNPCNYGCS CYECKINGY RPALOPLINN	VNECLESPGI IGSFECNCIM CKDLDECAEG GRCVNIIGSY CDGGRGWGHQ FRCFCKVGYT DLDECQTKQH PGSPSCECQR CVDENECSNP NTEGGYLCGC KKDSRQKRSI IRYVISOGND	CSNGQCINTD GPEPGPMMNC LHDCESRGMM RCECNEGFQS CELCPLPGTA TD I GGTSCID HCQFLCVNTL GFSLDATGLM NACGSASCYN PPGYYRVGQG HCQFPPTAVGQO DSVFRIHQRM	GSFRCECPMG EDINECAQNP CKNLIGFFMC SSSGTECLDN QYKKICPHGP LDBCSQSPK GGFTCKCPPG GEDVDECDGN TLGSYKCACP HCVSCMGPNX ISLESVDMDS GLSYLHTAKK	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG FTQHHTACID HRCQHGCQNI GGPSPDQPSS GQYLSLDTEV PVMMENLSH	VOTDECSIGN FGSYECTCPI DGEGCYDENE QTICQMASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL LGGYRCGCPQ ACHDVNECSS DEENALSPEA LGSKEHTLEL	2160 2220 2280 2340 2400 2520 2580 2580 2700 2760 2820
	PCGNGTCTNV GYALREDQKM CRTKPGICEN RNLVTKSECC NGQCINTMGS VLQEDGKTCK CCGKGICQNT GYIQHYGNNQ SKNPCNYGCS CYECKINGY RPALOPLINN	VNECLESPGI IGSFECNCIM CKDLDECAEG GRCVNIIGSY CDGGRGWGHQ FRCFCKVGYT DLDECQTKQH PGSPSCECQR CVDENECSNP NTEGGYLCGC KKDSRQKRSI IRYVISOGND	CSNGQCINTD GPEPGPMMNC LHDCESRGMM RCECNEGFQS CELCPLPGTA TDISGTSCII HCQFLCVNTL GFSLDATGLM NACGSASCYN PPGYYRVQQG HEPDPTAVEO	GSFRCECPMG EDINECAQNP CKNLIGTFMC SSSGTECLDN QYKKICPHGP LDBCSQSPK GGFTCKCPPG GEDVDECDGN TLGSYKCACP HCVSCMGPNX ISLESVDMDS GLSYLHTAKK	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG FTQHHTACID HRCQHGCQNI GGPSPDQPSS GQYLSLDTEV PVMMENLSH	VOTDECSIGN FGSYECTCPI DGEGCYDENE QTICQMASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL LGGYRCGCPQ ACHDVNECSS DEENALSPEA LGSKEHTLEL	2160 2220 2280 2340 2400 2520 2580 2580 2700 2760 2820
60	PCGNGTCTNY GYALREDQKM CRTKPOICEN RNLVTKSECC NGQCINTMGS VLQEDGKTCK CGGKGICQNT GYIQHYQNNQ SKNPCNYGCS CYECKINGYP ELKKLESSNE Seg ID NO:	VNECLESPGI IGSPECNICHE CIOLDECAEG GRCWNIGSY CDGGRGWGHG CDGGRGWGHG DIDECOTKQH GSSPSCECOR VTEGGYLCGC KKDSRQKRSI LTRYVISQGMD DDYLIGELGB 460 DNA se	CSNGQCINTD GPEPGPMNC LHDCESRGMM RCECNEGFQS CELCPLPGTA TDISGTSCID NCQFLCVNTL GFSLDATGLM NACGSASCIM PPGYYRVGQG HEPDPTAVEQ DSVFRIHGRM ALRMRLQIQL GUENCE	GSFRCECME EDINECACMP CKNLIGTFMC SSGTECLDN QYKKICPHGP QYKKICPHGP CEDVDECGGN CEDVDECGGN TLGSYKACCP HCVSGMGPNK ISLESVDMDS QLSYLHTAKK Y	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG FTQHHTACID HRCQHGCQNI GGPSPDQPSS GQYLSLDTEV PVMMENLSH	VOTDECSIGN FGSYECTCPI DGEGCYDENE QTICQMASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL LGGYRCGCPQ ACHDVNECSS DEENALSPEA LGSKEHTLEL	2160 2220 2280 2340 2400 2520 2580 2580 2700 2760 2820
60	PCGNGTCTNV GYALREDQKM CRTKPGICEN RNILVTKSECC USQCINTMGS VLQEDGKTCK CUGKGICQNT GYIQHYQMNQ SKNPCNYGCS CYECKINGYP RPAIQPLENH ELKKLEESNE Seq ID NO: Nucleic Ac	VNECLESPGI IGSPECNCHE CKDLDECAEG GRCVNIIGSY CDGGRGWGN FRCPCKVGYT DLDECGTKG91 FGSPSCECOR CVDENECSNP NTEGGYLCGC KKDSRQKRSI IRYVISQGND DDYLLGELGS 460 DNA se id Accessio	CSNGQCINTO GPEPOPMMNC LHDCESRGMM RCECMEGFQS CELCPLPGTA TDISGTSCID NCQFLCVNTL NACGRASCIN NACGRASCIN NACGRASCIN PPGYYNYQQO HEPDPTAVEQ DSVFRIEGRM ALRMRLQIQL Quence n #: NM_01	GSFRCECME EDINECACMP CKNLIGTFMC SSGTECLDN QYKKICPHGP QYKKICPHGP CEDVDECGGN CEDVDECGGN TLGSYKACCP HCVSGMGPNK ISLESVDMDS QLSYLHTAKK Y	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG FTQHHTACID HRCQHGCQNI GGPSPDQPSS GQYLSLDTEV PVMMENLSH	VOTDECSIGN FGSYECTCPI DGEGCYDENE QTICQMASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL LGGYRCGCPQ ACHDVNECSS DEENALSPEA LGSKEHTLEL	2160 2220 2280 2340 2400 2520 2580 2580 2700 2760 2820
60 65	PCGNGTCTNV GYALREDQKM CRTKPGICEN RNILVTKSECC USQCINTMGS VLQEDGKTCK CUGKGICQNT GYIQHYQMNQ SKNPCNYGCS CYECKINGYP RPAIQPLENH ELKKLEESNE Seq ID NO: Nucleic Ac	VNECLESPGI IGSPECNICHE CIOLDECAEG GRCWNIGSY CDGGRGWGHG CDGGRGWGHG DIDECOTKQH GSSPSCECOR VTEGGYLCGC KKDSRQKRSI LTRYVISQGMD DDYLIGELGB 460 DNA se	CSNGQCINTO GPEPOPMMNC LHDCESRGMM RCECMEGFQS CELCPLPGTA TDISGTSCID NCQFLCVNTL NACGRASCIN NACGRASCIN NACGRASCIN PPGYYNYQQO HEPDPTAVEQ DSVFRIEGRM ALRMRLQIQL Quence n #: NM_01	GSFRCECME EDINECACMP CKNLIGTFMC SSGTECLDN QYKKICPHGP QYKKICPHGP GCEDVDECGGN CEDVDECGGN TLGSYKACCP HCVSGMGFMK ISLESVDMDS QLSYLHTAKK Y	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG FTQHHTACID HRCQHGCQNI GGPSPDQPSS GQYLSLDTEV PVMMENLSH	VOTDECSIGN FGSYECTCPI DGEGCYDENE QTICQMASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL LGGYRCGCPQ ACHDVNECSS DEENALSPEA LGSKEHTLEL	2160 2220 2280 2340 2400 2520 2580 2580 2700 2760 2820
60	PCGNGTCTNY GYALREDGNO CRTKPGICEN RNLVTKSECC NGGCINTMGS VLQEDGRTCK CGGKGICGNT GYIGHYGNNO SKNPCHYGCS CYECKINGYP RPAIQPLNNH ELKLEESNE Seq ID NO: Nucleic Ac Coding seq	VNECLESPEGI IGSFECNCNE CKDLDECAEG GRCVNIIGSY CDGGRGWGRQ FRCFCKVGYT DLDECQTKQH PGSPSCECQR CVDENECSNP WTEGGYLCCC KKDSRQKRSI IRYVISQRND DDYLLGELGE 460 DNA se id Accessio uence: 63	CSNGQCINTO CSNGQCINTO LHDCESRGMM RCECMEGFQS CELCPLPGTA TDISGTSCID HOOPLCVNTL GFSLDATGLM NACGSASCTM PPGYTRVGQG HEPDPTAVEQ DSVPRIEQRM ALRMELQIQL Quence n #: NM_01: 617	GSFRCECMG EDINEZAONP CKNLIGTPMC SSSGTECLIM CYKKLCPHGP LDECSGSPKP GGFTCKCPPG CEDVDECDGN TLGSYKCACP HCVSGMGPNK ISLESVDMDS GLSYLHTAKK Y	YNLDYTGVRC LLCALRCMNT ICPPGMARRP RQGLCPABVL GYTTDGRDID CNYICKNTEG FTQHHTACID HRCQHGCQNI GGPSPDQPSS GQYLSLDTEV PVMMENLSH	VDTDECSIAN FGSYECTCPI DGEGCVDENE GYTCQNASSS ECKVMPNLCT SYQCSCPRGY NNECGSQPLL LGGYRCGCPQ ACHDVNECSS DEENALSPER LGSKEHILEI ITSIPLYKKE	2160 2220 2280 2340 2400 2520 2580 2580 2700 2760 2820
60 65	PCONSTITUTY GYALBEDORM CRITKPOICEN RNLYTKSECC NGQCINTMGS VLQEDGKTCK GGKGICONT GYIQEYQNNQ SKMPCNYGCS CYBEKINGYP ELKKLEESNE Seq ID NO: Nucleic Ac Coding seq	VNECLESPGI IGSFECNCNE CCDLDECABG GRCWNIIGSY CDGGRGMGMQ FRCFCKVGYT DLDBCQTTKCH FGSPSCECOR VTEGGYLCCE KKDSRQKRSI IRYVISQGMD DDYLLGELGE IA Accesto uence: 63	CSNGQCINTD GPERGPMSNC LHDCESRGMS RCECHEGEGS CELCPLPGTA TDISGTSCID GPSLDATGLM MACGSASCYN PPGYYRVGGG DSVFRIHORN ALMRLQIQL GUENCE n #: NM_01: 617	GSPRCECMB EDINECAONP CKNLIGTPMC SSSGTECLINN QYKKICPHGP LDECSQSPKP GGFTCKCPFG CEDVDECDGN TLGSYKCACP HCVSGMGPMK 1 SLESYDMDS GLSYLHTAKK Y	YNLDYTGYRC LLCALRCANT LCPGMARRP RGGLCPABVL GYTTGRDID CNYICKNTEG FTQHITACID HRCQHGCONI SGPSPDQFSS GGYLSLDTEY FYMMERILSH KIMPGTYTLE	VOTIBESIAN FGSYECTCPI DEGGCVDENE GTICQNASSS ECKWIPHLET SYOCSCPROY INNECGSQPLI LGGYRGGCPQ ACHDVNECSS DBENALSPER LGSKEHILEL ITSIPLYKKS	2160 2220 2280 2340 2460 2520 2520 2520 2700 2760 2820 2880
60 65	PCONGTOTING GYALREDORM CRITKPOICEM NUTURESECT NGQCINTHMSS VIQEOMSTORM GYACHTOMS SKMPCHYGGCS CYECKINGYP RPAIQPLANM ERKLESNE Seq ID NO: Nucleic Ac Coding seq	VNECLESPGI IGSFECNCHE CIDIDECANO GRCWNIGSY CDGGRGHGHG FREPCKVGVT DLDBCOTKGB FRESPCKVGVT DLDBCOTKGB FGSPSCECOR CVDRNECSNP NTEGGTLCOCC KKDSRQKRSI IRYVISQGND DDYLLGELGS 460 DNA se id Accessio uence: 63 11 TAGGGCCCCC	CSNGQCINTD GPEROPMENC LHDCSSRGMM RCECHEGFGS CELCPLFOTA TDISGTSCID NCOPILCVNTL GPSLDATGIN NACGISASCIN PPGTYTRVGQG DSVFRIHGNN LHSPDPTAVEQ GUENCE n #: NM_01: 617 21 GCGCTCGAAAG	GSPRCECMG GSPRCECMG CNILTOTPMC SSGTECLIN QYKKICPHGP GGPTCKCPPG GGPTCKCPPG GGPTCKCPPG GGPTCKCPRG GEDVDECDGN TLASYKCACF HCVSCMGPMK ISLESVDMDS GLSYLBITAKK Y 3372.1	UNLOYTONG LLCALECANT LCPGMARRA RGGLCPASVL GYTTGRDID GYTTGRDID HRCGRGCONI RGGPSCONI RGG	VDTDECSIGN FGSYECTCPI DEGGCVDENE CCVMPNLCT SYCCSCPRGY NNECGSOPLI LGGYRGGCQ ACHDVNECSS DEENALSPER LGSKEHILEI ITSIPLYKKE	2160 2220 2280 2340 2460 2520 2580 2760 2760 2820 2880
60 65 70	PCONFICTIVE GYALREDORM CRITKPOICEN RNLYTKSECC NGQCINTMGS VALEBGKTCK CGGKGICONT GITQHTQMNQ SKMPGNIYGCS CYECKINGYP ELKKLEESNE Seq ID NO: Nucleic Ac Coding seq	VNECLESPEGI IGSFECNCHE CIDLDECARO GRCVNI IGSY CDGGRGHGHG GRCVNI IGSY CDGGRGHGHG GRSPECCOR CVDENECSNP HTEGGYILCOC KKDSRQKRSI LTRYVI SQGID DDYLLGELGE 460 DNA see id Accessio uence: 63 11 CTCAGGGCCAC CRECKOCTEO	CSNGQCINTD CSNGQCINTD LHDCESRGMM RCECHEGFQS CELCPLPGTA TDISGTSCID NCQFLCVNTIL NACGSASCIN NACGSASCIN NACGSASCIN NACGSASCIN ANACGSASCIN ANAC	GSPRCECMB EDINECAONP CKNLIGTPMC SSSGTECLEN QYKKICPHGP LDECSGSPKP LDECSGSPKP LGSTCCPFG CEDVDECDGN TLGSYKCACP HCVSGMGPMK Y 3372.1	YNLDYTGWRC LLCALRCHNT LCPGMARRP RGGLCPABVL GYTTGGRDID CNYICGNTEG FTGHHTACID HRCGHGCMI SGPSPDQFSS GGYLSLDTEV PVMMKFNLSH KIMPGTYTLE	POTIBESIAN FGSYECTCPI DEGCYDENE ECKWINLCT SYOCSCPROY INNECGSOPLI LOGYRAGORY LOGYRAGORY LOSKEHILE: ITSIPLYKKE 51 GGCACTGACT ACCOTGCTG	2160 2220 2280 2340 2460 2520 2580 2580 2640 2760 2820 2880
60 65	PCONGTINY GYALREDORM GRIKEDORM GRIKEDORM GRIKEDORM GRIKEDORM GROGETHIMGS GYOGENIMGS L L GCGGGCGCAC GTATAGAGCGG	VNECLESPGI IGSFECNCHE CIDIDECANO GRCVNIIGSY CDGGRGHGHG FREPCKVGVT DLDBCOTKGB FRESPCKVGVT DLDBCOTKGB FRESPCKVGVT PGSPSECOR KVDRNECSNP NTEGGTLCOC KVDRNECSNP DYLLGELGH 460 DNA se id Accessio uence: 63 11 TCAGGGCCAC CCAGGCTAA	CSNGQCINTO CSNGQCINTO LHDCSSRGM RCECNEGGGS CELCPLFOTA TDISGTSCID NCOPILCVNTL GPSLDATGIN PROTYRVGQG DSVFRINGNN LARMELQTOL Quence n #: NM_01: 617 21 GGGTTCGAAAG ACGGTGGGAA ALAGGGGTTCCCC ALAGGGGTTCCC ALAGGGGTTCCC ALAGGGGTTCCC ALAGGGGTTCCC ALAGGGGTTCCC ALAGGGGGGGAGA ALAGGGGTTCCC ALAGGGGGGGAGA ALAGGGGTTCCC ALAGGGGGGGAGA ALAGGGGTTCCC ALAGGGGGGGAGA ALAGGGGTTCCC ALAGGGGGGGAGAGAGA ALAGGGGTTCCC ALAGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GSPRCECMG GSPRCECMG CNILTOTPMC SSGFECLIN QYKKICPHGP GGFTCKCPPG GGFTCKCPPG GGFTCKCPRG GEDVDECDGN TLASYKCACF HCVSCMGPMK ISLESVDMDS GLSYLBITAKK Y 3372.1 31 GCGCAGGCCCC GCGTGTTCC AAGGTGCCA	LICALROCHT LICARCHAT LICAR	POTIBESIAN FGSYECTCPI DEGGCVDENE GCCVDENE CCVMPNLCT SYQCSCPRCY NNECGSOPLL LGGYRGGCQ ACHDVNECSS DEENALSPER LGSKEHILEI ITSIPLYKKE 51 CGCACTGAC ACCCTCCTG ACCCTCCTG ACCCTCCTG ACCCTCCTG ACCCTCCTG ACCCTCCTG ACCCTCCTG ACCCTCCTG	2160 22280 2280 23400 2460 2520 2580 2640 2760 2820 2880
60 65 70	PCONFICTINY GYALBEDORM CRIVERSEC NGOCINTHOS VLOEDGETCH GOCINTHOS VLOEDGETCH GOCINTHOS SKMPCHYGGS CYBCKINGYP RPAIDPLINNE ELKKLESSNE Seq ID NO: Nucleic Ac Coding sect 1 GOGGGCGCAC GOGGCGCCAC GOGGCGCCAC GOGGCGCCAC GOGGCCCCAC GOGGCCCCAC GOGGCCCCAC GOGGCCCCAC GOGGCCCCAC GOGGCCCCAC GOGGCCCCAC GOGGCCCCCCAC GOGGCCCCCAC GOGGCCCCCAC GOGGCCCCCAC GOGGCCCCCAC GOGGCCCCCAC GOGCCCCCCAC GOGCCCCCAC GOGCCCCCCAC GOGCCCCCAC GOGCCCCCCAC GOGCCCCCAC GOGCCCCCCAC	VNECLESPGI IGSFECNCNE CIDLDECASO GRCVNI IGSY CDGGRWGRW CDGGRWGRW CDGGRWGRW CDGGRWGRW CDGRRWGRW CVDBECSNP HTEGGYLCGC KKDSRCKRP TRYVISQGND DDYLLGELGR 460 DNA see id Accessio uence: 63 11 TCAGGGCCAC CCACAGGCCAC AGGGANARG	CSNGQCINTD CSNGQCINTD CSNGQCINTD LHDCESRGMM RCECHEGFQS CELCPLPGTA TDISGTSCID NCQFLCVNTIL MACGASCIN NACGASCIN ANAGGASCIN ANAGGATCCC ACTCAATCCC ACTCAGTCCC CTCAGTCCC ACTCACTCC ACTCACTCC ACTCACTCC ACTCACTC	GSPRCECMG GSPRCECMG CNILGTPMC CNILGTPMC SSSGTECLIAN QYKKICPHGP GGFTCKCPPG GGFTCKCPPG GGFTCKCPRG GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCKCPK GGFTCK AGGGGCCCC CCCGGCTTCC AAGGTGCCAC CCCGGCAGCC CCCAGCAGCC CCCAGCC CCCAGCAGCC CCCAGCAGCC CCCAGCAGCC CCCAGCAGCC CCCAGCAGCC CCCAGCC LICALRONNI LICARRONNI LICARRONNI LICARRONNI LICARRONNI LICARRONNI ROBINI ROBINO ROBINI ROBINO ROBINI ROBINO ROBINI ROBINO ROBINI ROBINO ROBINI	POTRECTION FORSY TOTAL	2160 22280 2340 24400 2520 2520 2580 2640 2760 2820 2880	
60 65 70	PCONFICTINY GYALBEDORM CRITKPOICES RILVITESECC NGQCINTMGS VLQEDGETCK CGGGGCGCCC CYECKINGYP RPAIQPLINNE ELKKLESSE Seq ID NO: Nucleic Ac COding seq 1 CGGGCGCGCCC CTATGMACCG CGTATGMACCG CGCCCCCCA AGGGCCCACCA AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCACCAC AGGGCCCACCAC AGGGCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCCACCAC AGGGCCACCAC AGGGCCCACCAC AGGGCCACCAC AGGGCCACAC AGGGCCACAC AGGGCCACAC AGGGCCACCAC AGGGCCACAC AGGGCCACCAC AGGGCCACAC AGGGCCACAC AG	VNECLESPGI I IGSPECNCNE CXDLDECASO GRCVNI IGSY CDGGRMGHGG CRCVNI IGSY CDGGRMGHGG CRCVNI IGSY CMCDSROKESI IFYVI SQCMD DDYLLGELGE 460 DNA se id Accessio Uence: 63 11 TCAGGGCCAA CAGGGCAAAAAG GCGGGCAAT GGGGGCAAT GAGGGGCAT GAGGGGCAT	CSNGQCINTO CSNGQCINTO CSNGQCINTO LHDCSSRGM RCSCHEGGQS CELCPLFGTA TDISGTSCID RCSCHEGGQS CELCPLFGTA RCSCHEGGQS CELCPLFGTA RCSCHEGGQS CELCPLFGTA RCSCHEGGQS CELCPLFGTA RCSCHEGGQS REPDPTAVEQ DSVFRIEGGN ALRMELQIQL Quence n #: NM_01: 617 21 COCCTCGAAG ACCGTCGAAG ACCGTCGGAG ACCGTCGAGAG ACCGTCGAGAG ACCGTCGGAG ACCGTCGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGCGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGGAG ACCGTCGAG ACCGCAG ACCGTCGAG ACCGTCGAG ACCGTCGAG ACCGTCGAG ACCGTCGAG ACCGTCGAG	GSPRECEPHG GSPRECEPHG CINILITYPHG SSSOTECLIN QYEKICHEP GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCKEPHG GSPTCHEPHG GSPTCHEPHG GSPTCHEPHG GSPTCHEPHG GSPTCHEPHG GSPTCHEPHG GGGAGGCCCC GCCTGCTCT AAGGTGCAT GCCAGGAGCC GGGAGGCCCC GGGAGGCCC GGAGGCC GGGAGGCC GGGAGGCC GGGAGGCC GGGAGGCC GGGAGGCC GGGAGGCC GCAGGCAC GGGAGGCC GGGAGGCC GGGAGGCC GCAGGAGC GGGAGGCC GCAGGCAC GGGAGGCC GGGAGGCC GGGAGGCC GCAGGAGC GGGAGGC GCAGGAGC GGGAGGC GGGAGGC GCAGGAGC GCAGGAGC GGGAGGC GCAGGAGC CAGGAG GCAGGAG	YNLDYTOVIC LICALOGUE PROGRAPH CONTROL OF THE PROGRAPH	FIGSTRICTORY DESICTORY DESICTORY OFTICANASS ECKNYRPHICT SYCGECPRO ACHONICOS DEBNIASPRA LGSKREITLE LTSIPLYKKY 51 GCACTGACG GACAAGGCC AACHONICOS GACAAGGCC AACHONICOS CACAGGACG AACHONICOS CACAGGACG CACAGGACG CC CACAGGACG	2150 2220 2340 2440 2520 2580 2760 2760 2820 2820 1280 120 120 120 130 360
60 65 70 75	PCONFICTINY GYALREDORM CRITKPOICEN RILLYTKSPCC NGQCINTHOSS YOLOGICATION GYALREDORM REPLICATION SEMPCHYCOCS SEMPCHYCOCS SEMPCHYCOCS FREALDENBMM ELEKLESME Seq ID NO. Nucleic Au Coding seq I COGGCCGCAC GTATGAGCG GCGCTCCTAA AGCACAATTA GCGGCCAATG GCGGCCCAATG GCGGCCCAATG GCGGCCCAATG GCGGCCCAATG	WECLESPOI INSPECTION IN INSPECTION IN INSPECTION IN INSPECTION IN INSPECTION IN INSPECTION IN INSPECTION IN INSPECTION IN INSPECTION IN INSPECTION IN INSPECTION IN INVESTIGATION CSNGQCINTD GEPEOPHORIC LIDICISSIGNM RECENTEDES CELCPLOTA TDISCTSCII NCQFLCVNTL OFGLANDIA NACIGNACIA BEPTAVEQ GENERAL ALBERTAVE 1 CONTICABAGA AND CONTICABAGA CONTICABAGA CONTICABAGA AND CONTICABAGA CONTICABAGA CONTICABAGA AND CONTICABAGA CONTICABAGA CONTICABAGA AND CONTICABAGA	GSPRESCPNG GSPRESCPNG EDINECAGNE CNILLATIFIC SSSOTECLIA QYEKICHER GSPTEKCHER LSESSOTECH	YNLDYTOVIC LICALROSHI LICALROSHI LICALROSHI CHILDRASHI CHILDRASHI LICALROSHI	VITIBESTAN FORSTECTOR	2160 2220 2280 2340 2400 2580 2580 2760 2760 2820 2880 120 120 180 130 130 130 130 130 1420	
60 65 70	PCONFOTINY GYALBEDORM GRITHPOICES RILLYTISEC NGOCINTHOS SIMPHIYOCS CYECKINGY RPAIGPIANN ELKLESSE Seq ID NO: Nucleic Ac Coding seq I GCGGCCCAC GTATAGSCCCA GCGCTCCTA AGCACAATTA AGCACAATTA AGCACAATTA AGCACACCAT AGCACACCAT	VMECLESPOI INSPECTION IN INTERPRETARE IN INTERPRETARE INTERPRETARE IN INSPECTION IN INTERPRETARE INTERPRETARE IN I	CSNGQCINTD CSNGQCINTD	GSPRCECPHG GSPRCECPHG CNIL LOTPHG CNIL LOT	YHLDYTOVIC LICALROSHI	VITTEESTAM FORTER FORT FORTER FORT FORTER FORT FORTER FORT	2160 2220 2280 2340 2460 2520 2580 2760 2760 2820 2880 120 120 1300 240 360 480
60 65 70 75	PCONFOTINY OYALBEDOM CRITHPOICEM RINYTESEC NOOLINGO SKMPCHYOS SKMPCHYOCS CYBEKINGYP RPAIQPLANN ELKLESSIS OG GOOGOGOGO CON CONTROL CONT	WEECLESPOT I IGSPECKICHE I IGSPECKICHE CODULECTOR I IGSPECKICHE CODULECTOR I IGSPECKICHE CODUCTOR I IGSPECKICHE CODUCTOR I IGSPECKICHE CODUCTOR I IGSPECKICHE CODUCTOR I IGSPECKICHE I IGSPECKICHE I INTVI SOOND DIVILIGELIE	CSNGCLIFTD CSNGCLIFTD CSPECTOPE CLICAT	GSPRCECPHG EDINECAGNE CNIL TOTPHC SSOUTECLAN LDSEGGEPHG GGTCKCPB LDSEGGEPHG GGTCKCPB LDSEGGEPHG CEDVDECDGN TLGSPKCACC HCVSGGMGPN ISLSEVINDS 0LSYLWTAKK CGCAGGGCCC CGCAGGGCC GGGAGGGCCC GGGAGGGCCC GGGAGGGCCC GGGAGGGCCC AAGGTGCCACC AAGGTGCCACC AAGGGAGCCC AAGGTGCCACC AAGGGAGCCC AGGGAGCCC AAGGAGCCC AAGGGAGCCC AAGGAGAGCCC AAGGGAGCCC AAGGAGCCCC AAGGGAGCCCC AAGGGACCCC AAGGGACCCC AAGGGACCCC AAGGGACCCCC	YHLDYTOVIC LICALROPAT ICHORARDP ICHO	VITIBES INN FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORTECTION FORT	2160 2220 2280 23400 2460 2520 2580 2700 2700 2820 2880 120 120 180 1300 1420 1420 1480 1540 1540 1540 1540 1540 1540 1540 154
60 65 70 75	PCGNGTCTNY GYALREDGN GRTWGDIGEN GRTWGDIGEN RILYTESSCA RILYTESSCA RILYTESSCA VLQBDGKTCK CGGKGICQNT GYYQBYQRNQ GYALGPUNN ELKKLESSR ELKKLESSR ELKKLESSR ELKKLESSR I GCGGCCGCAC GCTATGAGAG GCGGCCACAC GCCAGTGCAA GCGGGCCAAG GCGGCCAAG GCGGCCAAG GCAGTGCAA GCCAGTGCAA GCCAG	WEELESPOT INSPECTION OF THE PROPERTY OF THE PR	CSNGQCIFTO CSNGQCIFTO	GSFREECPHG GSFREECPHG CNIL LOTPHG SSGOTECLIN QYEKI COHEP LDBCCQGPPC CNIL LOTPHG CNIL LOTPH	SILDITORIC LICALROSE LICALROSE ROSILOPASVI	SIL SERVICES OF STATE	2160 2220 2280 2340 2400 2520 2520 2580 2760 2760 2880 2880 2880 2880 2400 360 360 480 480 540 540 540 560
60 65 70 75	PONNTCTHY OTALEBOOM CRITEGICS RIVERIOR	WEECLESPOT I IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE IGSPECKICHE INTUISOOND DIVILIGELIEM INTUISOOND DIVILIGELIEM INTUISOOND DIVILIGELIEM INTUISOOND DIVILIGELIEM INTUISOOND DIVILIGELIEM INTUISOOND DIVILIGELIEM INTUISOOND INT	CSNGCITTO CSNGCI	GSPRCECPHG GSPRCECPHG CNIL LOTPHG SSOUTECLAN LOTPHG SSOUTECLAN LOTPHG GSPCCCPG HCYGGMGPH CEDVDECDGN TLGSPKCHC HCYGGMGPH GSPLCHC HCYGGMGPH GSPLCHC GGGAGGCCC GCGGGCT GCGGGGGGGGGGGGGGGGGG	YNLDYTOVIC LICALROPAT	VITIBES INN FORTERED TO THE PROPERTY OF THE PR	2160 2220 2280 23400 2460 2520 2580 2760 2760 2820 2880 2180 2180 240 360 360 420 480 480 480 540 660 660
60 65 70 75 80	PONNETTHY OTALBERGOM CHYPOLICE AND ADMINISTRATION OF THE ADMINISTRATION OF THE ADMINISTRATION OF THE ADMINISTRATION OF THE ADMINISTRATION OF THE ADMINISTRATION OF THE ADMINISTRATION OF THE ADMINISTRATION OF THE ADMINISTRA	VIECLESPOT I GEFERICATE CONCESSOR OF THE PROPERTY OF THE PROPE	CSMOQCCHTD CSMOQCCHTD CSMOQCCHTD CSMOQCCHTD CSMOQCCHTD CSMOQCCHTC CSMOQCC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSMOQCCHTC CSM	GSFRCECPHG ESUNECAGINE SESTITE LAN GSFTCKEPH LDSCGGSFK GGFTCKEPH LDSCGGSFK GGTCKCGCGCC CCCCCCCCCCCCCCCCCCCCCCCCCC	YILDYTOVIC LICCLINGS LICCLINGS ROGIC-PASVL GYTTORRID GYTTORRID HROGIGGRI HRO	VITUEES LAN VITUEES LAN PRISCUESSIA OTICONASS OTICONASS OTICONASS OTICONASS OTICONASS OTICONASS OTICONASS SOCIONASS ACCTOCTOCTOC CONCOCOLTY TYCTOCTOCOC AACTOCOC AA	2160 2220 2220 2340 24400 2520 2520 2520 2620 2820 2820 2820 2820 2820 2830 2420 2420 2420 2420 2520 2830 2640 2750 2650 2750 2750 2750 2750 2750 2750 2750 27
60 65 70 75	PONNETTHY OTALEBOOM CHARACTER OF THE CONTROL COMMISSION OF THE COM	VIELCLISTOTI INGSPENCISE CONLINEATE CONLINEATE CONLINEATE PROPERTY INVIENCE	CSNGCCIFTO CSNGCCIFTO CSNGCCIFTO CSNGCCIFTO CSNGCCIFTO CSNCCCIFC C	GSPRCECPHG SUNRCAGNE SSOTTECTAN SSOTTECTAN SSOTTECTAN SSOTTECTAN GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK LDECSGEPK GSPTCKCEP LDECSGEPK L	ALICATIONS CONTINUES OF THE CONTINUES OF	SI SI SECURIORI DE	2160 2220 2230 2340 2460 2520 2580 2790 2780 2880 2880 2880 2880 2880 2880 288
60 65 70 75 80	PONNETTHY OTALEBOOM CHARACTER OF THE CONTROL COMMISSION OF THE COM	VIELCLISTOTI INGSPENCISE CONLINEATE CONLINEATE CONLINEATE PROPERTY INVIENCE	CSNGQCINTD GSPEOTPHORE LINDESSAMM RECENSIONE	GSPRCECPHG SUNRCAGNE SSOTTECTAN SSOTTECTAN SSOTTECTAN SSOTTECTAN GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK GSPTCKCEP LDECSGEPK LDECSGEPK GSPTCKCEP LDECSGEPK L	ALICATIONS CONTINUES OF THE CONTINUES OF	SI SI SECURIORI DE	2160 2220 2230 2340 2460 2520 2580 2790 2780 2880 2880 2880 2880 2880 2880 288

	CTCACATCTA	AAGGGGCGGG	GCCGTGGTCT	GGTTCTGACT	TTGTGTTTTT	GTGCCCTCCT	960
	GGGGACCAGA	ATCTCCTTTC	GGAATGAATG	TTCATGGAAG	AGGCTCCTCT	GAGGGCAAGA	1020
	GACCTGTTTT	AGTGCTGCAT	TCGACATGGA	AAAGTCCTTT	TAACCTGTGC	TTGCATCCTC	1080
5	CTTTCCTCCT	CCTCCTCACA	ATCCATCTCT	TCTTAAGTTG	CARCARCEA	TGTCAGTCTA	1200
,	TTTTTTTTTT	TGCCAAGGTT ACCCTCCAGA	CTCTGGGAGA	GCTGCTGTG	GGCAAGGACA	AGCAGGATAG	1260
	TOGAGTGAGA	AAGGGAGGGT	GGAGGGTGAG	GCCAAATCAG	GTCCAGCAAA	AGTCAGTAGG	1320
	GACATTGCAG	AAGCTTGAAA	GGCCAATACC	AGAACACAGG	CTGATGCTTC	TGAGAAAGTC	1380
	TTTTCCTAGT	ATTTAACAGA	ACCCAAGTGA	ACAGAGGAGA	AATGAGATTG	CCAGAAAGTG	1440
10	ATTAACTTTG	GCCGTTGCAA	TCTGCTCAAA	CCTAACACCA	AACTGAAAAC	ATARATACTG	1500
	ACCACTCCTA	TGTTCGGACC	CAAGCAAGTT	AGCTAAACCA	AACCAACTCC	TCTGCTTTGT	1560
	CCCTCAGGTG	GAAAAGAGAG	GTAGTTTAGA	ACTOTOTOCA	TAGGGGTGGG	AATTAATCAA	1620 1680
	AAACCKCAGA	GGCTGAAATT	CCTAATACCT	TTCCTTTATC	GTGGTTATAG	TCAGCTCATT	1740
15	TCCATTCCAC	AGTGTACCTG	AATGCTTCTG	MANAGECACIA	ACTIGATION	CACTACTCTC	1800
13	GCCTCTGCTG	ARATATTKTG	COCCECTETT	TOTTTTARCT	AURUITIAGG	GATTGGGGTA	1860
	PAGAGAAGAC	GACGAGAGTA	AGGAAATAAA	GGGRATTGCC	TCTGGCTAGA	GAGTAAGTTA	1920
	GGTGTTAATA	CCTGGTAGAA	ATGTAAGGGA	TATGACCTCC	CTTTCTTTAT	GTGCTCACTG	1980
	AGGATCTGAG	GGGACCCTGT	TAGGAGAGCA	TAGCATCATG	ATGTATTAGC	TGTTCATCTG	2040
20	CTACTGGTTG	GATGGACATA	ACTATTGTAA	CTATTCAGTA	TTTACTGGTA	GGCACTGTCC	2100
	TOTORTTANA	CTTGGCCTAC	TOCCOATOCC	TACTTAGGAT	TGATCTAAGG	GCCAAAGTGC	2160
	AGGGTGGGTG	AACTTTATTG AAACTCCCTG	TACTTTGGAT	TTGGTTAACC	TGTTTTCTTC	AAGCCTGAGG	2220
	TTTTATATAC	AAACTCCCTG	AATACTCTTT	TTGCCTTGTA	TCTTCTCAGC	CTCCTAGCCA	2340
25	AGTCCTATGT	AATATGGAAA AGAGAACCCT	ACAAACACTG	CAGACTTGAG	ATTCAGTIGC	TOMICARGOC	2400
23	TCTGGCATTC	TCCCATCTAA	CONCTANCA	CONCCONTE	CANGGOGGG	CATATTTTAA	2460
	ACR CCCA A A A	TGTTGGGTCT	CATTETTCAAA	CHITTERARCE	CACTACTGAT	GATTCTCACG	2520
	CTAGGCGAAT	TTGTCCAAAC	ACATAGTGTG	TGTGTTTTGT	ATACACTGTA	TGACCCCACC	2580
	CCAAATCTTT	GTATTGTCCA	CATTCTCCAA	CAATAAAGCA	CAGAGTGGAT	TTAATTAAGC	2640
30	ACACAAATGC	TAAGGCAGAA	TTTTGAGGGT	GGGAGAGAAG	AAAAGGGAAA	GAAGCTGAAA	2700
	ATGTAAAACC	ACACCAGGGA	GGAAAAATGA	CATTCAGAAC	CAGCAAACAC	TGAATTTCTC	2760
	TTGTTGTTTT	AACTCTGCCA	CAAGAATGCA	ATTTCGTTAA	TGGAGATGAC	TTAAGTTGGC	2820
	AGCAGTAATC	TTCTTTTAGG	AGCTTGTACC	ACAGTCTTGC	ACATAAGTGC	AGATTTGGCT	2880
20	CAAGTAAAGA	GAATTTCCTC	AACACTAACT	TCACTGGGAT	AATCAGCAGC	GTAACTACCC	2940
35	TAAAAGCATA	TCACTAGCCA	AAGAGGGAAA	TATCTGTTCT	TCTTACTGTG	CCTATATTAA	3000
	GACTAGTACA	AATGTGGTGT GTCACTGATG	GTCTTCCAAC	TTTCATTGAA	AATGCCATAT	CTATACCATA	3060 3120
	TTTTATTCGA	ATATTTGTGG	ATGTAATGAT	ATATTTTTT	ATTATTATAG	BCBCCCBABTE	3180
	TIAIGGCAAG	GATGTACACT	TTCTCCTTCC	CATTABABAGA	AAAAAACACA	CATCCTGGAA	3240
40	GTCTCTAAGT	TGTTTTTTGT	TACTGTAGGT	CTTCAAAGTT	AAGAGTGTAA	GTGAAAAATC	3300
	TGGAGGAGAG	GATAATTTCC	ACTGTGTGGA	ATGTGAATAG	TTAAATGAAA	AGTTATGGTT	3360
	ATTTAATTTA	ATTATTACTT	CAAATCCTTT	COTCACTOTO	ATTTCAAGCA	TOTTTTCTTT	3420
	TTCTCCTTTA	TATGACTTTC	TCTGAGTTGG	GCAAAGAAGA	AGCTGACACA	CCGTATGTTG	3480
	TTAGAGTCTT	TTATCTGGTC	AGGGGAAACA	AAATCTTGAC	CCAGCTGAAC	ATGTCTTCCT	3540
45	GAGTCAGTGC	CTGAATCTTT	ATTTTTTAAA	TTGAATGTTC	CTTANAGGTT	AACATTTCTA ATGTATACAA	3600
	AAGCAATATT	AAGAAAGACT	TTAAATGTTA	TTTTGGAAGA	CTTACGATGC	ATGTATACAA	3660
	ACGAATAGCA	GATAATGATG	ACTAGTTCAC	ACATAAAGTC	CTTTTAAGGA	GAAAATCTAA	3720
	AATGAAAAGT	GGATAAACAG	AACATTTATA	AGTGATCAGT	TAATGCCTAA	GAGTGAAAGT	3780 3840
50	AGTTCTATTG	ACATTCCTCA AAAACGGCAA	AGATATITAA	TATCAACTGC	ATTAIGIATT	AIGICIGCII	3900
50	ARATCATTTA	AGTTGATAGT	CTCATAAAAC	TAATTTCCCT	TCAACTTTCA	TCAATCTGTA	3960
	ACTACAATTT	AATTTTCACC	CCANTANTO	TOTATATAGE	CTTTGCTAAA	GAGCAACTAA	4020
	TABATTARAC	AATTTTCACC CTATTCTTTC	AAAAAAAA	Territor			
55		461 Protein					
	Protein Ac	cession #: 1	NP_037504.1				
	i .	11	21	31	41	51	
60		1]	 	I moreowoon	CONCERNIBOR	60
UU	MSRTAYTVGA	LLLLLGTLLP EEVLESSQEA	AAEGKKKGSQ	GALPPPDRAQ	HNDSEQTOSP	DETTANDECYC	120
	OCHERATRON	IRKBEGSFQS	COPCUDENCE	THORETTACOR	CITHERCENS	TRYKOCRCIS	180
	IDLD	TRABBOOT QU	Cor Citrica I	LIMIT LANCE D	Dur I I I I I I I I I I I I I I I I I I I		
65	Seq ID NO:	462 DNA sec	quence				
	Nucleic Ac	id Accession	n#: Eos se	quence			
	Coding seq	uence: 12	733				
					41	51	
70	1	11	21	31	11	11	
70	1	ON OTHER PROPERTY.	OCHICA THEODOT	AMERICAN COMP.	TCACTGACGG	CCACCCTCCC	60
	TTCCTGGGGA	GAGTGCTGTG AAAATGATGG	CATCAAAACA	AAAAAAGAAC	TCATTGTGAA	TAAGAAAAA	120
	CATCTAGGCC	CAGTCGAAGA	ATATCAGCTG	CTGCTTCAGG	TGACCTATAG	AGATTCCAAG	180
	GAGAAAAGAG	ATTTGAGAAA	TTTTCTGAAG	CTCTTGAAGC	CTCCATTATT	ATGGTCACAT	240
75	GGGCTAATTA	GAATTATCAG	AGCAAAGGCT	ACCACAGACT	GCAACAGCCT	GAATGGAGTC	300
	CTGCAGTGTA	CCTGTGAAGA	CAGCTACACC	TGGTTTCCTC	CCTCATGCCT	GAATGGAGTC TGATCCCCAG	360
		TTCACACGGC	TOGACCACTC	CCAAGCTGTG	AATGTCATCT	CAACAACCTC	420
	AACIGCIACC			AAGATTTGGG	GCACTTTCAA	AATTAATGAA	480
	AGCCAGAGTG	TCAATTTCTG	TURGRGACA				
90	AGCCAGAGTG AGGTTTACAA	ATGACCITTT	GAATTCATCT	TCTGCTATAT.	ACTCCAAATA	TGCAAATGGA	540
80	AGCCAGAGTG AGGTTTACAA ATTGAAATTC	ATGACCITTT AACTTAAAAA	GAATTCATCT	TCTGCTATAT. AGAATTCAAG	ACTCCAAATA GTTTTGAGTC	TGCAAATGGA GGTTCAGGTC	540 600
80	AGCCAGAGTG AGGTTTACAA ATTGAAATTC	ATGACCITTT AACTTAAAAA GAAATGGAAG	GAATTCATCT AGCATATGAA CATCGTTGCT	TCTGCTATAT AGAATTCAAG GGGTATGAAG	ACTCCAAATA GTTTTGAGTC TTGTTGGCTC	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA	540 600 660
80	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC	TCAATTTCTG ATGACCTTTT AACTTAAAAA GAAATGGAAG TGTCAGCCAT	GAATTCATCT AGCATATGAA CATCGTTGCT TGAACATGTT	TCTGCTATAT AGAATTCAAG GGGTATGAAG GCCGAGAAGG	ACTCCAAATA GTTTTGAGTC TTGTTGGCTC CTAAGACAGC	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG	540 600 660 720
80	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC	TCAATTTCTG ATGACCTTTT AACTTAAAAA GAAATGGAAG TGTCAGCCAT TAGAAGACGG	GAATTCATCT AGCATATGAA CATCGTTGCT TGAACATGTT CTCTTTCAGA	TCTGCTATAT. AGAATTCAAG GGGTATGAAG GCCGAGAAGG GTGTTCGGAA	ACTCCAATA GTTTTGAGTC TTGTTGGCTC CTAAGACAGC AAGCCCAGTG	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG TAATGACATT	540 600 660 720 780
	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC CTGTTTCCAT	TCAATTTCTG ATGACCTTTT AACTTAAAAA GAAATGGAAG TGTCAGCCAT TAGAAGACGG TTSSETCCAA	GAATTCATCT AGCATATGAA CATCGTTGCT TGAACATGTT CTCTTTCAGA	TCTGCTATAT AGAATTCAAG GGGTATGAAG GCCGAGAAGG GTGTTCGGAA TATACCCTGC	ACTCCAATA GTTTTGAGTC TTGTTGGCTC CTAAGACAGC AAGCCCAGTG	TGCAAATGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG TAATGACATT TGGCTACAGG	540 600 660 720 780 840
80 85	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC CTGTTTCCAT	TCAATTTCTG ATGACCTTTT AACTTAAAAA GAAATGGAAG TGTCAGCCAT TAGAAGACGG TTSSETCCAA	GAATTCATCT AGCATATGAA CATCGTTGCT TGAACATGTT CTCTTTCAGA	TCTGCTATAT AGAATTCAAG GGGTATGAAG GCCGAGAAGG GTGTTCGGAA TATACCCTGC	ACTCCAATA GTTTTGAGTC TTGTTGGCTC CTAAGACAGC AAGCCCAGTG	TGCAAATGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG TAATGACATT TGGCTACAGG	540 600 660 720 780
	AGCCAGAGTG AGGTTTACAA ATTGAAATTC ACCCAATTTC TCTGAACTGC CTGTTTCCAT GTCTTTGGAT GGAACATCA CTCTCTCTGG CTCTCTCTGG	TCAATTTCTG ATGACCTTTT AACTTAAAAA GAAATGGAAG TGTCAGCCAT TAGAAGACGG TTGGGTCCAA CAGCCAAGTG TTGAAGAACT	GAATTCATCT AGCATATGAA CATCGTTGCT TGAACATGTT CTCTTTCAGA GGATGATGAA TGAGTCCTCT GAACAAGAAT	TCTGCTATAT AGAATTCAAG GGGTATGAAG GCGAGAAGG GTGTTCGGAA TATACCCTGC GGGTGGCAGG TTCAGTATGA	ACTCCAAATA GTTTTGAGTC TTGTTGGCTC CTAAGACAGC AAGCCCAGTG CCTGCAGCAG TCATCAGGGA TTGTAGGCAA	TGCAAATGGA GGTTCAGGTC CAGCAGTGCA CCTTCACAAG TAATGACATT	540 600 660 720 780 840 900

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	ACAGTGGGGA	ATCTGGCTTC	GGTGGTGTCG	ATTCTGAGCA	ATATTTCATC	TCTGTCACTG	1080
	GCCAGCCATT	TCAGGGTGTC	CAATTCAACA	ATGGAGGATG	TCATCAGTAT	AGCTGACAAT	1140
	ATCCTTAATT AGCTCACGGT	CAGCCTCAGT	AACCAACTGG	ACAGICITAC	TGCGGGAAGA	GACAGCTCTT	1260
5	CCTCTGAATT	TITCTCGGAA	ATTCATTGAC	TGGAAAGGGA	TTCCAGTGAA	CAAAAGCCAA	1320
-	CTCAAAAGGG	GTTACAGCTA	TCAGATTAAA	ATGTGTCCCC	AAAATACATC	TATTCCCATC	1380
	AGAGGCCGTG	TGTTAATTGG	GTCAGACCAA	TTCCAGAGAT	CCCTTCCAGA	AACTATTATC	1440
	AGCATGGCCT	CGTTGACTCT	GGGGAACATT	CTACCCGTTT	CCAAAAATGG	AAATGCTCAG	1500 1560
10	TTTTTTTCCA	AGATAGAGTC	ABACCTGAGC	CAGCCTCATT	GTGTGTTTTG	GGATTTCAGT	1620
10.	CATTTGCAGT	GGAACGATGC	AGGCTGCCAC	CTAGTGAATG	AAACTCAAGA	CATCGTGACG	1680
	TGCCAATGTA	CTCACTTGAC	CTCCTTCTCC	ATATTGATGT	CACCTTTTGT	CCCCTCTACA	1740
	ATCTTCCCCG	TIGTAAAATG	GATCACCTAT	GTGGGACTGG	GTATCTCCAT	TGGAAGTCTC	1860
15	ATTTTATGCC	TGATCATCGA GTATTTGCAT	GGCTTTGTTT	TGGAAGCAGA	TTAAAAAAAG	CCAAACCTCT	1920
13	TTTATTCTTY	GTGCCACAGT	GGACACCACA	GTGAACCCTT	CTGGAGTCTG	CACAGCTGCT	1980
	CAACALCALAAL V	CACACHTCHT	CALS CALCARAGE	THE PROPERTY OF THE PROPERTY O	GGATGCTCAT	CCTTGGCATC	2040
	CTGCTGGCTT	ACCGGATCAT	CCTCGTGTTC	CATCACATGG	CCCAGCATTT	GATGATGGCT	2100
20	GTTGGATTTT	GCCTGGGTTA	TGGGTGCCCT	CTCATTATAT	CTGTCATTAC	CATTGCTGTC	2160
20	ACGCAACCTA	GCAATACCTA TCCTGGCTTT	CAAAAGGAAA	GATGTGTGTT	GGCTTAACTG	GTCCAATGGA	2220
	AGCAMACCAC	TAGTTCTCAC	ABAGCTCTGG	AGGCCGACTG	TTGGGGAAAG	ACTGAGTCGG	2340
	GATGACAAGG	CCACCATCAT	CCGCGTGGGG	AAGAGCCTCC	TCATTCTGAC	CCCTCTGCTA	2400
~-	COCCTCACCT	GGGGCTTTGG	AATAGGAACA	ATAGTGGACA	GCCAGAATCT	GGCTTGGCAT	2460
25	GTTATTTTTG	CTTTACTCAA	TGCATTCCAG	GGATTTTTTA	TCTTATGCTT	TGGAATACTC	2520 2580
	TTGGACAGTA	AGCTGCGACA AGCAAAACTC	ACTTCTGTTC	AACAAGTTGT	CTGCCTTAAG	A ACCOUNTE	2640
	AACCCACTGC	AAAACAAAGG	CCATTATGCA	TTTTCTCATA	CTGGAGATTC	CTCCGACAAC	2700
	ATCATGCTAA	CTCAGTTTGT	CTCAAATGAA	TAA			
30							
	Seq ID NO:	463 Protein	sequence				
	Protein Acc	cession #: 1	sos sequenc	9			
	1	11	21	31	41	51	
35	Ī	Ī	1	ì	1	1	
	WKAGAFMFIR	PFTFTDGHGG	FLGKNDGIKT	KKELIANKKK	HLGPVBEYQL	LLQVTYRDSK	120
	EKRDLRNFLK	LLKPPLLWSH PSCECHLNNL	GLIRIIRAKA	PTUCHSLAGV	PRIMILINGS	SATYSKYANG	180
	TRIOLKKAYE	RIOGFESVOV	TOPRNGSIVA	GYEVVGSSSA	SELLSAIEHV	AEKAKTALHK	240
40	LFPLEDGSFR	RIQGPESVQV VFGKAQCNDI	VFGFGSKDDB	YTLPCSSGYR	GNITAKCESS	GWQVIRETCV	300
	LSLLEELNKN	PSMIVGNATE	AAVSSEVONL	SVIIRONPST	TVGNLASVVS	ILSNISSLSL	360
	ASHFRVSNST	MEDVISIADN	ILNSASVINW	TVLLREEKYA	SSRLLETLEN	ISTLVPPTAL	420 480
		WKGI PVNKSQ LPVSKNGNAQ					540
45	HIOWIDAGCH	LVNETQDIVT WKQIKKSQTS	COCTHLISES	ILMSPEVEST	IPPVVKWITY	VGLGISIGSL	600
	ILCLITEALF	WKOIKKSOTS	HTRRICMVNI	ALSLLIADVW	PIVGATVDTT	VNPSGVCTAA	660
							720
	TOPSNTYKRK	DVCWLNWSNG KSLLILTPLL	SKPLLAFVVP	ALATVAVNEV	VVLLVLTKLW	RPTVGERLSR	840
50	DDKATIIRVG	NKLSALSSWK	OTEROMSCOT.	TADSÖNDVAR	NPLONKGHYA	PSHTGDSSDN	900
50	IMLTOPVSNE	NKDSKDSWK	Q1BNQN33DD	OAKEKE SKEF	Ar DQUIGHTA	r Sili Coboobii	
	Seq ID NO:	464 DNA 886	uence				
55	Coding seg	id Accession	10219	109.1			
	searny						
	1	11	21	31	41	51	
	GGGCATGCAG	1		1	CON NOGRACIA	AGAAGAAGGA	60
60	CACTTOTACT	B B B B G G G B G B	ACATCAATAT	ACCATOTTC	TTAGCAATAG	AAAAAGAAGG	120
00	CCAAGAGGAA	TTAGGGAGAG AGCATACAGT	AGTTATAAGA	GATCAGCAAG	GGGACAGGGT	TAGATTTGGT	180
	TTGGTTTGAA	AGCATACAGT	AAATATGATG	TCTGTCCCTG	GCAGTGTTGG	CAGAGTAGGA	240
	DOMADDADOM	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACTGT	ACTTACATAT	300 360
65	GAGACTATTT	CCCTCTCTGC	TTTTCAAACC	Tracigaci	ATGTATACAT	ATCTATATCT	420
05	GTAGACAGAA	TOCTTOGGAA	TACAGTAATT	GACATATATT	CTGTTATTTG	ATGCTTGAAA	480
	B B TOTAL CONTROL	BCTBACCBGT	TTCCCTATAG	ATTRICCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGT	TCTCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAAACTTTA	CAGCCTTCAT	600
70	AAGGAAGTGA	GGTCCAGGAA	AATCTAGGAG	ATATTTCTTA	ACCAATCTAT	AAAGGCATTA	660 720
70	GTAATGACAG	GATATTTCCT AGCCAATGAA	GAAAGTGTAA	TTTCCCATTG	AGGATTIGIT	CATARCTTCC	780
	Chacterica	TATGCAAAA	CTTCTTGGAA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCACCATATC	TOCAGTOTOR	CACACCAGGA	TATGTCCTTT	CTAGCCTGTC	TATCACATGC	900
75	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCATT	TGAACTCATC	960
75	CAAGCTTTCT	CTARATTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCCTTAAG	1020
	COATAGATAG	AUGGCAAACC GTCCCCTCTA	ACCOCCCCTC	GTCTCAGCTT	GTTATCCTGT	AAATTCTCTT TTTTTTTCTTC	1140
	CCTCCATTCC	CAGGATGAGC	TTGTTGCTTC	TGTCCTATGA	GACATTAGAT	TCCTTTTCTT	1200
	TOGTACCOGA	GTAAATCCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTTG	TCTTATAGCG	1260
80	CTGGATGCAG	ACTCAGCTGA	GARGACCATT	ATTCATTTTT	GGAATTCTTT	ATCTCAGATA	1320
	TTTCCTCTTC	TTTCTTTTTC	TTCTATCTTT	GGATTTTTAG	TCCATCAACG	CCCCATTAGT	1380 1440
	CTATTCCCCG	ACTICARTCA	CCTARGACC	CCATCTCAAA	GGGGTTGAGA	GACTCAAAAC AAACAGGCAG	1500
	GTGAGAAATT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTCAG	1560
85	CCTATGTGTT	TCTGGCACCT	TGTTGTAGAT	AAATCTCCCT	TGACTTTGTG	ATGTGCTGAG	1620
	AAAACAAACT	CACGGCTGGT	GTTAAAAAGG	GCCCATGACA	ATACCAAGIG	TTGGGGAGAA	1680
	TGTGGAGAAA	TCAGAACTCT	ATTCACGGTC	GGTTGGAATG	CACACTTGTG	CAGAATTCTA	1740

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	TGGAGAAGAG	TCTGGCATTT AGGTTTATAC	CCTCAAAATG	TTAACCTGGA	TTTACCATAT	GACCCAGCGA	1800 1860
	TTTCATTCAT	AGGTTTATAC	TCAAAAGAAA TATTCATAAT	TGAAGAAATA	TGGGAAACAAC	ACABATGTCC	1920
_	ATCAACTTAT	ACAACATCAT GATTAAAGAA	AATCTGGTCT	ATTCATAGAA	TGGAATATTA	TTCGACCACA	1980
5							2040
	TTARAGARGC	CAGTCACAAA CCATAGAAAC	AGGACTTACT	TTCCTGGTTT	CAGGGTCTC	CAGGAAGGGA	2160
							2220
10	GATGATAGCA	CAACTTTGTG ATATGTTAAT	AATATAATAA	AATCATTGAA	TTGTACAGTT	GAATTTATGG	2280 2340
10	TATATAAATT	ATATGTTAAT	AAAAAGGGGG	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTCTTCAGA	ATATTGGATT TTACAAGATA ACCATTGAGA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
							2520
15	CTTCATTTTT	AAATGTAAAA GTGTCAGCCT GAGACTGGCA CAGAATCACA	GTTAGAAAGCT	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAGAG	GTTTAATTGG	GCTTAGAGTT	CCACGTGATT	2700
	GGGGAGGCCT	CAGAATCACA	GTAGGAGGCA	AAAGTTATTC	TTACATGGTG	GCTGCAAGAG	2760 2820
	AAGATGAGGA	AGAAGCAAATAG	CACAAGAAAG	ACCGGCCCCC	ATGATTCAAT	TACCTCTACC	2880
20	TGGGTCCCTC	AGAAGCAAAA ATGAGAATAG CAATAACATG	TGGAAATTCT	GGTAGATACA	ATTCAAGTTG	AGATTTGGGT	2940
		CCAAACCATA CATCTGGGAT					3000 3060
							3120
~-	ACTGAAGTAC	ACTTCTTCAC TTACTAAGGA	TATCTCTTTG	GACTTAGAAT	TAGCACTACA	TTCCTTGTTA	3180
25							3240 3300
	CAAGAAAAGA	ATGGTGGGGT GGGATGGAGT AGAAAGGCAC	TTTTGTTTGT	TTGGTTTTGT	TTTTGTTTTA	CAGCTGGAGT	3360
	AGAATACAAA	GGGATGGAGT	TGAAACAAAT	GAGAGGAAAT	TGGAATTCTA	AACTTATTCT	3420
30	CATTGGCATT	AGAAAGGCAC TTCCCTATAG	CTACATGTAT	TTCACATGAG	CCGGTGACTG	AATCCTGTCC	3480 3540
50	TTTGTCATAA	ATTTTCATAT	TCATAAAGGT	GAGTGTTAGC	CCGCTTGTGA	AATCTGAAGT	3600
							3660 3720
	GGATCTCACC	CTTCATTCCA TAAGAGCTTC	CAGACACACA	AGCTTAATAA	CATGAATTAT	TTTTGAGAAT	3780
35							3840
							3900 3960
		AGTAAACCAA AAGGAGATGT					4020
	AGGTCTCCTG	TTAGCATTCA TAAAGAGGGT	TTGTAAAGCC	ATCCTACCTA	GCTCTAGTGT	AACCAGCAAT	4080
40	GAAAGAAAGA	TAAAGAGGGT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTTG	4140 4200
	TAAGCCTTCT	AATTAGGACA AAGAGAAAAA TTGTACTACA	CTTTAATATATT	CANANTCTCA	CAACCCAGAT	ATATCATTTC	4260
	TTTAAGAAAA	TTGTACTACA	AAATACCATT	CCATTTATTA	AAGTCATTCI	GACAGGAATC	4320
45							4380 4440
45	CARCACCAAG	TTCATGTTCG CCTATCAGCA	TCACATCAGC	ATTAGGGATG	GTCCTCTTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATO	ATTACGTTGT	CCTGTTGCAG TCTGATGGGT AACAGATCTT	4560 4620
	TTTTTCTCTG	GTTCCGTCGG	CTAGCACGCA	ACTOTORAGE	CACTGACTTA	AACAGATCTT	4620
50	TTGAGTAAAG	TTTTCTTGTC	CCGCTTCATG	TCTCTTCCAG	GTTCTTCACT	TTGATCAAGT CACTCTGATT AACTAAGAAA	4740
	CACAGAGAAC	ACCACAGAAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CACTCTGATT	4800 4860
	CAGCTTTAGA	TCCCTGAACA	GGTCATAGTT	AAGATTGAGA	CATACAGAGI	GGGTTGGCAT	4920
	TTCATGGCAC	ATAATTATTA	TTCCTCATTT	CTGCGTTACT	AAAAGACAGT	GGGTTGGCAT CAGCACTGTA TGCTCTTCAC	4980
55	CCTCAGAGCA	TAGGTCTGGA	TCAGGATAGG	CTGGGTTCAG	ACTCCAGCTT	TCCCAGAAAA	5040 5100
	AADTADTAAA	TAAGAGCAGG	GACTCAATAC	ATGCAAATAC	ATGCAAATG	TTACAACAGT	5160
	GCCTTGCCCA	TAAAAGTCAT	AATAAATGTT	ATTATTATTA	TAAAGTAGCT	TTACAACAGT	5220
60	TAATCATAAT	AATGTGAAAA	TAATTTAATT	TTCATTGAGT	CATTAATGAG	ATTCAGAGGA	5280 5340
60	ATAAGCACAA	GTCCAAGTAT	TTCCTCCAAC	GTAGAAAGTT	CTAGATTTA	ATTCAGAGGA TGGTTTAGAG ACAGGCTTAG	5400
							5460
						TGTAAAGTCC ATGAGGAAAG	5520 5580
65	AGCCACAGAT	CAGTCAATGT	GTCCTACAAG	ATAATAGCAG	CAACAGGTA	AACAGGGCTT GATGACTGTT AGCTAAACCT	5640
	CCTGGCATAA	TCTATTTAAA	ATATCCAACC	TTCAACATAC	TCGTATCCT	GATGACTGTT	5700
	AGAAGTGAAA	TATGGTCCTT	GCCCATAAGG	AGCTGAGAGT	COCCTGCAT	TTTAGTTCAG	5760 5820
	AAGAGAAAAG	ATTGCAGTAC	GTTAGAGCA	GAAGAATTT	CTGGAAGAA	TTTAGTTCAG TCAAATATAA AACATCAAAG	5880
70	GGTGGATTT	GAAGGGTATT	TGAGGTGAA	TACACCAATT	ATCAGGGAA	* AACATCAAAG	5940 6000
	A MANUAL CITA STATES	*********	THE REPORT OF	· Contributed and a	DAARYT"PERT	TGGGTTTAGT	6060
							6120
	ATATCACCTC	ANDROTABAA I	ACARGETETT	CGGAGAAAAA	ACGTATCAA	TTTTACAGGT	6180
75	AATTTCACCT	GGCCTACCCA	CATTICATT	GCATCCTGA	CTCCAGACC	TTTACTCAGA	6240 6300
	GTGCATTAG	TCCATTTCCA	CAACTCTCCC	CCACTGGAG	GTCCCAGAC	CCAACGATAC TGTAATAGAG CAGTCACATA	6360
	ATCACTGAAC	TGTGGATTTA	GGGATAATC	LAAATABTET	GAGGAGGTT	TGTAATAGAG	6420
80	TGAGTAAGAG	TAATAAGTAA	TARGATACC	A TOGGGATARACT	ATTGGAATG	G GCAGGCTTGG	6540
00	GTGAGTTCC	GAGAATAGTT	GAGGAAGTA	CAGGAAATA	TGAATGCAC	G GCAGGCTTGG A GGATGAAAGA I GAGAAGCAAT	6600
	CAAAAACAA	GATCAGAAAC	ATCATGGTT	AAATTACTG	AGAGAAGTC	T GAGAAGCAAT	6660 6720
	GAATCTCCT	CARCATATTO	ACCUTCACIO	ACCTETTE	TGTGCCAGC	CACATTCCCC	6780
85	TTTTGCATT	CCTACATGAC	ACCTGTATA	AAATATCCA	GGACAGGAG	A TACTGCATCT T AATATATAGT	6840
	ATTCAGGGT	TGGATTCAGC	TTACTGTTG	TACAAATAA	TAAGTTTGG	T AATATATAGT T ATTTAGATGC	6960
	TACATAAAT	ACTOCTAATT	CCTACTTCT	CLICATAT	- LUNNOUNH		0,000

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	CATCAAGAAA	TTTTACCAGA	CCAGTGTGGA	ATCTACTGAT	TTTGCAAATG	CTCCAGAAGA	7020
	AAGTCGAAAG TTATAGAAAC	AAGATTAACT ACCTTTGAGA	AACCTATGCC	AAGTCAAACG	GTGCTTGACA	CTGCATGGGG	7140
	GAACAGGTGT	GGGGATTGAG	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
5	AGGATTTGTC	CABATGBATA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
	GCCAATTAGA	TGGAAACACA	TCTGGAGAAT	TATTTGCTTA	TGGCCCTGCA CATATCCTTT	TGACAATAGC	7320 7380
	TTTGTGGATC AGACTCAAAT	CCCTGTCTCC	GCTCAGACCT	AGAAAACATT	AGAAAGCGTC	TCTCGTCTCC	7440
	TTTACTAATT	GGGAAACAAG	CAGCTCTCTG	GTAAATCACC	CTTTTGTCTC	TGAGCTGGAG	7500
10	CTGCCTGGAT	CACATCTGTA	GCCAATGTGT	TCTGCAGGGA	TTATCACAGC	TCTCTTCCCC	7560
	ATCAAGGGCA	AAGAGCTTGA	CAAAGTCTCC	ATTCTACAGA	CATCITTCTT	ACCTCCCACC	7620
	TCTCATTACA	GGCCAAACTT	ACAGCAACTC	AACATGAGAG	TGAATAGGAA	GATACCCCCG	7680 7740
	GAAGTAGTGT	ATCAGGGCCT	CCTTCCTCTG	AATGGGGACC	CCGTAGTTAA	AAAAAAAAA	7800
15	BACTACCAAC	ACCRECATE CO.	CAGAAAGGAA	AGACACATGT	TGGAAGAGTA	GACAAAATCA	7860
	GTTTATCAGT	ATTCCAAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAACTCC	7920
	TTCTCTATCA	CAAGAAGTGA	TGTCTCCATC		TTATACGACT CAATTCAAAG	GGAGCCTTGA	7980 8040
		ATCTGGTGAA AGCAGGGATT	TOCOTCARTA	ATTAACGATC	AGTCACGAAC	ATTTGCAAAG	8100
20	CATCTTCCAG	N CA ACCCATT	TOTACCTTOT	CTABAGACT	CTTTTATTCT	TTCCCTTGCA	8160
	GAAAAAATTA	AAAACCTATT	TCCTGATGGG	ACTATTGGCA	ATGATACGAC	ACTGGTTCTT	8220
	CTCAACCCAA	TOTATTTOAA	AGGGCAGTGG	GAGAATAAAT	TTAAAAAAAGA	AAACACTAAA	8280 8340
	GAGGAAAAAT	TTTGGCCAAA AATGTTAAAC	CAAGGTATTG	CARTATATT	TGATAAGTAA	AAAATAAAA	8400
25		CTGTTATTTT	GTTGTTTTAC	TCTTATAACT	TTATTTAGTT		8460
23		TGTTTCTAAC	TCATGGAATT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCBATAATAT	TATCTTTTT	GTCTTGTGTT	TCACGTGTTA	TTTGTTGGAC	8580
		ATTGCAGAAT	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATTCCT	8640 8700
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	CARCCTARA	GCTTATGACC	GAGTTGCCTC	AAAATGATGA	AAAATTCTAA	ATGAGGAATG	8880
	ATGACTCACC	TTCATATTAC	AAATATTTGA	GCATAGGGCC	TGACACAAAC TACTTTAAGC	TGAAAGCTTA	8940 9000
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	CACCCCACAA	CAGTCCTCAG	AGTGTGATGT	TACCTTCCTG	TGTCCAAGTG	TTCTCATTGT	9180
	TOTAL PROCESS	TOTATOATTT	AATTOCATOT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
40	TTACATGCAT	TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA GAGTAGAAAA	CTTGACTGGG	9300 9360
40	AGAAATATAT ATTTAGGAAT	ACCAATGTGA	GGAAAGTTTA	AATTGCAATG	TOTACTABAT	AATGTATACA	9420
	G11111	* TOTAL COOKER A.M.	TRABARTINA	CACATOTACT	AGGCTGTTGG	CACAAGAAAT	9480
	AGTGATACAT	ACAGTTCATT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
40	ACAGTTGTAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600 9660
45	ACATACATGT	ATATACATAT TAGAATAATA	ACACATATAA	CCCAATGTAT	TTATATATTC	ACATTTATI	9720
	TTTTACCTAT	GAATCTCCAC	ATAGTCARTT	CATTGTTAAG			9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTTGT	ATAGCTTGAA	GAGAAACTCA	CTGCTGAGAA	9840
	ATTYCATYCCAA	TOGACAAGTT	TGCAGAATAT	GAGAGAGACA	TGTGTCGATT	TACACTTACC	9900 9960
50	TCGGTTCAAA	ATGGAAGAGA	GCTATGACCT	CAAGGACACG	TYGAGAACCA	GTCTCTCAGT	
	ATCTAAAGTC	AATGGGGATG	CCTTTCTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TOCCACOGOT	GTAGTAGTAG	TOGRATTATO	ATCTCCTTCA	ACTAATGAAG	AGITCIGITG	10140
	TAATCACCCT	TTCCTATTCT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
55	CAGATTCTCA	TCCCCATAGA	TGCAATTAGT	CTGTCACTCC	TCTTGGCTCA		10260
	GAGGTGTTCT	GGTAAACTGA TTGATGATGA	TTGCTGGCAA	CAAGAATTTA	ATGATTAAAA		10380
	defected the beat	CTCTTAATAA	CCCCACATAT	AAATGTACTT	TTCCTTCCAG	AAAAATTTCC	10440
	CTTCACCAAA	DAGGOTTOTAG	ATANGATGAA	TCATTTAATA	CCGTGTCTTC	TAAATTTGAA	10500
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	ATTTAGCAAC	CTAGAAACAC	ACATTTCTTT	GAATTTAGGT ATCATCAATA	GATACCTAAA	ATABABATCAT	10620
	GTTTCTAAAT	CONCRETEDITOR	CTCTCGGAAAG	GGCAAGTGTC	CACTTACACA	TAGGAAAGAT	10740
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	CTATTTTATG	CTAAAGGGAT	AAGAAACTCA	TTACAGGCTT	TGATGGTTGT	TTGTCAAAGA	10920
	GGGGCATAAA	GAAAGAACAG	CCACATCTAG	AAAATACATC	TAGGAAATCA	CTGATATCAA	11040
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70							11160
	GAGAGAAAA	AAGACTTTGG					11220
	TCAAATGGAT	TTGCCTGGCA	GGCACTTGAA	GATATTAGTC	TAAATCTCAG	AAACAGAATA TTGGGATAAA	11280
	TATOCTACTT	GTAGCTAAAA	GCAAAAATAA	GATACTAGGG	AGAAAGGATA	AAGTTAGAAG	11400
75	BARCHACHAT	CTACAATTCA	COTTOLAGOTA	TATCAGCATG	TCTAAAGATC	AGGAATTGAT	11460
,,,	CATTTTTATT	TTCCAGAAAG	TAGCTTTTCT	TAGGGTTCCA	TATTTACTCC	CATAGATTCT	11520
	TCCC						
80	protein *	465 Protei cession #:	BAB21525.1				
00	TTOCGAR AC	acceson #1					
	1	11	21	31	41	51	
	1	FMFDLFQQFR	l	I DYSTESSTON	M.T.CVKD	OOTSKVI PPD	60
85							120
05	DATFFFFFF	THEOTOPANAD	PESDERTNS	VESOTNEKIK	NLFPDGTIGN	DITLULUNAI	180
	YFKGQWENKF	KKENTKBEKE	WPNKNTYKSV	QMMRQYNSFN	PALLEDVQAK	VLEIPYKGKD	240

LSMIVILIPNE IDGLOKLEEK LTAEKLMEWT SLONMRETCV DLHLPRFKME ESYDLKDTLR 200 TMGMVNIFNG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAVV VVELSSPSTN 360 PERCOMPRI, PRIPONKING ILPYCRESCP 5 Seg ID NO: 466 DNA sequence Nucleic Acid Accession #: NM_001910.1 Coding sequence: 50..1240 10 GGAGAGAGA AAGGAGGGG CAAGGGAGAA GCTGCTGGTC GGACTCACAA TGAAAACGCT CCTTCTTTTG CTGCTGGTGC TCCTGGAGGT GGGAGAGGCC CAAGGATCCC TTCACAGGGT 120 GCCCCTCAGG AGGCATCCGT CCCTCAAGAA GAAGCTGCGG GCACGGAGCC AGCTCTCTGA 100 GEOCHIOGA AGRANTENI TEGACATEAN COASTICACE GASTECTEC CANTEGACA GASTGOCAAG GAACCCTCA TCAACTACTI GGATATGAA TACTTCOGGA CTATCTCAG TEGGCTCCCCA CCACAGAAT TACTTCTCAT CTTCGACACT GGCTCCTCA ACCTCTGGST 240 15 360 CCCCTCTGTG TACTGCACTA GCCCAGCCTG CAAGACGGAC AGCAGTTCC AGCCTTCCCA GTCCAGCACA TACAGCCAGC CAGGTCAATC TTTCTCCATT CAGTATGGAA CCGGGAGCTT 420 GTCCGGGATC ATTGGAGCCG ACCAAGTCTC TGTGGAAGGA CTAACCGTGG TTGGCCAGCA 20 GTTTGGAGAA AGTGTCACAG AGCCAGGCCA GACCTTTGTG GATGCAGAGT TTGATGGAAT *** TOTGGGCCTG GGATACCCCT CCTTGGCTGT GGGAGGAGTG ACTCCAGTAT TTGACAACAT
GATGGCTCAG AACTGGTGG ACTTGCCGAT GTTTTCTGTC TACATGAGCA GTAACCCAGA 660 720 ACCITATIONS GEGAGEGAGE TEATITITIES AGGETACGAE CACTECEATT TETETEGGAG 700 AGGINGTING GGGAGCGAGC TOATTITTIG AGGINACIAC CACTCOCATT TCTURGGAG CCTRAATTIG GTCCAGERG. CCAAGCAGC THACTGEGAG ATTROCACTG ATRACATCA GGTGGGAGG ACTGITATOT TCTGCTCCGA GGGCTGCCAG GCCATTGTGG ACACGGGA TTCCCTCATC ACTGGCCCTT CCGACAGART TAAGCAGCTG CAAAACGCCA TTGGGGCAGC CCCCGTGGAT GGAGAATATG CYGTGGAGTG TGCCAACCTT AAGGTCATGC CGGATGTCAC 840 25 900 1020 CTTCACCATT AACGGAGTCC CCTATACCCT CAGCCCAACT GCCTACACCC TACTGGACTT 1080 CHICACCATT AACGAGTICE CUTATACCUT CAGGLEAACH GCUTACACUL INCIGGACITY CGTGGATGGA ATGCAGTICT GCAGCAGTGG CTTTCAAGGA CTTGACATCC ACCCICCAGC TGGGCCCCTC TGGATCCTGG GGGATGTCTT CATTCGACAG TTTTACTCAG TCTTTGACCG 30 1200 TGGGAATAAC CGTGTGGGAC TGGCCCCAGC AGTCCCCTAA GGAGGGGCCT TGTGTCTGTG 1260 1320 ACATGAGAAT ACACACACA ACACACATAT ACACACACA ACACTTCACA CATACACACC 1440 35 ACTCCCACCA COGTCATGAT GGAGGAATTA CGTTATACAT TCATATTTTG TATTGATTTT 1500 1620 1680 1740 40 1800 TANCHICCTI AMATATACAA TCOGMATTCA MGCATCTCCC ATTRICCCAC MAMIGITIES CHOTITITOTI AGTOGMATE TITGTATTAG GATTCAMCCA AGGCCATRA TATGCATTA TTIGAMATGI CHGTAGATCI CITICCATCI ACAGAGTTTA GCACATTGA ACQTGCTGG TIGAMATCI CHGGGGTCTAT TOMACATGI TCTCTQMACT TATCTTTCCT ATAMATGGT AGTTAGATCI GGAGGTCTGA TITTCTGGCA MAMATACTTC CHAGGGGTG CTGGGTACT 1860 1920 2040 45 CTTGTTGCAT CCTGTCAGGA GGCAGATAAT GCTGGTGCCT CTCTATTGGT AATGTTAAGA 2100 CTGCTGGGTG GGTTTGGAGT TCTTGGCTTT AATCATTCAT TACAAAGTTC AGCATTTT Seg ID NO: 467 Protein sequence Protein Accession #: NP_001901.1 50 51 SMDOSAKEPL INYLDMEYPG TISIGSPPON FIVIFDTGSS NLWVPSVYCT SPACKTHSRP 120 55 OSSISTING POORFEITYS TSSISSIIOA DOVSVEGITY VGQQPGESVI ERQQTFVDAE
POGLIGIGYP SLAVGGVTPY ENONAQNIV DIEMPSVYMS SNEEGAGSE LIFGGITHEN
POSSILMEVEY TKQAYKQIAL DNIQVGGTVM FGSECQAYU DTGTSLITGP SBKIKQLQNA 180 240 IGAAPVDGEY AVECANLINVM PDVTFTINGV PYTLSPTAYT LLDFVDGMQF CSSGPQGLDI HPPAGPLWIL GDVFIRQFYS VFDRGNNRVG LAPAVP 60 Seq ID NO: 468 DNA sequence Nucleic Acid Accession #: NM_018058.1 Coding sequence: 319..1575 65 TACGCGCTGC GGGACCGGCA GGGGAACGCC ATCGGGGTCA CAGCCTGCGA CATCGACGGG GACGGCCGGG AGGAGATCTA CTTCCTCAAC ACCANTAATG CCTTCTCGGG GGTGGCCACG 120 TACACCGACA AGTTGTTCAA GTTCCGCAAT AACCGGTGGG AAGACATCCT GAGCGATGAG 180 GTCALGOTGS CCGTGGTGT GGCCAGCCTC TTTGCGGGAC GCTCTGTGGC CTGTGTGGAC AGAAAGGGCT CTGGACGCTA CTCTATCTAC ATTGCCAATT ACGCCTACGG TAATGTGGGC 70 300 CCTGATGCCC TCATTGAAAT GGACCCTGAG GCCAGTGACC TCTCCCGGGG CATTCTGGCG 360 CCTUATROL: THATTGAMAT GARCCITEMS GEOMETRIC: TLANCOSSISS CATTURBES CONTROLLED TO CONTRO 420 75 E40 600 720 GTCCGCACGG TCATCACCGC CGACTTTGAC AATGACCAGG AGCTGGAGAT CTTCTTCAAC
AACATTGCCT ACCGCAGCTC CTCAGCCAAC CGCCTCTTCC GCGTCATCCG TAGAGAGCAC 780 80 840 GGAGACCCCC TCATCGAGGA GCTCAATCCC GGCGACGCCT TGGAGCCTGA GGGCCGGGGC ACAGGGGGTG TGGTGACCGA CTTCGACGGA GACGGGATGC TGGACCTCAT CTTGTCCCAT 960 GGAGAGTCCA TGGCTCAGCC GCTGTCCGTC TTCCGGGGCA ATCAGGGCT CACCACAACAAC
TGGCTGGGAG TGGTGCCACG CACCGGGTT GGGGCCTTTG CCAGGGGAGC TAAGGTCGTG 1020 1080 85 CTCTACACCA AGAAGAGTGG GGCCCACCTG AGGATCATCG ACGGGGGCTC AGGCTACCTG TGTGAGATGG AGCCCGTGGC ACACTTTGGC CTGGGGAAGG ATGAAGCCAG CAGTGTGGAG GTGACGTGGC CAGATGGCAA GATGGTGAGC CGGAACGTGG CCAGCGGGGA GATGAACTCA

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	GTGCTGGAGA		CCGGGATGAG	GACACACTTC	AGGACCCAGC	CCCACTGGAG	1320
	ACACCAATGA	ATGCATCCAG	TTCCCATTCG	TGTGCCCTCG	AGACAAGCCC	GTATGTGTCA	1380
	ACACCTATGG	AAGCTACAGG	TGCCGGACCA	ACAAGAAGTG	CAGTCGGGGC	TACGAGCCCA	1440
5	ACGAGGATGG	CACAGCCTGC	GTGGGGACTC	TCGGCCAGTC	ACCGGGCCCC TGCTGGAGCT	CCCCCACCA	1500 1560
,	CCCCCACCGC	TGCTGCTGCC CGTAGATGGA	CATCTCAATC	TOGGOTTOGT	GCTTBAGGAG	AGCTGCGAGC	1620
	CCAGCTGCTG	AGCAGGGGTG	CGACATGAAC	CAGCGGATGG	AGTCCAGCAG	GGGAGTGGGA	1680
	AAGTGGGCTT	GTGCTGCTGC	CTAGACAGTA	GGGATGTAAA	GGCCTGGGAG	CTAGACCCTC	1740
10	CCCAAGCCCA	TCCATGCACA	TTACTTAGCT	AACAATTAGG	GAGACTCGTA	AGGCCAGGCC	1800
10	CTGTGCTGGG	CACATAGCTG GTCTAATGAC	TGATCACAGC	AGACAGGGTC	GCTGCCCTGA	TGGCGCTTAC	1860
	ATTCCAGTGG	AGTATGAGGA	CATATUTIAG	CTGAGTTCAA	ATCCTGATTC	AGGAACTCAC	1980
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	AAATGGGGAT	TAAGAATAGA	ATCTTGGGGT	TAGTGTGGAG	ATTAGATTAA	ATGTATGTAA	2100
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	Seg ID NO:	469 Proteir	sequence				
20	Protein Acc	ession #: b	P_060528.1				
20	_	11	21	31	41	51	
	ì	Ĭ.	ī .	1	i	i	
	MDPEASDLSR	GILALRDVAA	EAGVSKYTGG	RGVSVGPILS	SSASDIFCON	ENGPNFLFHN	60
	PCDCTFVDAA	ASAGVDDPHO	HGRGVALADF	NRDGKVDIVY	GNWNGPHRLY	LOMSTHICKVR	120
25	FRDIASPKFS	MPSPVRTVIT	ADPONDQELE	IPPNNIAYRS	SSANRLFRVI	RREHGDPLIE	180 240
	ELNPGDALEP	EGRGTGGVVT AKVVLYTKKS	CANTERTING	SUAL CEMEBA	AHEGIGEDEA	SSVEVTWPDG	300
	KMVSDNVASG	EMNSVLETLY	PRDEDTLODP	APLETPMNAS	SSHSCALETS	PYVSTPMEAT	360
	GAGPTRSAVG	ATSPTRMAQP	AWGLSASHRA	PAPPPPPLLL	PPDPPPDFB	LPLLHRSS	
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	I TOTOCACOA	TGTTACCGTT	CCTGCTGCTG	CTCTGGTTTC	TGCCCATCAC	TGAGGGGTCC	60
		AACCCATGTT	CACTGCAGTC	ACCAACTCAG	TTCTGCCTCC	TGACTATGAC	120
40	AGTAATCCCA	CCCAGCTCAA	CTATGGTGTG	CCACTTACTC	ATGTGGACCA	TGATGGGGAC	180
40	TTTGAGATCG		GTACAATGGA CGCGGTCGAT	CCCAACCTGG	TTCTGAAGTA	COCCUCTOCCO	240 300
	CAGAAGCGGC	TGGTGAACAT GGAACGCCAT	CGGGGTCACA	GCCTGCGACA	TOGACGGGGA	CGGCCGGGAG	360
	GAGATCTACT	TCCTCAACAC	CAATAATGCC	TTCTCGGGGG	TGGCCACGTA	CACCGACAAG	420
4.5	TTGTTCAAGT	TCCGCAATAA	CCGGTGGGAA	GACATCCTGA	GCGATGAGGT	CAACGTGGCC	480 540
45	CGTGGTGTGG	CCAGCCTCTT	TGCCGGACGC TGCCAATTAC	COTACGCTA	GTGTGGACAG	TOATGCCCTC	600
		ACCCTGAGGC	CAGTGACCTC	TCCCGGGGCA	TTCTGGCGCT	CAGAGATGTG	660
	GCTGCTGAGG	CTGGGGTCAG	CARATATACA	GGGGGCCGAG	GCGTCAGCGT	GGGCCCCATC	720
50			TATCTTCTGC	GACAATGAGA	ATGGGCCTAA	CTTCCTTTTC	780 840
30		GCGATGGCAC	CCCCTGGCT	GACTTCAACC	GTGATGGCAA	AGTGGACATC	900
	GTCTATGGCA	ACTGGAATGG	CCCCCACCGC	CTCTATCTGC	AAATGAGCAC	CCATGGGAAG	960
	GTCCGCTTCC		CTCACCCAAG	TTCTCCATGC	CCTCCCCTGT	CCGCACGGTC	1020
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33	ATCCAGCAGC	TCAATCCCGG	CGACGCCTTG	GAGCCTGAGG	GCCGGGGCAC	AGGGGGTGTG	1200
	GTGACCGACT	TCGACGGAGA	CGGGATGCTG	GACCTCATCT	TGTCCCATGG	AGAGTCCATG	1260
	GCTCAGCCGC	TGTCCGTCTT	CCGGGGCAAT	CAGGGCTTCA	ACAACAACTG	GCTGCGAGTG	1320 1380
60	GTGCCACGCA	CCCACCTGAG	GGCCTTTGCC	AGGGGAGCTA	AGGTCGTGCT	TGAGATGGAG	1440
00	CCCGTGGCAC	ACTTTGGCCT	GGGGAAGGAT	GAAGCCAGCA	GTGTGGAGGT	GACGTGGCCA	1500
	GATGGCAAGA	TGGTGAGCCG	GAACGTGGCC	AGCGGGGAGA	TGAACTCAGT	GCTGGAGATC	1560
	CTCTACCCCC	GGGATGAGGA	CACACTTCAG	GACCCAGCCC	CACTGGAGTG	TGGCCAAGGA	1620 1680
65	TTCTCCCAGC	AGGAAAATGG GAGACAAGCC	CCATTGCATG	BACACCAATG	AATGCATCCA CAAGCTACAG	GTGCCGGACC	1740
05		GCAGTCGGGG	CTACGAGCCC	AACGAGGATG	GCACAGCCTG	CGTGGGGACT	1800
	CTCGGCCAGT	CACCGGGCCC	CCGCCCCACC	ACCCCCACCG	CTGCTGCTGC	CACTGCCGCT	1860
	GCTGCTGCCG	CTGCTGGAGC		GCACCGGTCC		AGATCTCAAT	1920 1980
70	CTGGGGTCGG	TGGTTAAGGA GAGTCCAGCA	GAGCTGCGAG	CCCAGCTGCT	GAGCAGGGGT	GGGACATGAA	2040
70	AGGGATGTAA	AGGCCTGGGA	GCTAGACCCT	CCCCAAGCCC	ATCCATGCAC	ATTACTTAGC	2100
	TAACAATTAG	GGAGACTCGT	AAGGCCAGGC	CCTGTGCTGG	GCACATAGCT	GTGATCACAG	2160
	CAGACAGGGT	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ATGGCGCTTA	CATTCCAGTG	GGTCTAATGA	CCATATCTTA	2220
75	GGACACAGAT	GTGCCCAGGG AATCCTGATT	AGGTGGTGTC	ACTGCACAGG	AAGTATGAGG	CCAGTCACTT	2280 2340
13	A A COMPONER OF	CCATCCATTA	TOTAL TOTAL	ABAATGGGGA	TTAAGAATAG	AATCTTGGGG	2400
	TTAGTGTGGA	GATTAGATTA	AATGTATGTA	AGACACTTGG	CACAAAACCT	GGCACATAGT	2460
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80							
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	- LOCELII AC	CCEBTON #1					
	1	11	21	31	41	51	
85	1	 LWPLPITEGS	1	Threat Docum	 CANDETOLARYON	AVERDADHDGD	60
85	PRIVVAGYNG	PNI.VI.KYDRA	OKRLVNIAVD	ERSSPYYALR	DROGNAIGVT	ACDIDGDGRE	120
	EIYFLNTNNA	FSGVATYTOK	LPKPRNNRWE	DILSDEVNVA	ROVASLPAGE	SVACVDRKGS	180

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GRYSIYIANY	AYGNVGPDAL	IEMDPEASDL	SRGILALRDV	AAEAGVSKYT	GGRGVSVGPI	240
LSSSASDIFO	DNENGPNFLF	HNRGDGTFVD	AAASAGVDDP	HQHGRGVALA	DFNRDGKVDI	300
VYGNWNGPHE	LYLOMSTECK	VRFRDIASPK	PSMPSPVRTV	ITADFONDQE	LEIPFNNIAY	360
	VIRREHGDPL					420
	QGFNNNWLRV					480
	EASSVEVTWP					540
	DTNECIQEPE					600
LGQSPGPRP	AATAAAATAT	ATAAAAAAA	APVLVDGDLN	LGSVVKESCE	PSC	

10 Seq ID NO: 472 DNA sequence
Nucleic Acid Accession #: FGENESHH

	Coding sequ	ence: 147	94				
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15	1	1	l	1	1	1	
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	GTTCTGAAGT	ATGACCGGGC	CCAGAAGCGG	CTGGTGAACA	TCGCGGTCGA	TGAGCGCAGC	180
	TCACCCTACT	ACGCGCTGCG	GGACCGGCAG	GGGAACGCCA	TCGGGGTCAC	AGCCTGCGAC	240
20	ATCGACGGG	ACGGCCGGGA	GGAGATCTAC	TTCCTCAACA	CCAATAATGC	CTTCTCGGGC	300
		CAGCGCAGGT					360 420
	CCACCTACAA	GTCAGGCTTC	TOTCCIGGGT	ACCCACGGAG	AGAGGGGGGGG	GGTTCCCTGC	480
	TOTOGGGGGG	GACTGAGACC	TACCCATGAA	CCAGAACCAT	TTCTTCTGAG	ACCCAAATCA	540
25	GGGGTGGCCA	CGTACACCGA	CAAGTTGTTC	AAGTTCCGCA	ATAACCGGTG	GGAAGACATC	600
	CTGAGCGATG	AGGTCAACGT	GCCCCGTGGT	GTGGCCAGCC	TCTTTGCCGG	ACCCTCTGTG	660
	GCCTGTGTGG	ACAGAAAGGG	CTCTGGACGC	TACTCTATCT	ACATTGCCAA	TTACGCCTAC	720 780
	GGTAATGTGG	GCCCTGATGC CGCTCAGAGA	CCTCATTGAA	CACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TCACCABATA	TACAGAAGGC	840
30	TTCTCCCACA	CTGCCTCTCC	AAGCATTGGT	GAGATATCTG	GCAGAACCGA	GGAGCGGGAA	900
	GGAGGAGACC	CAGAGGAGGC	AGATGAGGAG	CACAGTGGGG	ATGGAAGCAC	CAGCCAACTG	960
	TGCCGGCTGG	GCTGGAAGGA	CGGGCAGTTC	AAGGAAGAAG	CAGCAGCTTT	GGTGGAGGAA	1020
	CAGAGGGAGG	CTGGGGCAGC	TGGCGTGCCC	AGAGGACGTG	TTCGAACAGC	TCTGCAGACT	1080
35	TCCAAAAGCC	ATTTGGCTGA CAGCCCACCC	CAAGAACCTA	CCCCAAGCCC	CCCAACACTA	CCCTGTAGCC	1200
33	CCCCTTCTC	CTCAGCTAAT	GACACATGGA	COTCTGGCTG	GAAAACTAGC	CCGGAGTGTC	1260
	CCCACCCC	GAGCCCCAGG	AATGGACCCC	AAATGTAAGG	GCCGCCATGC	TGAGCCCGGC	1320
	CTCATGGCTG	AGGCTTTGGG	CGCGTGGCCA	GCGCTCAGCA	CCACTGTGGT	GCCAGGGGGC	1380
40	CTGAGAAGCT	GGGAGGAAAG	CAGGCAGAAG	GGGCAGGCCA	TGTCCAGATG	TGCACTCAGG	1440
40	GAGCTGGGAG	GTCCCTGGAG	CCAAGCCACA	CAGCACCTGC	CIGCIAGAGA	GCTGTATGAC AAGGGACTCG	1560
	CCCAAGGTCA	CACAGGAGTG	CCATCTAGTG	GCCACCATGC	CAGCTCTCGG	GGGACTCGAG	1620
	GGCCCCCGGGA	GGGTGGCCAA	GCGAGAGATT	GGGAGAGAGA	CTGGGGCAGT	AGGAAGACCA	1680
40	CTCTCCCATC	CCCTGGTCCC	CAACTTCCCC	AGCTGCTTGA	GGCCTCTTGA	AGCCGGGACA	1740
45	GTGCCGGGAG	CTGCCCTGCC	TGGGAATCCT	GGGAACTGGG	TTCTGGACAT	GGCCAAGGCC TGAGCCCAGA	1800
	CTGGCGTGGA	GGANAGCACG	GGAAGCAGAA	TTCCCCCCAG	GCTCCTCTGA	GGAGCCTCTG	1920
	COMPANDE COMPANDE	COTOROGCCT	Chahaachac	COTOTOCTOC	AGGTGGGCCT	GGGGCTTGCT	1980
	TOTGCCACTC	ACTOTOGGTC	GATGTCTTTT	CTAGGGGGGCC	GAGGCGTCAG	CCTGGGCCCC	2040
50	ATCCTCAGCA	CCACTCCCTC	COATATOTTO	TGCGACAATG	AGAATGGGCC	TAACTTCCTT	2100
	TTCCACAACC	GGGGCGATGG	CACCTITGTG	GACGCTGCGG	CCAGTGCTGA	ACGTCGTTTA CCTGTGCCAC TCTTCAGGCT	2220
	GCCTTCATCG	CINCOTCOM	CTCCTCCTCC	TGCCCGTGGC	ATGCACGTCT	TCTTCAGGCT	2280
55							
	CAGGGGGCCC	CACCCTGCCT	TCTGGCAAGA	GCTCCCTGTG	TCCTGGGGTC	TCTGATCCCC CCACAGCTAT	2460
	ACTGCCTATT	ACATTGTCCT	GTGGTCTGCC	ATCCCAGAGA	ACCTGATGAC	GCGAGGTGTC	2520
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60	CCCCACCGCC	TCTATCTGCA	AATGAGCACC	CATGGGAAGG	TCCGCTTCCG	GGACATCGCC	2700
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	GACCAGGAGC	TGGAGATCTT	CTTCAACAAC	ATTGCCTACC	GCAGCTCCTC	AGCCAACCGC	2820 2880
	CTCTTCCGAT	GCTCCATCCT	GGCTCGTGGC	CONCECTOR	CAGGGGGGAGG	TGGGAGGAAC GGGTCAGGCC	2940
65	BACCTCAACA	CAGGTCCCCT	GATGAAGAAA	CAGAAAGGAA	GGAAGGACGA	GGACTGGGCA	3000
••	AGAGGCTGTG	GGAATGCAGG	GCAAAGCCTG	GCCAAGGAGC	CGGCCTCTGC	TATTGCAGGG	3060
	AAAGGGAAGG	GAAATGTGGC	CCAAAGTGTG	CCCAGAACCC	AAGCGCCACA	AGATACAAAG	3120
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70	GTCCAATCAC	TACCAGGAAA	AGGGGGCTACG	TACGGGGGTCC	ACTACCAGGA	AAAGGGGCTA AGGAAAAGGG	3240 3300
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	AGGGGCTACG	GGCTCCAATC	ACTACCAGGA	AAAGGGGCTA	CAGGGTCCAA	TCACTACCAC	3420
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/3	ACTACCAGGA	AAAGGGGCTA	CGGGCTCCAA	TCACTACCAG	CCAGGAAAG	TACGGGGTCC GGGCTACAGG	
	CTCCA ATCAC	TACCACAGAA	AGGGGGCTACG	GGCTCCAATC	ACTACCAGGA	AAAGGGGCTA	3720
	CGGGGTCCAA	TCACTACCAG	GAAAAGGGGC	TACGGGCTCC	AATCACTACC	AGGAAAAGAG	3780
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	AGAGAGCACG	GAGACCCCCT	CATCGAGGAG	TTCAATCCCG	ACCIGINATION	GGACCTCATC	4020
	TTGTCCCATT	GAGAGTCCAT	GGCTCAGCCG	CIGICCGTCT	TCCGGGGCAA	TCAGGGCTTC	4080
	AACAACAACT	GGCTGCGAGT	GGTGCCACGC	ACCCGGTTTG	GGGCCTTTGC	CAGGGGAGCT	4140
85	AAGGTCGTGC	TCTACACCAA	GAAGAGTGGG	GCCCACCTGA	GGATCATCGA	CGGGGGGCTCA	4200
	GGCTACCTGT	GTYGAGATGGA	GCCCGTGGCA	CACTTTGGCC	TGGGGAAGGA	TGAAGCCAGC	4260
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	ATGAACTCAG	TGCTGGAGAT	CCTCTACCCC	CGGGATGAGG	ACACACTTCA	GGACCCAGCC	4380
	CCACTGGAGT	GTGGCCAAGG AGTTCCCATT	ATTCTCCCAG	CAGGAAAATG	COCTATOCAT	CAACACCAAT	4440
	GAATGCATCC	GGTGCCGGAC	COLGIGOCCCI	TOCA CTOCCC	COMMISSION	CAACCACCAT	4560
5	GGAAGCTACA	GCGTGGGTAC	TOLCOTAGO	TOTACCORTA	CANTONGCC	CARACCARGO	4620
,	GGCACAGCCT	AGCTGCAACT	TOAGCTAGGC	TCTAGGCATA	CANTONCOTO	CERTIFICATO	4680
	CCCAAAAAAAGG	GGCTGCTCCT	CALANGOC	ATCTOCACCC	CCGTCTGGTC	Checepter	4740
	CCGGGTTGCC	CAGGTATTCC	CAAAAGAGCI	CHGCICCAGG	ANCATCACCA	PAGE LICIC	4/40
	CAGAGAAGCTC	CAGGIATICE	MONOGCCCAN	GIGIAIGAAC	MIGHT CHOOM	A.A.A	
10	Sec ID NO.	473 Protein	semience				
10	Dretain her	ession #: 1	Dedagnice	licted			
	Process Acc	COBLOIL W	demon pro				
	1	11	21	31	41 .	51	
	î	î	ī-	ĭ	i	ī	
15	MACPGGLPAR	CSGWMGLGGP	SGSSPASPPH	SSSRYNGPNL	VLKYDRAOKR	LVNIAVDERS	60
	SPYYALRDRO	GNAIGVTACD	IDGDGREEIY	FLNTNNAFSG	HSSSAQVPSG	LHRNRPVLKP	120
	PPTTPAGLLG	LPPLSGRDFS	SSLGQASPDS	ROGERVPVPC	CRGGLRPTHE	PEPPLLRPKS	180
	GVATYTDKLP	KFRNNRWEDI	LSDEVNVARG	VASLPAGRSV	ACVDRKGSGR	YSIYIANYAY	240
	GNVGPDALIE	MDPEASDLSR	GILALRDVAA	EAGVSKYTEG	FSHTASPSIG	ei sgrteere	300
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	SKSHLADKNL	FGPPCYYSVC	APSPAHPPPA	ROAPOHYPVA	PLVTQLMTHG	RLAGKLARSV	420
							480
	ELGGPWSQAT	QHLPARELYD	LGEPPILQRT	DCDPGRRRDS	PKYTQECHLV	ATMPALGGLE	540
25	GPGRVAKREI	QHLPARELYD GRETGAVGRP	LSHPLVPNPP	SCLRPLEAGT	VPGAALPGNP	GNHVLDMAKA	600
25	LAWNOMEKEE	GKIHGDHEPR	PRLRKAREAE	PPPGSSEEPL	LOPPSGLRGS	PVLQVGLGLA	660 720
	SATHCGSMSP	LGGRGVSVGP	ILSSSASDIF	CONENGPNPL	PHNKGDGTFV	DAAASAERKL	780
	AFIVHLKYHL	CRDPPHSLCH HRRTLSLQGS	LAETGPSSSC	CPWHARLLQA	PHCHHGLSMS	TODOTHUM	840
	FLTQGLASSA	DDPHQHGRGV	QUAPPELLIAR	APCVIGSLIF	DUDY WY OMOT	TEROPHINOI	900
30	LSSERVNVGV	DDPHQHGRGV	DODE DE DEDOL	ADTAIGNMING	PREDITABLE	COULTACODA	960
30	SPRESMESEV	RIVITADEDA	PADDETLENK	THIRDSONNA	DERCOTORO	SSSLTAGGRN AKEPASAIAG	1020
	GOGEGERIKK ROYCHTINOCH	PRIQAPQUIK	DUMINACI OU	DITTEDUDENA	VOCT DOVONT	GENHYOFKGI.	1080
	DODLEGANIST	YGVQSLPGKG	ATTENUOUS	CLOCALLACOLA	PGVGI OR DG	KCVACKEAR	1140
	ROFITIRARO	DADGAGAGAG	DCKUTAGOM	VORWGIRGET	TTPERROYGIA	SLPGKGATGS	1200
35	MANOBACTUL	DITTERDOVE	VOST-POKGAT	GSNHYOEKGI.	RGPITTREEG	SLPGKGATGS YGLQSLPGKE	1260
55	MUCCHHANER	GLRAPITTRK	RGYGVOSLPO	KGATGSNVIR	RENGDPLIE	LNPGDALEPE	1320
	CRCTCGVVTD	PDGDGMLD1.T	LSHGESMAOP	1-SVFRGNOGF	NNNWLRVVPR	TREGAFARGA	1380
	RUVI.YTKKSG	FDGDGMLDLI AHLRIIDGGS	GYLCEMEPVA	HPGLGKDEAS	SVEVTWPDGK	MVSRNVASGB	1440
	MNSVLBILYP	RDEDTLODPA	PLECGOGPSO	OENGHOMDTN	ECIOFPPVCP	RDKPVCVNTY	1500
40	GSYRCRINKK	CSRGYEPNED	GTACVGTELG	SRHTMTWKPR	PKKELQLSQG	ICTPVWSFFL	1560
	PGCRLLLKRA	QLQAAPSTLL	QKAPGIPEAQ	VYEQDQE			
	Seq ID NO:	474 DNA sec	quence				
	Nucleic Act	id Accession	#: NM_003	661.1			
45	Nucleic Act	id Accession Lence: 11	1 #: NM_003 L52	661.1			
45	Nucleic Act	id Accession	152				
45	Nucleic Act Coding sequ	id Accession sence: 11	1 #: NM_003 L52 21	31	41	și	
45	Coding sequ	pence: 11	152 - 21 	31 	1	I	
	Coding sequents	ience: 11	21 TGTGGGAGTG	31 AGGGCAGAGG	AAGCTGGAGC	J GAGGGTGCAA	60
45 50	Coding sequents	11 TITTCCTTGG	21 TGTGGGAGTG	31 AGGGCAGAGG	AAGCTGGAGC	GAGGGTGCAA CGGTGACTGG	120
	Coding sequence of the coding sequence of the	11 TTTTCCTTGG CAAGTGGGAC CCATGGACCC	21 TGTGGGAGTG AGATACTGGA AGAGAGCAGT	31 AGGGCAGAGG GATCCTCAAA ATCITTATTG	AAGCTGGAGC GTAAGCCCCT AGGATGCCAT	GAGGGTGCAA CGGTGACTGG TAAGTATTTC	120 180
	Coding sequence of the control of th	11 TTTTCCTTGG CAAGTGGGACC CCATGGACCC TGAGCACACA	21 TGTGGGAGTG AGATACTGGA AGAGAGCAGT GAATCTGCTA	31 AGGGCAGAGG GATCCTCAAA ATCITIATIG CTCCTGCTGA	AAGCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAAC	120 180 240
	Coding sequence of the control of th	11	21 TGTGGGAGTG AGATACTGGA AGAGAGCAGT GAATCTGCTA ACTGCCCAGG	31 AGGGCAGAGG GATCCTCAAA ATCITTATIG CICCIGCIGA AATGAGGCAG	AAGCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAAC TAAAGCTCTG	120 180 240 300
50	Coding sequents 1 ATGAGTGCAC CAAAACGTTC GCTGCTGGCA AAGGAAAAAG GGATTCGTGG GBCAACCTTG	11 TTTTCCTTGG CAAGTGGACC CCATGGACCC TGAGCACACA CTGCTGCTGA	21 	31 AGGGCAGAGG GATCCTCAAA ATCITTATTG CTCCTGCTGA AATGAGGCAG GACAAAAACT	AAGCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GGCACGATAA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAAC TAAAGCTCTG AGGCCAGCAG	120 180 240 300 360
	Coding sequence of the control of th	11	21 TOTGGGAGTG AGATACTGGA AGAGGCAGT GAATCTGCTA ACTGGCCAGG GATCATGAAA AGAGTTTCCT	31 AGGCCAGAGG GATCCTCAAA ATCITTATTG CTCCTGCTGA AATGAGGCAG GACAAAACT CGGTTGAAAA	AAGCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GGCACGATAA GTGAGCTTGA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAAC TAAAGCTCTG AGGCCAGCAG GGATAACATA	120 180 240 300 360 420
50	Coding sequence of the control of th	11 TTTTCCTTGG CAGTGGGAC CCATGGACCC TGAGCACACA CTGCTGCTGA CAGACACAT GGTTTCTGA GGTCCCTTGC	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT GATCTGCTA ACTGCCCAGG GATCATGAAA ACAGGGTTTCCT AGATGGGGTT	31 AGGGCAGAGG GATCCTCAAA ATCTTTATTG CTCCTGCTGA AATGAGGCAG GACAAAAACA CAGAAGGTCC	AAGCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GGCACGATAA GTGAGCTTGA ACAAAGGCACA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAAC TAAAGCTCTG AGGCCAGCAG GGATAACATA CACCATOGCC	120 180 240 300 360 420 480
50	Coding sequence of the control of th	11 TTTTCCTTGG CAGTGGGAC CCATGGACCC TGAGCACACA CTGCTGCTGA CAGACACAT GGTTTCTGA GGTCCCTTGC	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT GATCTGCTA ACTGCCCAGG GATCATGAAA ACAGGGTTTCCT AGATGGGGTT	31 AGGGCAGAGG GATCCTCAAA ATCTTTATTG CTCCTGCTGA AATGAGGCAG GACAAAAACA CAGAAGGTCC	AAGCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GGCACGATAA GTGAGCTTGA ACAAAGGCACA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAAC TAAAGCTCTG AGGCCAGCAG GGATAACATA CACCATOGCC	120 180 240 300 360 420
50	Coding sequence of the control of th	11 TITTCCTTGG CANGTGGGAC CCATGGACCC TGAGCACAC CTGCTGCTGA CAGACCACA CTGCTGCTGA CAGCCCTTGC CTGCCCTTGC CTGCCTCCT TCACAGAGGG	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT GAATCTGCTA ACTGCCCAG GATCATGAAA AGAGTTTCCT AGGCAGCCTT CAGCATTTCC	31 AGGGCAGAGG GATCCTCAAA ATCTTTATTG CTCCTGCTGA AATGAGGCAG GACAAAACT CGGTTGAAAA CAGAAGGTCC CTCTGGCATCC GTACTCTTGG	AGCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GCCACGATTA ACAAGGCAC TGACCCTCGT AACCTGGAA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAAC TAAAGCTCTG AGGCCAGCAG GGATAACATA CACCATCGCC CGGCATGGGT GGAGTTGGGA	120 180 240 300 360 420 480 540
50	Coding sequence of the control of th	11 TITTCCTTGG CANGTGGGAC CCATGGACCC TGAGCACAC CTGCTGCTGA CAGACCACA CTGCTGCTGA CAGCCCTTGC CTGCCCTTGC CTGCCTCCT TCACAGAGGG	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT GAATCTGCTA ACTGCCCAG GATCATGAAA AGAGTTTCCT AGGCAGCCTT CAGCATTTCC	31 AGGGCAGAGG GATCCTCAAA ATCTTTATTG CTCCTGCTGA AATGAGGCAG GACAAAACT CGGTTGAAAA CAGAAGGTCC CTCTGGCATCC GTACTCTTGG	AGCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GCCACGATTA ACAAGGCAC TGACCCTCGT AACCTGGAA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAAC TAAAGCTCTG AGGCCAGCAG GGATAACATA CACCATCGCC CGGCATGGGT GGAGTTGGGA	120 180 240 300 360 420 480 540
50	Coding sequence of the control of th	11 TITTCCTTGG CANGTGGGAC CCATGGACCC TGAGCACAC CTGCTGCTGA CAGACCACA CTGCTGCTGA CAGCCCTTGC CTGCCCTTGC CTGCCTCCT TCACAGAGGG	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT GAATCTGCTA ACTGCCCAG GATCATGAAA AGAGTTTCCT AGGCAGCCTT CAGCATTTCC	31 AGGGCAGAGG GATCCTCAAA ATCTTTATTG CTCCTGCTGA AATGAGGCAG GACAAAACT CGGTTGAAAA CAGAAGGTCC CTCTGGCATCC GTACTCTTGG	AGCTGGAGC GTAAGCCCCT AGGATGCCAT CTGATAATGA ATGAGCTCCG GCCACGATTA ACAAGGCAC TGACCCTCGT AACCTGGAA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAAC TAAAGCTCTG AGGCCAGCAG GGATAACATA CACCATCGCC CGGCATGGGT GGAGTTGGGA	120 180 240 300 360 420 480 540 600
50	Coding sequilibrium sequilibriu	11 TITTCCTTGG CAAGTGGGAC CATGGACC TGAGCACAC CTGCTGCTACA CAGCACACA CTGCTGCTACA CAGCACACA CTGCTCCTTGC CTGGTCTTGC CTGGCTCTCT TCACCAGAGG CTTTACCGG AGCCACACA GTGAGACACA TTGAGAGACAT TTGGCAAGACA TTGAGAACACA TTGAGAACACA TTGAGAACACA	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT GAATCTGCTA ACTGCCCAGG GATCATGAA AGAGTTTCCT AGGCAGCCTT CAGCATTTCC GATTACCAGC CCTGGTCATC ATCCAACTTT	31 AGGCCAGAGG GATCCTCAAA ATCTTATTG CTCCTGCTGA AATGAGGCAG GACAAAAACT CGGTTGAAAA CAGAAGGTCC GTACTCTTGG AAGTACCATGG AATACCATGG AAAAGCCTTG CTTCCTTAG CTCAGACGAG	AAGCTGGAGC GTAAGCCCT AGGATGCCAT CTGATAATGA ATGAGCTCGG GGCACGATAA GTGAGCTTGA ACAAAGGCAC TGACCCTCGT AACCTGGGAAT ACTACGGAAA ACAAATTGAA CTGGCAATAC CCGAGACCAA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC GGCCTGGAC TAAAGCTCTG AGGCCAGCAG GGATAACATA CACCATCOCC CGGCATGGGT GGAGTTGGGA GAAGTGGTG GGAGGTGAGG TTACCAACTC TCTTCAACTC	120 180 240 300 360 420 480 540 600 660 720 780 840
50	Coding sequence of the control of th	11 TITTCCTTGG CAGGTGGGAC CAGTGGACC TGAGCACACA CTGCTGCTGA GTTCTGAA GGTTTCTGAA GGTTTCTGAA GTTCCTGAGGACC TCACAGAGGG CTGCCTTGC CTGACCTTCC TCACAGAGGG CTTCACAGAGGA GTTTCACAGAGGA TCACGGAACAAT TTGGAAAGAA TTGGGAAAGAA	21 TOTGGGAGTG AGATACTGGA AGAGGGGGAGTG GAATCTGCTA ACTGCCCAGG GATCATGAAA AGAGTTTCCT AGAGGGGTT CAGCATTTCC AGGCAGCCTT GATTACCAGC CCTGGTCATC ATCCAACTTT CATCCGTGGC	31 AGGCCAGAGG GATCCTCAAA ATCTTTATTG CTCCFGCTGA AATGAGCCAG GACAAAAACT CGGTTGAAAA CAGAAGGTCC TCTGGCATCC GTACTCTTGG AAAAGCCTTG CTTCCCTTAG CTTCCCTTAG CTTCCCTTAG CTCAGACCAG GTCACTCTTAG CTCAGACCAG GTCACTCTTAG	AAGCTGGAGC GTAAGCCCT AGGATGCCAT CTGATAATGA ATGAGCTCG GGCACGATAA ACAAAGGCAC TGACCCTGGT AACCTGGGAA ACTACGGAAA ACTACGGAAA CTACGGAAATTGAA CTAGGCAATAC CCAGAGCCAA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC TAAGCTCTG AGGCCAGCAG GGATAACATA CACCATCGC CGGCATGGGT GAGTTGGTG GAGTTGGTG GAGTTGGTG TACCAACTC TCTTCAGTCA	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55 60	Coding sequence of the control of th	11 TITTCCTTGG CAGGTGGGAC CAGTGGACC TGAGCACACA CTGCTGCTGA GTTCTGAA GGTTTCTGAA GGTTTCTGAA GTTCCTGAGGACC TCACAGAGGG CTGCCTTGC CTGACCTTCC TCACAGAGGG CTTCACAGAGGA GTTTCACAGAGGA TCACGGAACAAT TTGGAAAGAA TTGGGAAAGAA	21 TOTGGGAGTG AGATACTGGA AGAGGGGGAGTG GAATCTGCTA ACTGCCCAGG GATCATGAAA AGAGTTTCCT AGAGGGGTT CAGCATTTCC AGGCAGCCTT GATTACCAGC CCTGGTCATC ATCCAACTTT CATCCGTGGC	31 AGGCCAGAGG GATCCTCAAA ATCTTTATTG CTCCFGCTGA AATGAGCCAG GACAAAAACT CGGTTGAAAA CAGAAGGTCC TCTGGCATCC GTACTCTTGG AAAAGCCTTG CTTCCCTTAG CTTCCCTTAG CTTCCCTTAG CTCAGACCAG GTCACTCTTAG CTCAGACCAG GTCACTCTTAG	AAGCTGGAGC GTAAGCCCT AGGATGCCAT CTGATAATGA ATGAGCTCG GGCACGATAA ACAAAGGCAC TGACCCTGGT AACCTGGGAA ACTACGGAAA ACTACGGAAA CTACGGAAATTGAA CTAGGCAATAC CCAGAGCCAA	GAGGGTGCAA CGGTGACTGG TAAGTATTTC TAAGCTCTG AGGCCAGCAG GGATAACATA CACCATCGC CGGCATGGGT GAGTTGGTG GAGTTGGTG GAGTTGGTG TACCAACTC TCTTCAGTCA	120 180 240 300 360 420 480 540 660 720 780 840 900
50	Coding sequi	INTERPRETATION OF THE PROPERTY	21 1 TOTIGGACTE GARACTIGA AGAGEAGT GARTCTGCA AGACTIGCA AGACTICCA AGACTITCC AGACTITCC AGACTITCC AGCAGCCT ATCAACTIT CATCACCT CATCACTIC CAT	31) AGGGCAGAGG GATCCTCAAA ATCHTEATAG CTCCTGCTAA AATGAGGCAG GACAAAAACT CTCTGGCATC GTACTCTTAG GAGTACCATGG AAAAGCCTTG CTTCCTTAG CTCTGGACAAG GTCACTGAGCA GTCACTGAGCA GTCACTGAGCA GTCACTGAGCA GTCACTGAGCA GTCACTGAGA GTCACTGAGA GTCACTGAGA GTCACTGAGA GTCACTGAGA GTGCTGGAGA	AAGCTGGAGC GTAAGCCCT AGGATGCCAT AGGATGCCAT ATGAGCTCCG GGCACGATRAA ACTAAGCACC TGACCCTCGT AACCTGGGAT ACTACGGAAA ACTAACTGAAC CCAGGCAATAC CCAGGCAATAC CCAGGCAATAC TGAGCCATTCAGC TGAGCCATTCAGC TGAGCCAAGCT TGAGCCATTCAGC TGAGCCAAG	GAGGGTGCAA CGGTGACTCG TAAGTATTTC GGCCTGGAC TAAGCCTGA GGATAACATA AGGCCAGCA GGATTAGGC GGAGTTGGG GAGTTGGG GAGTTGGG GAGTTGGG TAACAACTC TTACCAACTC TCTTCAGTCA AGTCAAGCTC TGTAAGGAGA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60	Coding sequilibrium sequilibriu	INTEGRAL AND AND AND AND AND AND AND AND AND AND	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT AGAGGAGCAGT ACTGCCAGA GATCTCCT AGAGGATTCC AGGAGTTCCT AGAGGAGCCTT AGAGGAGCCTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTC AGGCACACCAGC TGAACCCAGG TGAACCCAGG CTTCTTTCTTT	31 AGGCCAGAGG GATCCTCAAA ATCCTTATTG CTCCTGCTGA AATGAGGCAG GACAAAAACT CGGTTGAAAC CTCTGGCACC GTACTCTTGG AGTACCATGG CTCAGACGAG CTCAGACGAG GTCACTCAGA ATCCTGGAA ATCCTGGAA ATCCTGGAA ATCCTGGAA GAGACGGGGGAA	AGCTOGAGC GTAAGCCCT AGGATGCCAT CTGATAATGA ATGAGCTCGA GGCACGATGA ACAAAGCAC TGACCTCGGAA ACTAGGCTTGA ACTGGGAA ACTAGGAA ACAAATTGA CTGGGAA CCAGGGAA CCAGGGAA CCAGGGAA CCAGGGAA CAATTCAGA CTGGGAA CAATTCAGA CAATTCAGA CAATTCAGA CAATTCAGA CAATCTCAGC CAGGGCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCCAA CAGGCCCCCAA CAGGGCCCCCAA CAGGGCCCCCAA CAGGGCCCCCAA CAGGCCCCCAA CAGGCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCCC	GAGGGTGCAA CGGTGCAAC CGGTGCAAC CGCCTTGCAAC CGCCATGCAC CGCCATGCC CGCCATGCGC CGGCATGGGC CGAGTTGGGC CGAGTTGGGC CGAGTTGGGC TCTCCACTC TCTCACTC TCTCACTC TCTCAGTC CGTTACGAC CGTTACGAC CGTTACGAC CGTTACGAC CGTTACGAC CGTTACGAC CGTTACGAC CGTTACGAC CGTTACGAC CGTTACGAC CGAGGTTGCGC CGTTTACGAC CGTTACGAC CGAGGTTACGAC CGTTACGAC CGAGGTTACGAC CGTTACGAC CGAGGTTACGAC CGAGGTTACGAC CGAGGTTC CGTTTACGAC CGAGGTTC CGTTCACGAC CGAGGTT CGAGGTC CGAGGTT CGAGGTT CGAGGTC CGAGGT CGAGG CGAGGT CGAG	120 180 240 300 360 420 540 600 660 720 780 840 900 960 1020
50 55 60	Coding sequi	III II ITTTCCTTGG CAAGTGGAC CCATGGACC CCATGGACC CCATGGACC CTGGTCTGA CAGGACAAT GTGTTCTGAA GTGTCTTGAA GTGCCTTGC CTTGGCCTTCT CACAGGGG AGCCACGA AGGCACACT TGGGAAGGA CTCAGGCTTAGA CTCAGGGTTAA CCCCTGTAAG TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA AGGAGAAAGCT	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT AGAGGAGCAGT ACTGCCAGA GATCTCCT AGAGGATTCC AGGAGTTCCT AGAGGAGCCTT AGAGGAGCCTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTC AGGCACACCAGC TGAACCCAGG TGAACCCAGG CTTCTTTCTTT	31 AGGCCAGAGG GATCCTCAAA ATCCTTATTG CTCCTGCTGA AATGAGGCAG GACAAAAACT CGGTTGAAAC CTCTGGCACC GTACTCTTGG AGTACCATGG CTCAGACGAG CTCAGACGAG GTCACTCAGA ATCCTGGAA ATCCTGGAA ATCCTGGAA ATCCTGGAA GAGACGGGGGAA	AGCTOGAGC GTAAGCCCT AGGATGCCAT CTGATAATGA ATGAGCTCGA GGCACGATGA ACAAAGCAC TGACCTCGGAA ACTAGGCTTGA ACTGGGAA ACTAGGAA ACAAATTGA CTGGGAA CCAGGGAA CCAGGGAA CCAGGGAA CCAGGGAA CAATTCAGA CTGGGAA CAATTCAGA CAATTCAGA CAATTCAGA CAATTCAGA CAATCTCAGC CAGGGCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCCAA CAGGCCCCCAA CAGGGCCCCCAA CAGGGCCCCCAA CAGGGCCCCCAA CAGGCCCCCAA CAGGCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCCC	GAGGGTGCAA CGGTGCAAC CGGTGCAAC CGCCTTGCAAC CGCCATGCAC CGCCATGCC CGCCATGCGC CGGCATGGGC CGAGGTTGGGC CGAGGTTGGGC CGAGGTTGGGC TCTCCACTC TCTCACACTC TCTCACACTC TCTCAGTC TCTTCAGTC TCTTCAGTC TCTTCAGTC TCTTCAGTC TGTAGGAGT CGTTTAGGAGT CGTTTAGGAGT CGTTTAGGAGT CGTTTAGGAGT CGAGGTTAGGGGT CGTTTAGGAGT CGAGGTGGGGT CGTTTAGGAGT CGAGGTGAGGGGT CGTTTAGGAGT CGAGGTGGGT CGAGGTGGGGT CGAGGTGGGGT CGAGGTGGGGT CGAGGTGGAGT CGAGGT CGAGGTGGAGT CGAGGT CGAGGTGGAGT CGAGGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60	Coding sequilibrium sequilibriu	III II ITTTCCTTGG CAAGTGGAC CCATGGACC CCATGGACC CCATGGACC CTGGTCTGA CAGGACAAT GTGTTCTGAA GTGTCTTGAA GTGCCTTGC CTTGGCCTTCT CACAGGGG AGCCACGA AGGCACACT TGGGAAGGA CTCAGGCTTAGA CTCAGGGTTAA CCCCTGTAAG TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA AGGAGAAAGCT	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT AGAGGAGCAGT ACTGCCAGA GATCTCCT AGAGGATTCC AGGAGTTCCT AGAGGAGCCTT AGAGGAGCCTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTC AGGCACACCAGC TGAACCCAGG TGAACCCAGG CTTCTTTCTTT	31 AGGCCAGAGG GATCCTCAAA ATCCTTATTG CTCCTGCTGA AATGAGGCAG GACAAAAACT CGGTTGAAAC CTCTGGCACC GTACTCTTGG AGTACCATGG CTCAGACGAG CTCAGACGAG GTCACTCAGA ATCCTGGAA ATCCTGGAA ATCCTGGAA ATCCTGGAA GAGACGGGGGAA	AGCTOGAGC GTAAGCCCT AGGATGCCAT CTGATAATGA ATGAGCTCGA GGCACGATGA ACAAAGCAC TGACCTCGGAA ACTAGGCTTGA ACTGGGAA ACTAGGAA ACAAATTGA CTGGGAA CCAGGGAA CCAGGGAA CCAGGGAA CCAGGGAA CAATTCAGA CTGGGAA CAATTCAGA CAATTCAGA CAATTCAGA CAATTCAGA CAATCTCAGC CAGGGCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCCAA CAGGCCCCCAA CAGGGCCCCCAA CAGGGCCCCCAA CAGGGCCCCCAA CAGGCCCCCAA CAGGCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCCC	GAGGGTGCAA CGGTGCAAC CGGTGCAAC CGCCTTGCAAC CGCCATGCAC CGCCATGCC CGCCATGCGC CGGCATGGGC CGAGGTTGGGC CGAGGTTGGGC CGAGGTTGGGC TCTCCACTC TCTCACACTC TCTCACACTC TCTCAGTC TCTTCAGTC TCTTCAGTC TCTTCAGTC TCTTCAGTC TGTAGGAGT CGTTTAGGAGT CGTTTAGGAGT CGTTTAGGAGT CGTTTAGGAGT CGAGGTTAGGGGT CGTTTAGGAGT CGAGGTGGGGT CGTTTAGGAGT CGAGGTGAGGGGT CGTTTAGGAGT CGAGGTGGGT CGAGGTGGGGT CGAGGTGGGGT CGAGGTGGGGT CGAGGTGGAGT CGAGGT CGAGGTGGAGT CGAGGT CGAGGTGGAGT CGAGGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	120 180 240 300 360 420 540 600 660 720 780 840 900 960 1020
50 55 60 65	Coding sequi	III II ITTTCCTTGG CAAGTGGAC CCATGGACC CCATGGACC CCATGGACC CTGGTCTGA CAGGACAAT GTGTTCTGAA GTGTCTTGAA GTGCCTTGC CTTGGCCTTCT CACAGGGG AGCCACGA AGGCACACT TGGGAAGGA CTCAGGCTTAGA CTCAGGGTTAA CCCCTGTAAG TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA TACATGAAGGA AGGAGAAAGCT	21 TOTGGGAGTG AGATACTGGA AGAGAGCAGT AGAGGAGCAGT ACTGCCAGA GATCTCCT AGAGGATTCC AGGAGTTCCT AGAGGAGCCTT AGAGGAGCCTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTT ATCCAACTTC AGGCACACCAGC TGAACCCAGG TGAACCCAGG CTTCTTTCTTT	31 AGGCCAGAGG GATCCTCAAA ATCCTTATTG CTCCTGCTGA AATGAGGCAG GACAAAAACT CGGTTGAAAC CGGTTGAACC GTACTCTTGG AGTACCATGG AGTACCATGG CTCAGACGAG CTCAGACGAG GTCACTCAGAA ATCCTGGAA ATCCTGGAA ATCCTGGAA ATCCTGGAA GAGACGGCTGGAAA	AGCTOGAGC GTAAGCCCT AGGATGCCAT CTGATAATGA ATGAGCTCGA GGCACGATGA ACAAAGCAC TGACCTCGGAA ACTAGGCTTGA ACTGGGAA ACTAGGAA ACAAATTGA CTGGGAA CCAGGGAA CCAGGGAA CCAGGGAA CCAGGGAA CAATTCAGA CTGGGAA CAATTCAGA CAATTCAGA CAATTCAGA CAATTCAGA CAATCTCAGC CAGGGCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAATCTCAGC CAGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCAA CAGGGCCCCCAA CAGGCCCCCAA CAGGGCCCCCAA CAGGGCCCCCAA CAGGGCCCCCAA CAGGCCCCCAA CAGGCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCAA CAGGCCCCCCCC	GAGGGTGCAA CGGTGCAAC CGGTGCAAC CGCCTTGCAAC CGCCATGCAC CGCCATGCC CGCCATGCGC CGGCATGGGC CGAGGTTGGGC CGAGGTTGGGC CGAGGTTGGGC TCTCCACTC TCTCACACTC TCTCACACTC TCTCAGTC TCTTCAGTC TCTTCAGTC TCTTCAGTC TCTTCAGTC TGTAGGAGT CGTTTAGGAGT CGTTTAGGAGT CGTTTAGGAGT CGTTTAGGAGT CGAGGTTAGGGGT CGTTTAGGAGT CGAGGTGGGGT CGTTTAGGAGT CGAGGTGAGGGGT CGTTTAGGAGT CGAGGTGGGT CGAGGTGGGGT CGAGGTGGGGT CGAGGTGGGGT CGAGGTGGAGT CGAGGT CGAGGTGGAGT CGAGGT CGAGGTGGAGT CGAGGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGTGGAGGAGT CGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	120 180 240 300 360 420 540 600 660 720 780 840 900 960 1020
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50 55 60 65 70	Coding seq. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Jennes 1: TITTCCTTGG CAMAGGACACA CATGGACC TGAGCACACA CATGGACC TGAGCACACA CATGGACC TGAGCACACA CATGGACC TGAGCACACA CATGGACC TGAGCACACA CATGGACC TGAGCACACA CATGGACACA CATGGACACA CATGGACACACA CATGGACACA CATGGACACACA CATGGACACACA CATGGACACACA CATGGACACACA CATGGACACACACACACACACACACACACACACACACACA	152 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	31 AGOUCAGAGG GATCCTCAAA ATCTTAATA CTCCTCAA ATTAGACCA GACAAAACT CCGCTGAAAACT CCGCTGAAAACT CCGCTGAAAACT CTCGCACA ATCACCATGA AATAGACCTC AATAGACCTC AATAGACTC GTTCCTTAG CTCCTCTTAG ATCCTCGGAA ATCCTCGGAA ATCCTCGGAA TCCTCGGAA TCCTCGGAA TCCTCGGAA TCCTCGGAA TCCTCGGAA TCCTCGGAA TCCTCGGAA TCCTCGGAA TCCTCGGAA TCCTCTCGGAA TCCTCTCTTAG TCCTCTTAG TCCTCTCTTAG TCCTCTTAG AGGREGACCE AAGGREGACCE AAGGREGACCE AAGGREGACCE AAGGREGACCE ACAAAGGREGACCE ACAAAGGRACCACA ACAAAGGRAC ACAAGGRAC ACAAAGGRAC	GAGGGTGCAA GAGGGTGCAA GAGGGTGCAA GAGGGTGCAA GAGGCAACAA GAGCAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAACAACAACAACAACAACAACAACAACAAC	120 180 240 300 480 540 660 720 960 1020 1140	
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50 55 60 65 70 75	Coding sequi- ATRIGUTOCAC ANALOSTIC GENTOCTOCAC ANALOSTIC GENTOCTOCAC GENTOCTO	Janes 11: 11 11 11 11 11 11 11 11 11 11 11 11	152 21 1 TOTTOGGAGTO AGATACTOCA AGATACTOCA AGATACTOCA AGATACTOCA AGATACTOCA AGATACTOCA AGATACTOCA AGATACTOCA AGATACTOCA AGATACCAGA AGATACCAGA AGATACCAGA AGATACCAGA AGATACCAGA AGATACCAGA AGATACCAGA AGATACCAGA AGATACCAGA AGATACCAGA AGATACCAGA AGATACCAGA AGATACAGAC AGATACCAGAC AGATACCAGAC AGATACCAGAC AGATACAGAC CACACACACACACACACACACACACACAC	31 AGGICAGAGG GATCCTCAAAA CATCATCAAAA CATCATCATAAAA CATCATCATCAAAAA CATCATCATCAAAAA CATCATCATCAAAAA CATCATCATCAAAAA CATCATCATCATCATCAAAAAA CATCATCATCATCATCATCATCATCATCATCATCATCATC	AGGREGACCE AAGGREGACCE AAGGREGACCE AAGGREGACCE AAGGREGACCE ACAAAGGREGACCE ACAAAGGRACCACA ACAAAGGRAC ACAAGGRAC ACAAAGGRAC	GAGGGTGCAA GAGGGTGCAA GAGGGTGCAA GAGGGTGCAA GAGGCAACAA GAGCAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAA GAGCAACAACAACAACAACAACAACAACAACAACAACAAC	120 180 240 300 480 540 660 720 780 840 900 900 1020 1080 1140
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50 55 60 65 70 75 80	Coding sequi-	HERCE 1: THITTCCTTGG CAAGTGGAC CAAGTGGAC CAGGACAA GOTTCTGAA AGCCCTGTAAG TACATGAGGA AGCCCTGTAAG TACATGAGGA AGCCTGTAAG TACATGAGGA AGCCTGTAAG TACATGAGGA TACATGAGA TACATGAGGA TACATGAGA TACATGAGA TACATGAGGA TACATGAGA TAC	152 21 1 TOTOGGAGTO AGATACTICA AGAGAGGGAT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGGTT AGAGAGGTT AGAGGTT A	31 AGGICAGAGG GATCCTCAAAA CATCATCAAAA CATCATCATAAAA CATCATCATCAAAAA CATCATCATCAAAAA CATCATCATCAAAAA CATCATCATCAAAAA CATCATCATCATCATCAAAAAA CATCATCATCATCATCATCATCATCATCATCATCATCATC	AGGREGACCE AAGGREGACCE AAGGREGACCE AAGGREGACCE AAGGREGACCE ACAAAGGREGACCE ACAAAGGRACCACA ACAAAGGRAC ACAAGGRAC ACAAAGGRAC	STATEMENT OF THE STATEM	120 180 240 300 480 540 660 720 780 840 900 900 1020 1080 1140

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_					ACCGCCATGT		180
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						GATTGAGAAA	\$ 360
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13					ACCTTCAGGT		900
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Seq ID NO: 478 DNA sequence Nucleic Acid Accession #: XM_044533

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                               TRETICITAT GIAMACTARG CONTITUTTI NAMARCAMI TOCAMITRIS MARCHARAT 3066 AGRAGGARA GATROCATO GARROCAGO CACCOGGOT CICCARTCA TOGATOCA 3120 GOGUTUCTO GARROCATO AMOTGOTTO TOTAGARCAG AGTTGGAMAC COTCACCAC 110 TOGACCTOTTO ACTOCAGO TOGATOCATO TOCATOCAGO TOGATOCAGO 
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                                CHARACCARC TYRARCTREAU TRANTICTRE CITTECRATE ASCURAGANT GRATTETTS
CTGCCGTGGT CCCACCACT CAGGGACCA ASGCCTAGGT TGGCACTGG GCCCTACCA
GCGTCCTGGG TCGAACCCAA CTCCTGGAC TTTCCAGCCT GTATCAGCGT GTGGCCACA
GAGAGGACAG CGCGAGCTCA GGAGAATTT CGTGACAATG TACGCCTTTC CCTCAGAATT
                                                                                                                                                                                                                                                                                                                                                  3360
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                                                                                                                                                                                                                                                                                                                                                  3480
 30
                                CAGGGAAGAG ACTGTCGCCT GCCTTCCTCC GTTGTTGCGT GAGAACCCGT GTGCCCCTTC
                                                                                                                                                                                                                                                                                                                                                  3540
                                CARCRARMING AUTOICECT CONTETTED ACTORAGES ONGACCOST GROCECTED CONCENTRAL CACCOCTOR CONTETTED ACTORAGES GRAGGARCTAN CTGCACCOCTO GTCCTCTCCC CAGTCCCACT CTRAGGGATA
                                                                                                                                                                                                                                                                                                                                                  3600
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                                TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTTATAAG
ATGCACTTTA TGTCATTTT TAATAAGTC TGAAGAATTA CTGTTT
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                                  Sec In NO: 479 Protein semier
                                Protein Accession #: XP_044533.3
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 40
                                MIRTAMGLES WLAAPWGALP PRPPLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPPL
REFARHISMY TALLLSROOR TLYVGAREAL FALSSMISFL PGGEYGELM GADAEKKQQC
SPKGGDQRD CONYIKILLP LSGSHLFTCG TAAFSPMCTY INNEMPTLAR DEKGNVLLED
                                                                                                                                                                                                                                                                                                                                                        120
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                               SPECINOPIDE CONTISTLIB LOSSHIFTCO TARFSHOTT INHOSPITLAR DEKONVLED (GRIGOEPOR) PETSIALVOR ELITOTUSES (COMENTESS GIBERTETS SIMMIQUES) VASANIPESL OS LOGODORI YPPESCOUR FEFENTIUS RIALICEGOS CORRICAGIM FEFENCIAL RIALICEGOS CORRICAGIM FEFENCIAL RIALICEGOS CORRICAGIM FEFENCIAL RIALICEGOS CORRICAGIM FEFENCIAL RIALICEGOS CORRICAGIM FEFENCIAL RIALICEGOS CORRICAGIM FEFENCIAL RIALICEGOS CORRICAGIM FEFENCIAL RIALICEGOS CORRICAGIM FEFENCIAL RIALICEGOS CORRICAGIM FEFENCIAL OPOLYTORIA VIRUPCHINI TINDIFICATION GELISARAVSIA PRIVILIFICACIO RELISARAVSIA PRIVILIFICACIO RIALICEGOS CARRICAGIM FORMATION FORMATION CORRICAGIO LIBERCOSTA PRIVILIFICACIO LIBERCOSTA CORRICAGIM FORMATION CARRICAGIM FORM
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                                  EGFOOLVASY CPEVVEDGVA DOTDEGGSVP VIISTSRVSA PAGGKASWGA DRSYWKEFLV
                                                                                                                                                                                                                                                                                                                                                          720
                                  MCTLPVLAVL LPVLPLLYRH RNSMKVPLKQ GECASVHPKT CPVVLPPET PLNGLGPPST
PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV
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                                120
 65
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                                GRIGHATTIGO CHRATECTET MATENTETE CATEGORIOS MATENTATA CONSIDERACIONA MAGICARRAN ATTOCCOTTA ROSCOPICARIO GRADAGOTTA ROSCOTTOS CONSIDERACIONAS CONSIDERACIONAS CONSIDERACIONAS CONSIDERACIONAS CONSIDERACIONAS CONSIDERACIONAS CONSIDERACIONAS CONSIDERACIONAS CONSIDERACIONAS CONSIDERACIONAS CONTROLOGRAM CONTROLOGRAM CONTROLOGRAM CONTROLOGRAM CONTROLOGRAM CONTROLOGRAM CONTROLOGRAM CONTROLOGRAM CONTROLOGRAM GONTROLOGRAM GONTRO
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                                   TCAGCCCACC CTTGGGTCCG GGCCAACTCT CGGAGGGTGC TGCCTCCCTC TGCCCTTCAA
                                                                                                                                                                                                                                                                                                                                                     1080
  80
                                  TETGTCGCCT GATGGTCCCT GTCATTCACT CGGTGCGTG TGTTTGTATG TCTGTGTATG
TATAGGGGAA AGAAGGGATC CCTAACTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT
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10	Nucleic Aci	482 DNA sec id Accession dence: 381	#: AKO5566	3			
15	1 AGAACGGCTT	11 CCGGCGGGAG	21 CTGTGCAGCT	31 CCTTATCATG	41 GGGACAATTC	51 ATCTCTTTCG	60 120
	CCGBAGGTCC	AGATCCTTTT TGGAAGATAC TGCAGTTCTA TTTAGTTTAA	TGCTCTTTGG	TGTAATAAAC	TTGATATGTA	CTCCCTTCCT	120 180 240 300
20	AGTOTTEGCA	TATTCATTTG CAGTTGGGAG ATACACACGG ATGCTTTCTA	GGTTTGAAAG	ATTAGAAGAA ATTAAAAGAA	CTGGCTGTAT	GCTTTTTGGA	360 420 480 540
25	TACGAGCTGG GGGACTTAGC AGCATTTGCT	CTTCAAGAGC AGTATCTTCC CTTTGTATTA	ATGTTGCAGA TTCCCCGAAT CATATATGCT	TCTTAGTCGA GAATCCATTT CATTGAAATT	AGCTTGTGTG GTTTTGATTG AATAATTATT	GAATTATTCC ATCTTGCTGG TTGCCGTAGA	600 660 720 780
30	GTACAGTGGG ACTCATCAGA GACCCTAGGT	GCTATAGCTA AAAGTCTTAC GAGGTATCTA TTTGGCTCAT	TCCAGACAAC CCTTAGATGG TGGCTGGATC	ACCACCCCAT AGTTTTAGAA AGTGCATGTA	GTTATTGGTC GTCCGAAATG AGAATTCGAC	AGTTGGACAA AACATTTTTG GAGATGCCAA	900 960 1020
	TGTTCAAATT CAATGTCCTA TGATTTGAAC	GTTCTTGCTC TTCAAGGATG AACTTTTCAG CCAGTTACAT CCTGGGAAAA	ACTGGATTAG ATCATCACGT CAACTCCAGC	GCCTGCCTTA AATCCCAATG TAAACCTAGT	TTGTCTGGGC CCTCTTTTAA AGTCCACCTC	CTGTTGCAGC AGGGTACTGA CAGAATTTTC	1080 1140 1200
35	TTATGGTTTT	GGAATTGGAG	CANCTCAAGG	ACCTTACAGC	AGCATGCTTA	ATCAAGGACT	1260 1320 1380 1440
40	TGTTTAATCA TATGAAACTA GCTTTAAATA	ACTAATAATA TATTGACTCC TTTACTCTAA TATTTTTGTA GGCTTCCTTT	ATGTTAGATA AAATGTATTT AGAAAATGTG	ATAGTAGTCT GTGACAGTGA TTTCTTTAAA	TGTTCACATT AATCCTCGTA TTTGGATTTT	AATGTTAAAG GGTATCTTTG	1500 1560 1620 1680
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55	AATTGCTAAA TTTTTAGCAG	TTTTTCTTTG AAATTTTGGA AAAGTTTCTC	AGGTTCTCCT	GAATTATGTC	TTTGAATTTT	AAAGCAAAAA TAATTATCAA	2340 2400
	Seq ID NO: Protein Acc	483 Protein cession #: 1	sequence				
60	1 MGTIHLPRKP	11 QRSFFGKLLR LFSLMTCLIS	21 EFRLVAADRR	31 SWKILLFGVI	41 NLICTGFLLM	51 WCSSTNSIAL	60 120
65	ESAERPLEQP RSLCGIIPGL GTMYPMSVYS VRIRRDANEQ MPLLKGTDDL	EIHTGRLLVG SSIFLPRMNP GKVLLQTTPP MVLAHVTNRL NPVTSTPAKP	TFVALCENLE FVLIDLAGAP HVIGQLDKLI YTLVSTLTVQ SSPPPEFSEN	TMLSIRNKPF ALCITYMLIE REVSTLDGVL IFKDDWIRPA TPGKNVNPVI	AYVSEAASTS INNYFAVDTA EVRNEHFWTL LLSGPVAANV LLNTOTRPYG	WLQEHVADLS SAIAIALMTF GFGSLAGSVH LNFSDHHVIP	180 240 300 360 420
70	Seq ID NO: Nucleic Ac:	PGIGATQGLR 484 DNA ser id Accession uence: 19	quence				
75	1 -	11 GGGAGCTGAG	21 GBAGGCCGAG	31 -	41 TOORGGOOG	51 GACCCCTCCC	60
80	CCGCGGGGGC GCCGTGGGCA CGGCCCACTG GGCTGCGGCG GGACCCCGGG	GTAGCGCGCC AGAGCAGCCT CGCTGGACAC GGGCTGTGCA GAGGAGACTG	CCCAGAGCTG CATCGTCAGC CTTCTCTGGT CCGGGGAGCT GAGCAGGCCC	GGCATCAAGT TACACCTGCA ACGTACGTTC GGGGCGGGCG CGAGGTGGCG	ATGGGTACCC AATGGCCCGT TCTCGGCGGG CTGGTGCGGC	GGGCGACGC CGCGCGCTAC GCGGCCGCGT AGGGCGCAGA CCAGGACGCT	120 180 240 300 360 420
85	CCGGTGCGCA CTTTGCTACC TTTCAAAACA	CAGGCTCTCC TTGAGCTCTG CGGATACCGA TCACAGAGAA TGGGCACCCA	GGACACAGCG TGTCTTCCTG ATGGCTGCCC	GGACAGGAGG GCGTGCTTCA GAGATCCGCA	GCGTGGTGCA CGCACAACCC	GCCCAGCTCC CCAGGCGCCT	480 540 600 660

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	GCCAAAGGTG	CTATTCTCAG TGCGCACCCT	CTCCCGCTGC	CGCTGGAAGA	AGTTCTTCTG	CTTCGTTTGA	
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	MPPRELSEAE	PPPLRAPTPP	PRRRSAPPEL	GIKCVLVGDG	AVGKSSLIVS	YTCNGYPARY	60 120
	RPTALDTFSG	TYVQSPVRPR	GCGGAVHRGA	GAGVSAGGRR	GPRGGDWSRP	RGGAGAAQDA	180
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25	GTGCGCACCC	TCTCCCGCTG	CCGCTGGAAG	AAGTTCTTCT	GCTTCGTTTG	A	
35	Com ID NO.	487 Protei	- romionce				
	Protein Ac	cession #:	KP 063832.1				
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40	į.	11	21	31	41	51	
40	WDDDIT COAT	PPPLRAPTPP	PROPERTY.	CINCAL AGDG	AUGKSSI-TVS	YTCNGYPARY :	60
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50 55 60	Seq ID NO: Nucleic Ac Coding seq I GCACCUATT ACATGCOC CACGATGGCA ACTGCACCAA ACAGTAAAAA ACAGTAAAAA ACAGTAAAAAA ACAGGGC ACTGCACCAGGTAACACCC CCACGGGTAACA	QKNLKEVPDS 488 DNA se sid Accessio Luence: 64 11	ATLEATERNA quence n #: NM_01: 1314 21 COGGACTTOS GSACATAANA ANGATTCATG TACCCAGCS ACCARGCTTA AACCAGGCC CCCTRAGCTTA AACCAGTTCA CACCGTTCCA CACTGCCTCCA ACTGACTTCA ACCAGTTCA	31 COGCACGCTO GOGGCTCTTOCAGAAA AAACCTGTCO GATGGTCATA ACTACAAAA GCCCTTATT TCAACCGTCA GCACCTTATT CATGCCOCAG ACGTTCTAAACGTCAACAGCTCATGTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGCTAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAACGTTCATGTTCTAAAAAAAA	41 	51 	120 180 240 300 360 420 480 540 660 720 780
50 55	Seq ID NO: Nucleic Ac Coding seq I GGCACCGATT ACCATGGCCC CACGATGGCA CCTCACCGAA ACTACAGCA GTTACTAAAA ATTACTACA ACTACACCA ACAACCGGC CCACGATGGCA CCACAGCGC CACAACCGC CCACAGCGC CCACAGCGC CCACAGCGCC CCACAGCCC CCACAGCGCC CCACAGCCC	488 DNA se sid Accessio puence: 64 11 GGGGGCCTGG GGGAGCTCAG GTAAATGAG CTTTCCAACAAG TTTCAACAAG TTTCAACAG GTAACAGAG CATACAGAG CATACAGAG CATACAGAG GTAACAGAG GTAACAGAG GTAACAGAG GTAACAGAG GTAACAGAG GTAACAGAG GGAGAGCCTAG GGAGAGCCTAG GGAGAGCGTG TCAAGACTAG GGAGAGGGGG TCAAGACTAG GGAGAGGGGG TCAAGACTAG TCAAGACT	quence n #: NM_01. 1314 21 CCGGACTTCG GGCGGGGC GGCATAANA ANGATTCATG TACCCAGCA AACCCAGCC CACCAGCTTCA AACCCAGCT CAACCCACC ACCTGCTTCA ACCCAGCTCCA ACCCAGCTCCA ACCCAGCTCCA ACCCAGCTCCA ACCCACCACCACCACCTCCAATTTATCAGA	31 1 CCGCACGCTG GCGCTCTTCG GTTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAA ACACCCAACA GCCCCTATT TCAACCGTCA GCAACTTTAT CATGCCCCAG ACGGTTCCTG GTTCTTAAACG GACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	41 CAGAACCTCG COTCCCTGGC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACTCACACAC CACTGCACC GACTACACAC GACACACAC GACACACAC GACACACAC GACACACCC GACACCCC GAGCAGCAC GACCACCCC GAGCAGCACCC GAGCAGCACCC GAGCAGCACCCC GAGCAGCACCCC CAGTTTTTC	51 CCCAGGGGCCC GGTAATTTN TTCTCAACCT TAAGCAAGCA AACAGGGGCCA AGCTCCTCCA AGCTCCTCCA GGCACAAAGC AGCTGCCAC TGCACCTCAC TGCACCTCAC TGCACCTCAC TGCACCTCAG CTGTATAAAA ACCTCGAGGAGA	120 180 240 300 360 420 480 540 600 660 720 780
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50 55 60 65	Seq ID NO: Nucleic Ac Coding seq	GENERAPPS 488 DNA se id Accessio puence: 64 11	ATLISATIERIA quence n #: NN_01 314 21 1 COGGGOGGCC AGCANAGCA GGACATAMA AGATTCAC TACCCCAGGC CCCTAGCTTA AACCAGGC CCCTAGCTTA AACCAGGC AGCACAAGCA GGACATAMA GGACACGAGC GGACATAMA CCAGGCC GGACATAMA CCAGGCC CCAGGCC CAGGCC AGCTTCA CACCCCAGGCC AATTATCAG GGACACGAGC GGACACGAG GGCGCAGTTC GGGGCGCAGTT GGGGCGCAGT GGGGGGCCAT GGGGGCGACT GGGGGGCGAT GGGGGGCGAT GGGGGGCCAT GGGGGGCCAT GGGGGGCCAT GGGGGGCCAT GGGGGGGCCAT GGGGGGCCAT GGGGGGCCAT GGGGGGCCAT GGGGGGCCAT GGGGGGCCAT GGGGGGGCCAT GGGGGGGCCAT GGGGGGGCCAT GGGGGGGCCAT GGGGGGGCCAT GGGGGGGCGAT GGGGGGGGCAT GGGGGGGGCAT GGGGGGGGCAT GGGGGGGGCAT GGGGGGGGCAT GGGGGGGGAT GGGGGGGGAT GGGGGGGGAT GGGGGGGG	31	41 CAGAACCTCG COTTCCTGGG CAGAGATTA AGCAACCAG ACCACACAG ACCACACAG GCCACACAG GCAACACG GAAAGAGG GGCCACCCT GAAGAGGG CATTTACCA ACTGGGCATAGCAC ACTGGGCACACAG CGATTGGCAC ACTGGGCACACAG CGATTGGCACACAG CGATTGCACACAG CATTTACCAG CATTACCAG CATTTACCAG CATTTACCAG CATTTACCAG CATTTACCAG CATTTACCAG CATTACCAG CATTTACCAG CATTTACCAG CATTTACCAG CATTACCAG CAT	51 CCCAGGGGCCC GOTARTTTIS TTCTCAACCT TAAGCAAGCA AACAGGGGC CACCAGCCGA AACAGCGGCC AACATCACC TGGGAACACC GCACATCACC TCGGACACCA ACTCGGACCA CCTCAACCCC TCGCACCCCA CCTCAACCCC TCGCACCCCA ACCTCGGAGA CCTCAACCCCA GGATGAAAATCC GGATGAAGAA AACAGTTTAC CTTCAACTGC CTTCAACTGC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
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50 55 60 65 70	Seq ID MO, Nucleic Recognition and Part Part Part Part Part Part Part Part	485 DNA se id Accession de la constitución de la co	ATLSATERIA Quence 1 9: NM_01: 21 COGGACTTOS GGGAGGGC GGACTANAN ANGATTANG GGACTANG GG	31 COCCACCTO GOOGLETTICA AND COCCACCTO GOOCLETTICA AND ANACCTOTICA GOOCLETTICA CATALON ANACCTO AND COCCACCO	41 CAGAACCTCG COTCCCTGGC COTCCCTGGC COTCCCTGGC COTCCCTGGC COTCCCTGGC COTCCCTGGC COTCCCTGGC COTCCTGGC COTCGGGCATC GGCATACCGGC GGAACGCGC GGAACGCGC GGAACGCGC GGAACGCGC GAACGCGC GAACGCGC CATTTCCGGCATC CATTTCGGCATC CATTTCGGCATC CATTTCGGCATC CATTTCGGCATC CATTTCGGCATC CATTTCGGGCATC CATTCGGGCATC CATTTCGGGCATC CATTTCGGCATC CATTTCGGGCATC CATTTCGGGCATC CATTTCGGGCATC CATTTCGGGCATC CATTCGGGCATC CATTTCGGGCATC CATTTCGGGCATC CATTTCGGGCATC CATTTCGGCATC CATTTCGGGCATC CATTTCGGGCATC CATTTCGGGCATC CATTTCGGGCATC CATTTCGG	S1 COGNOCICE COCNOCICE COCNOCICE COCNOCICE ACROCICE ACROCICE COCCOCICE ACCOCICE COCCOCICE ACCOCICE COCCOCICE COCOCICE COCOCICE COCCOCICE COCCOCICE COCOCICE COCOCICE C	120 180 240 300 360 420 480 660 660 720 780 960 1020 1140 1260 1320
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50 55 60 65 70 75 80	Seq ID NO. Nucleic Accounts Seq ID NO. Nucleic Accounts GOTHER GOTHER GOTHER ACCOUNTS ACCOUNT	488 DNA se id Accessio Lagorita (1986) 11 12 13 13 14 15 16 16 16 16 16 16 16 16 16	ATLEATIERA Quence n #: NM_01. 3114 21 1 COUGACTTOS GEGGGGGGC AGCAMAGGA AGCAMAGGA AGCAMAGGA AGCAMAGGA AGCAMAGGA AGCAMAGGA AGCAGGGA AGCAMAGGA AGCAGGAGA AGCAGAGAA AGCAGGAGA AGCAGAGAA AGCAGGAGA AGCAGAGAA AGCAGGAGA AGCAGAGAA ACCAGAGAA ACCAGAA ACCAGAGAA ACCAGAAA ACCAGAGAA ACCAGAAA ACCAGAAAA ACCAGAAA ACCAGAAAA ACCAGAAAA ACCAGAAAA ACCAGAAAAA ACCAGAAAAAA ACCAGAAAAAA ACCAGAAAAAAAA	3198.1 31 1000CCCCCCCAMA 31 1000CCCCCCCAMA 31 1000CCCCCCCAMA 31 1000CCCCCCCAMA 31 1000CCCCCCCAMA 31 1000CCCCCCCAMA 31 31 1000CCCCCCCAMA 31 31 31 31 31 31 31 31 31 3	41	51 COMMODICATE COMMODICATE COMMODICATE THATGAMEA ANGEGGGGG CACCAMICAC CACCAMICA CACCAMICAC CACCAMICA CACCAMICAC CACCAMICA	120 180 240 300 420 480 660 660 660 960 1020 91 1080 1140 1200 1200 1200 1320 1340 1560 1680 1740 1800 1800 1800 1800 1900 1900 1900 190

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50				***************************************			
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		493 Protein					

Seg ID NO: 493 Protein sequence Protein Accession #: NP_000568.1

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85	CCACCCCCC	CTGGATAGTT	AAGGGCTTTT	CCAAACATGC	ATCCATTTAC	TGACACTTCC	3000
00	TOTAL CONTROL OF THE PARTY OF T	CATGGAGAGC	TOTTOGCTCC	TCCCAGATGG	CTTCGGAGGC	COGCAGGGCC	3060
	CACCTTOCAC	CCTGGTGACC	TCCTGTCACT	CACTGAGGCC	ATCAGGGCCC	TGCCCCAGGC	3120
		COLONICACC	- 501010101				

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10	TCCTTGTATG	AATAAAAGGC	TGGAAACCTA	AA AA	GIGACGIGIG	TICITITIONS	3000
	Seq ID NO: Protein Acc	495 Protein cession #: N	Bequence P_002072.1				
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25	RGRYLPEVMG ASDDGSGSGS	DGLANQINNP	EVEVDITED	MTIRQQIMQL	KIMTNRLRSA	YNGNDVDFQD	480
20	Nucleic Ac	496 DNA sec id Accession Lence: 40.10	#: NM_001	650.2	1		
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70	Nucleic Ac	498 DNA se id Accessio quence: 11	n 🖟: AB020	684.1			
75						51 TTTTGGCCAG AGATATGTTG	60 120
80	GACGGTTACC TGCTTGCTTT CATATATGGC	AGAGGAGAAG TATGTTGCTG ACATATTTAA CATGGAGAGT	GACTCAGTCC TAATTTTTAT GTGGCAGCCC GTACCCGTGT	TATTGAAAGG TTTAAATGGA ATTAGGAGGG AATGTGGACA	TGTGAAGGAT CTAATGATGG CTGGTTACAG CCACCTCTCC	TGGGAGATCC	180 240 300 360 420
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	CATCCCCACC	ATGGCAAGTG	TTARGETETE	TECACTTCES	CCCATTGTGA	ATCATCCACA	1440
	CATGCCCACG	GCAGGCTTGA	CLOCOCICIC	TOCACTICOO	TACTOR ATTOR	ATACTCCCAA	1500
	TTATGAAGAC	GCAGGCTTGA	GAGCCAGAAC	MONAMINGIA	COCCUPATION	ALMOTOGOMA	1560
15	AGCAGCCGAA	GAAGTGAAGC TGTGTAAGAA	GAGAACIGAT	ANAGIIANAA	GIGMACIAII	MONTTOTAGA	1620
13	AGAGTCATGG	TGTGTAAGAA	GATCCAAGCC	TGGTTGCAGT	ATGCCTGAAA	TTTGGGATGT	
	AGAAGATCCT	GCCAATGCTG	GGAAAACTCC	CITATGTAAC	CTCTTGGTGA	AGGATTCCAA	1680
	ACCTCACTTC	ACCACTGTAT CATGACCTGC	TCCAGAACAG	TGTTTACAAA	GTCCTAGAAG	TTGTAAAAGA	1740
	ATGACTGCTA	CATGACCTGC	TGCCTACGGA	GAACTACATC	TGTAATGGTT	TTAATGTTTT	1800
	GCTAAGTCAT	GTGTTGTTCA	TATCCCAAAA	ACTITITATAG	GTAACTGTTT	TCAAATAGAA	1860
20	AACCTTTTAT	TTGGTCAATT	TGAATGTCAT	TCTAATTATA	AAAATGACTT	ACACCTTTAT	1920
	CAATTGGTTA	CTATTTCAAT TAATATTTGT	GCACCCTTTA	AAATTTGCTA	TGCAAATGAG	TATATGCTTG	1980
	TACTTGACTT	TAATATTTGT	GCTAAAGTGA	GCAAAGCTAC	CTGTATAAAG	AAAACACAGT	2040
							2100
	TATAGTGTAA	GAACTATTAA AGTGATTGTA	TOCCCCTTGC	TTCTTTTTTC	TGCCTCTTGC	TCTTGTCTTT	2160
25	TOGACATTTC	ACTGATTGTA	AGTTCTTCGG	TCATGTCAGC	CCCTGTCATC	AACTTGAGTT	2220
							2280
	CERCECCCCC	TTTTGTTCTC GGACCTTGTG	TYPETTY	TTAATCAACC	THEFT	CATTATTAAT	2340
	CITOTOCCCI	CCACCTTCTC	CTTACCANAT	TOCCTTANCE	TOTAGOCATA	TOCCATTATO	2400
	COORTCICIT	CTCTCTCTCT	CHINGGAMAI	CTCCTTAACT	CTTCCCCATA	TTTTCTYTCA	2460
30	GIGICICITI	CICICICICI	CTIGCTCTCT	PAGE POMPON	TA TOCCOMIN	TTTABARAAA	2520
30	AATAAGTACT	GTTTACTCAT ACTGTATTTT	TIMGTIGCTI	ATCAAGIACI	TATICITION.	TITIOOON AMAG	2580
	ATTAATGGTA	CTTTAAAGTT	TCTCATTTTT	AGCATTATTC	AMAIGITIAL	ATTITANTAC	2640
	CTTTAAACCA	ATATAGTGCA	TITTCATGIT	TAATTATAGT	TITANGANAA	ACTATTTGA	2700
	ACAACCCCAA	ATATAGTGCA	TCTAGAAACT	AATGTATATT	TGATTAGACA	CATTIALAG	2760
35	TGGAACAGTA	GACTOTAGTA TGCTGTCAAA	CATGGTAATT	TITCITITAC	TATTAAGATA	CANTAGONACA	2820
33	TGACTAATTT	TGCTGTCAAA	AATGTAAAGA	ATAATGATAA	ATGGAGTTTT	TTATATTTTA	
	CTTTTAAGAT	TGCCTGTCTT	TAATAAGACA	AAGCCTTAAG	CCTTATGTTA	TAATTTTGGT	2880
	TCTAAAAACC	ATCATTTCAG TTATTTTTAT	TATAAGGAAT	AAGTATATTT	CGTCCTCCTC	TTTAGTTTTT	2940
	TTCTTCCTAT	TTATTTTTAT	TITGAAAAAT	TTCTACACCT	TCTTTGAATT	CCTTGTATGA	3060
40	ATTTTTGTTT	CTTAGAAGTT	AATTTGTGTG	AAATGAGATT	CTTCAAAACG	ATGAAACCTC	3120
40	ATAGCTCTGA	GAAAAGGTTT TTTAATTATA	TAGGGTTTTA	AATTCTAAGC	AAAGCGTGAC	TATGGCTGAC	3120
	AGACTACACA	TTCAGACCTT	CAGCTTCTCT	TICTIMECA	CAGGCAGATT	WCCTCVIIG	3240
	TGGATTGTCC	TTCAGACCTT	AGTCCTCAGG	CATGGTTTCT	GGTGCCCACT	CCIGOMAGCC	3300
	GCTGTTCCCT	TTCTACCTTC ACATAAGTCA	TTACCAGAGC	CCAAGGGCAG	GCCTGGTCCC	CA A COLO COCO	3360
45	CAGCTTGCTG	TGTGCCAGCG	GCTGCAAAGG	CIGAGGAGIG	COLOCOTOR	TOOOTCCACC	3420
43	CCCCCAGTCT	TGTGCCAGCG	CCTAGAGCCG	CAGCICCCAG	MONTOCICCI	TCCCTGGMGG	3480
	CAGCCCAGGA	GAGGGACTCT	GGCAGCGTTC	TTCAGATTTG	TOGCCACTGT	CLICATING	3540
	CTGGTTGACT	GTTTTTATTT	CITAGGCITI	TGCTAGTTTT	MUMMATAGG	CONTRACCO	3600
	TTGATTTGTG	TTGAGGCTGA	AACATTIGAG	CGATGATGCA	CAACAGICCA	0000001000	3660
50	CGGTGGACAC	TIGAGGCTGA	GGATGGGAGT	CONCATOROC	AUGUAUAGOU	AGGI GCGCGC	3720
50	IGCTTATCIG	TGATTGTTGC ATTATACTTT	TCACCTGAGT	GIGGCIGATI	GIGINCAICC	CENTRACE	3780
	ATTTTTAAAA	ATTATACTTT	TACATTTATT	TIMIMITITI	CICACCCCA	DIMMITTICCI	3840
	TCCAAAGAAG	TTCACATGTA	ATAAGTAGAA	ATTCTGTATA	GGMUUMMGC	ATTAKAKATA	3900
	CTATTATAAC	TGCTTCATTT TTTGTAGCAG	GCTGGGAACC	ATTAAAAGTA	ATATAAATTA	GCTTTTTCCA	3960
55	GAAGGATCCT	TTTGTAGCAG	TGTTTATGAA	TGTAACCCCC	AGCAAAATAT	GGCTATATAT	
22	TAGGGGAGCC	AGTTTGGAGC	AGAGGCCTGA	AGGTCCCTGC	TATGCAGCCG	TGGCCACAGC	4020
	TCGCAGCCCA	AGCACTGTGG GTACAAAACA	AGCATCCACA	CCTTTGATGG	CAATGCAGAT	TGGTAGCAGG	4080
	TTCCATAGGC	GTACAAAACA	GTATTAAAGC	TCAGTGTTTT	GCATATTGTT	AGCATTTACA	4140
	AATATTTTTG	CTTTAGTATG	AGGAAAGTAA	GGATGGGCAA	AGAAGCGATC	AAAATAGCTA	4200
	TTGCTACAAC	ATTTTCGAAA	ACAAAGTTGG	GGCTGTATTT	CTTTAAAAAG	ATAAGCCTCT	4260
60	AAAAATGCTT	ATTITCGAAA GGCAAAAAA	ATATAGTGTT	AAAATAGGCC	AGTGATATTA	ATGAGAAAAT	4320
	GAAAGTATGT	ATCAGGAATA	AAGTGATATT	GCATAGGAGT	ATTGTATTT	TATGAATTT	4380
	ATGCCAGTTG	TTTACATGTA	CTATATATGT	TAAATTAAAA	AAAATCATGA	GAAATG	
	Seg ID NO:	499 Protein	n sequence				
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	1	11	21	31	41	51	
	i	1	1	1	i	1	
	PLVINTLKRF	NLYPEVILAS LNGLMMALFF	WYRIYTKIMD	LIGIOTKICW	TVTRGEGLSP	IESCEGLGDP	60
70	ACTYVAVIFI	LNGLMMALFF	IYGTYLSGSR	LGGLVTVLCF	PPNHGECTRV	MWTPPLRESF	120
	EXPERIMENT ONE.	LVTHILRATK	LV9CGLTALC	T SNUREMI, DW	OPAGEVIATO	TASLPAVYVV	180
	CALLTANTOR	IIYIHMISLA	LOBIT MECHE	MITTOVVACO	LUTTWATTAM	KDHBI'K LNAS	240
	O'IDICKUKK	TALE DOMESTIC	AL MONTHOUS	DDAUTOUT LT	CABBUARDED	TILVECANDE	300
	PREPARATORC	PWLFGTVILK YTKTLLLPVV	TIOTHER TITLE	TTERMUM	PULL COLUMN TO	DUNCOL VALLE	360
75	DIMERRIPLE	TIKTPPPDA	PAALAKK	T SUMMGVLA	WATHARRED	PATTARMOTO	420
13	LULLAYTALG	ILIMRLKLPL	TEHMCVMASL	TORKOTEGNE	FUNDAMENTA	EUTTWARDIÖ	480
	GSANLQTQWN	IVGEPSNLPQ	EETIEMIKA8	TKPDAVPAGA	MPTMASVKLS	ALRPIVNIPH	200
	YEDAGLRART	IVGEPSNLPQ KIVYSMYSRK	AABEVKRELI	KTKANAAITE	ESWCVRRSKP	GCSMPEIWDV	540
	EDPANAGKTP	PCMPTAKDRK	PHFTTVPQNS	AAKAFEAAKE			
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00	seq ID NO:	500 DNA se	Ineuce				
	Nucleic Ac	id Accession	n.#: XM_001	1276.1			
	coding seq	uence: 127.	.1278				
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85	1	11	21	31	41	51	
92	1	1		Non-personal	COUNTRACTOR	I CONCUENCE NO	60
	AUTGGAGTGG	GACAGGTATA CAGGAGCCGT	IMAAGGAAGT	ACAUGUCCTG	COCCACAGGC	CCIGICING	120
	TAGCTGGCAC	CAGGAGCCGT	GGCAAGGGA	MUAGGCCACA	CCCTGCCCTG	CICIGCIGCA	120

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	GCCAGAATGG	GTGTGAAGGC	GTCTCAAACA	GGCTTTGTGG	TCCTGGTGCT	GCTCCAGTGC	180
	TGCTCTGCAT	ACAAACTGGT	CTGCTACTAC	ACCAGCTGGT	CCCAGTACCG	GGAAGGCGAT	240 300
	GGGAGCTGCT GCCAATATAA	CCAGATGC	CATCCACACC	TICCICIGIA	ATCATCTCAC	COTOTAGGCTTT	360
5	ATTOTOTOTO	CACTCAAGAA	CATCGACACC	A A COTTON A CA	CTCTCTTGTC	TOTOGRAGIA	420
•	TGGAACTTTG	GGTCTCAAAG	ATTTTCCAAG	ATAGCCTCCA	ACACCCAGAG	TCGCCGGACT	480
	TTCATCAAGT	GGTCTCAAAG CAGTACCGCC	ATTCCTGCGC	ACCCATGGCT	TTGATGGGCT	GGACCTTGCC	540
	TGGCTCTACC	CTGGACGGAG	AGACAAACAG	CATTTTACCA	CCCTAATCAA	GGAAATGAAG	600
10	GCCGAATTTA	TAAAGGAAGC	CCAGCCAGGG	AAAAAGCAGC	TCCTGCTCAG	CGCAGCACTG	660
10	TCTGCGGGGA	AGGTCACCAT	TGACAGCAGC	TATGACATTG	CCAAGATATC	CCAACACCTG	720
	GATTTCATTA	GCATCATGAC TGTTCCGAGG	CTACGATTTT	CATGGAGCCT	GGCGTGGGAC	CACAGGCCAT	780 840
	CACAGTCCCC	CCTLCLGAGG	CACCCTCCCC	CCTCCTCCCC	CTARCETCOT	CANCACIGAC	900
	CCCACCTTCG	GGTACATGTT GGAGGAGCTT	CACTCTGGGG	TCTTCTGAGA	CTGGTGTTGG	AGCCCCAATC	960
15							1020
	ATCTGTGACT GCCACCAAGG	TCCTCCGCGG	AGCCACAGTC	CATAGAACCC	TOGGCCAGCA	GGTCCCCTAT	1080
	GCCACCAAGG	GCAACCAGTG	GGTAGGATAC	GACGACCAGG	AAAGCGTCAA	AAGCAAGGTG	1140
							1200
20	TTCCAGGGCT	CCTTCTGCGG CAACGTAGCC	CCAGGATCTG	CCCTTCCCTC	TCACCAATGC	CATCAAGGAT	1260
20	GCACTCGCTG	CTCCAGCTGG	CTCTGTTCTG	CACACAGCAC	CONCORDA	CCCACCCCCC	1380
	CCCCCTCTGG	CCCTCCCTTG	GGGCCTATGC	AGAGGTCCAC	AACACACAGA	TTTGAGCTCA	1440
	GCCCTGGTGG	CCCTCCCTTG GCAGAGAGGT	AGGGATGGGG	CTGTGGGGAT	AGTGAGGCAT	CGCAATGTAA	1500
	GACTCGGGAT	TAGTACACAC	TTGTTGATGA	TTAATGGAAA	TGTTTACAGA	TCCCCAAGCC	1560
25	TGGCAAGGGA	ATTTCTTCAA	CTCCCTGCCC	CCTAGCCCTC	CTTATCAAAG	GACACCATTT	1620
							1680
	TACCCCCTGC	AAAGCCAGCT	TGAAACCTTC	ACTTAGGAAC	GTAATCGTGT	CCCCTATCCT	1740
	ACTTCCCCTT	CCTAATTCCA	CAGCTGCTCA	ATAAAGTACA	AGAGTTTAAC	AGTGTGTTGG	1800
30	CGCTTTGCTT	TGGTCTATCT TCCTTCCTCT	TTGAGCGCCC	ACTAGACCCA	CTGGACTCAC	CTCCCCCATC	1860 1920
30	ATGTT	recreerer	GAGCCTTGGG	ACCCCTONGC	TIGCAGAGAT	GAMGGCCGCC	1920
	AIGIT						
	Sea ID NO:	501 Protein	sequence				
	Protein Acc	cession #: 1	IP_001267.1				
35			-				
	1	11	21	31	41	51	
	J	<u> </u>	!	1			60
	MGVKASQTGF	VVLVLLQCCS WNDVTLYGML	AYKLVCYYTS	WSQYREGOGS	PORCHESTA	CIMILIYSPAN	120
40	VOUDDDT DTU	GFDGLDLAWL	ADGDDDAVAD	TTLIKENKAP	PARENDECKK	OLLIGABLEA	180
-10	GKVTTDSSYD	IAKISQHLDF	TSIMTYDENG	AWRGTTGHHS	PLPRGOEDAS	PDRPSNTDYA	240
	VGYMLRLGAP	ASKLVMGIPT TLGQQVPYAT	FGRSFTLASS	ETGVGAPISG	PGIPGRFTKE	AGTLAYYEIC	300
				QESVKSKVQY	LKDRQLAGAM	VWALDLDDFQ	360
4.0		TLGQQVPYAT PLTNAIKDAL		GESAKSKAĞA	LKDRQLAGAM	VWALDLDDFQ	360
45	GSFCGQDLRF	PLTNAIKDAL	AAT	GESAKSKAĞA	LKDRQLAGAM	VWALDLDDFQ	360
45	GSFCGQDLRF Seq ID NO:	PLTNAIKDAL 502 DNA sec	AAT		LKDRQLAGAM	VWALDLDDFQ	360
45	GSFCGQDLRF Seq ID NO: Nucleic Ac:	PLTNAIKDAL 502 DNA sec Ld Accession	AAT quence 1 #: NM_006		LKDRQLAGAM	VWALDLDDFQ	360
	GSFCGQDLRF Seq ID NO: Nucleic Ac:	PLTNAIKDAL 502 DNA sec	AAT quence 1 #: NM_006		LKDRQLAGAM	VWALDLDDFQ	360
45 50	GSFCGQDLRF Seq ID NO: Nucleic Ac:	PLINAIRDAL 502 DNA sec Ld Accession Jence: 181.	AAT quence 1 #: NM_006		LKDRQLAGAM	VWALDLDDFQ 51	360
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50	GSFCGQDLRF Seq ID NO: Nucleic Ac: Coding sequence GCTGCCTAGG	PUTNAIRDAL 502 DNA sec Id Accession Jence: 181. 11 GTCTGGAAAG	AAT Quence 1 #: NM_006 669 21 CTCGGGGCACC	31 CTCCTCTCC	41 GGGGCTCCTG TGGCCGCGGT	51 CTCCCACCCC	60 120 180
	GSFCGQDLRF Seq ID NO: Nucleic Ac: Coding sequence GCTGCCTAGG TCCGGCCCCC ATGTGGAAGG	PUTNAIRDAL 502 DNA sec Id Accession sence: 181. 11 GTCTGGAAAG CCACGTCGC TCAGAATCTT TGTCAGCTCTT	AAT Nuence 1 #: NN_006 669 21 CTCGGGCACC GCTCTCCAG GCTGCTCGGC GCTCTTCGTT	31 CTCCCTCTCC GCTGGGCTG CCCCAGGAGA TTGGGAAGCG	41 GGGGCTCCTG TGGCCGCGTG GCAACAACTC CGTCGCTCTG	51 CTCCCACCCC GCTTTAATT AACGGAACG GGTCCTGGCA	60 120 180 240
50	GSFCGQDLRF Seq ID NO: Nucleic Ac: Coding sequ Coding sequ CCGGCCCCC TCCCGCCCCC TCCCCCAGC ATGTGGAAGG GAAGGAGCCA	PUTNAIRDAL 502 DNA Beeld Accession sence: 181. 11 GTCTGGAAAG CCACGTCGC TCAGAATCTT TGTCAGCTCT GGACAGGCCA	AAT quence 1 #: NM_006 669 21 CTCGGGGCACC GCTCCTCCAG GCTGCTCGGG GCTCTTCGTT GCCAGAAGAT	31 CTCCCTCTCC CCTGGGCCTG CCCCAGGAGA TTGGGAAGCG GACACTGAGA	41 GGGGCTCCTG TGGCCGCGGT GCAACAACTC CGTCGCTCTG CTACAGGTTT	51 CTCCCACCCC GCTTTTAATT AACGGAACG GGTCCTGGCA GGAAGGCGGC	60 120 180 240 300
50	GSFCGQDLRF Seq ID NO: Nucleic Ac: Coding seq GCTGCCTAGG TCCGGGCCCC ATGTGGAAGG GAAGGAGCCA GTTGCCATGC	PUTNAIRDAL 502 DNA sec id Accession sence: 181. 11 GTCTGGAAAG CCACGTCGC TCAGAATCTT TGTCAGCTCT GGACAGGCCA ACAGGTCCA ACAGGTCCA ACAGGTCCA ACAGGTCCA ACAGGTCCA	Quence 1 #: NM_006 669 21	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA TTGGGAAGCG GACACTGAGA GTGACTCCAG	41 GGGGCTCCTG TGGCCGCGGT GCAACAACTC CGTCGCTCTG CTACAGGTTT GAACCAGCGA	51 CTCCCACCCC GCTTTTAAT AACGGGAACG GGTCCTGGCA GGAAGGCGGC AGACCGCTAT	60 120 180 240
50 55	GSFCGQDLRF Seq ID NO: Nucleic Ac: Coding seq 1	PLINAIRDAL 502 DNA sected Accession dence: 181. 11	AAT Quence 1 #: NM_006 669 21	31 	41 GGGCTCCTC TGGCCGGGT GCAACAACTC CTMCAGGTTT GAACCAGGA GTGTAACAGG BACAAAGTCC	51 CTCCACCCC GCTTTTAATT AACOGGAACG GGTCCTGCA AGACCGCTAT CATTOGCATC	60 120 180 240 300 360
50	GSFCGQDLRF Seq ID NO: Nucleic Ac: Coding seq 1	PLINAIRDAL 502 DNA sected Accession dence: 181. 11	AAT Quence 1 #: NM_006 669 21	31 	41 GGGCTCCTC TGGCCGGGT GCAACAACTC CTMCAGGTTT GAACCAGGA GTGTAACAGG BACAAAGTCC	51 CTCCACCCC GCTTTTAATT AACOGGAACG GGTCCTGCA AGACCGCTAT CATTOGCATC	60 120 180 240 300 360 420 480 540
50 55	GSFCGQDLRF Seq ID NO: Nucleic Ac: Coding sequ GCTGCCTAGG TCCCCCAGC ATGTGGAAGG GAAGGAGCA GTTGCCATGC AAGTCTGGCT GAGGATCTGG GCTCAAACG GCTTCAAAAG GTTGAAAAG GTTGAAAAG	PLINAIRDAL 502 DNA sec dd Accession cence: 181. 11	AAT Quence 1 #: NM_006 669 21	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA TTGGGAACGG GACACTGAGA AGTGTCAACA CACCCGCAAG GAGAAATTGG CTGGTTGGAA	41 GGGCTCCTG TGGCCGCGTG GCACAACTC CGTCGGCTCTG CTACAGGTTT GAACCAGGA ATGTAACAGG AACAAAGTCC ATGGAGACAC TCATAGTTGG	51 CTCCCACCCC GCTTTTAATT AACGGGAACG GGTCCTGCA AGGACGCGCA AGACGCCACA AACGGCCACA ACAGACAACA ACAGACAACA	60 120 180 240 300 420 480 540 600
50 55	GSFCGQDLRF Seq ID NO: Nucleic Ac: Coding sequ 1 GCTGCCTAGG TCCGGGGCCC TTCCCCCAGG AAGTGGAAGA GAAGTACTGGCT GAGAATCTGGCT GAGAAACG GTCTGAAAACG GTCTGAAAACG GTCTGAAAACG GTCTGAAAACG GCCTTAGAAACG GTCTGAAACG GCCTTAGAAACG	PLINAIRDAL 502 DNA sec td Accession cence: 181. 11 GTCTGGAAAG CCACGGTGGC TCAGAATCTT TGTCAGCTCT GCACAGGCCA CAGGTGCCGA CAGGTGCCGA TGACTACTCAGA TGGCCACCAG ATGGTTTGCACACT CAATGGTTTGCACACCAG ATGGTTTGTGATGGTGGCACAG ATGGTTTGTG	AAT Quence 1 #: NM_006 669 21 CTCGGGCACC GCTGCTCCAG GCTGTCGGT GCCAGAAGAT AGATGATGTG GGTGGCAACA AAGCACAGTC TCACTCCACG AACAGTGACC AACAGTGACC AATCATCGTT	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGC GACACTGAGA GTGACTCAGA AGTGTCAACA CACGGCAAG GAGAAAGTGG CTGGTTGGAA	41 GGGGCTCCTG TGGCCGGGGT GCAACAACTC CTACAGGTTT GAACCAGGGA AACAAGTCC ATGGAGACAC TCATAGTTGG GAAAAATGTC	51 CTCCCACCCC GCTTTTAATT AACGGGAACG GGAAGGCGGC AGACCGCTAT CATTCGCATC AACGGCCACA ACAGACAACA GGTCTTACTA GGGAAGGTAC	60 120 180 240 300 360 420 480 540 600 660
50 55	GSFCGQDLRF Seq ID NO: Nucleic Ac: Coding sequ 1 GCTGCCTAGG TCCGGGGCCC TTCCCCCAGG AAGTGGAAGA GAAGTACTGGCT GAGAATCTGGCT GAGAAACG GTCTGAAAACG GTCTGAAAACG GTCTGAAAACG GTCTGAAAACG GCCTTAGAAACG GTCTGAAACG GCCTTAGAAACG	PLINAIRDAL 502 DNA sec td Accession cence: 181. 11 GTCTGGAAAG CCACGGTGGC TCAGAATCTT TGTCAGCTCT GCACAGGCCA CAGGTGCCGA CAGGTGCCGA TGACTACTCAGA TGGCCACCAG ATGGTTTGCACACT CAATGGTTTGCACACCAG ATGGTTTGTGATGGTGGCACAG ATGGTTTGTG	AAT Quence 1 #: NM_006 669 21 CTCGGGCACC GCTGCTCCAG GCTGTCGGT GCCAGAAGAT AGATGATGTG GGTGGCAACA AAGCACAGTC TCACTCCACG AACAGTGACC AACAGTGACC AATCATCGTT	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGC GACACTGAGA GTGACTCAGA AGTGTCAACA CACGGCAAG GAGAAAGTGG CTGGTTGGAA	41 GGGGCTCCTG TGGCCGGGGT GCAACAACTC CTACAGGTTT GAACCAGGGA AACAAGTCC ATGGAGACAC TCATAGTTGG GAAAAATGTC	51 CTCCCACCCC GCTTTTAATT AACGGGAACG GGAAGGCGGC AGACCGCTAT CATTCGCATC AACGGCCACA ACAGACAACA GGTCTTACTA GGGAAGGTAC	60 120 180 240 360 420 540 600 660
50 55 60	GSFCGQDLRF Seq ID NO: Nucleic Ac Coding seq I GCTGCCTAGG TCCGGCCCCA TTGCCAGG AAGTATGAAAGG GCATCGGCT GGCCTAAAG GCCTAAAAG TCTAGAAAG TTGAGAAAG TTTAGAAAGA TTTAGAAAGA TTTAGAAAAG TTTAGAAAAG TTTAGAAAAG TTTAGAAAAG TTTAGAAAAG TTTAGAAAAG TTTAGAAAAG TTTAGAAAAG TTTAGAAAAG TTTAGAAAAG TTTAGAAAAG	PLINAIRDAL 502 DNA set 6d Accession Dence: 181. 11	AAT Number 1 #: NM_006 669 21 CTCGGGCACC GCTCCTCCAG GCTGTTCGGCACA GCTGATGATGATGA GGTGATGATGA AGAGACAGTC TCACTCCACG AACAGTGACC AATCAACGTG GTTAGGCCT GTTAGGCCT GCCTGAGGTC CCCTGAGGTC	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA TTGGGAGCG GACACTGAGA GTGACTCACA CACGGCAAG GAGAAAGTGG GAGAAAGTGG GTGTGCGAAC GTGGTTGCAAC	41 	51 CTCCACCCC GCTTTTAATT AACGGAACG GGTACGCGCACA AGACCGCTAT AACGGCACA ACAGCAACA GGTCTTACTA AGAGACAACA GGGAAGGTAC AAAGACCATTG GGAACATTTG GGAACATTTG	60 120 180 240 300 360 420 480 540 600 660 720
50 55	GSFCGQDLRF Seg ID NO: Nucleic Ac: Coding sequence GCTGCCTAGG TCCGGGCCCC TTGCCCCAGG ATGTGGAAGG GAAGGAGCTGGCT GAGGATCTGGCT GAGGATCTGGCT GAGGATCTGGCT GTTGGAAAG GCATCGATT TTGCCTAAACT GTTGAAAAG GCATCGGTT TTGGCCTAA	PLINAIRDAL 502 DNA sec Ld Accession Gence: 181. 11 GTCTGGAAAG CCACCGTGGC TCAGAATCTT TGTCAGCTCT GCACAGCCA CAGGTGCCAA CAGGTGCCAA TGACAACTCT CAACTTCAGA TGCCACCAG GGCCACCAG GGGCACCAG GGGCACCAG GGGCACAG GGGCACAG GAGGTGCAAG	AAT quence 1 #: NM_006 669 21	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA TTGGGAGCG GACACTGAGA GTGACTCACA CACGGCAAG GAGAAAGTGG GAGAAAGTGG GTGTGCGAAC GTGGTTGCAAC	41 	51 CTCCACCCC GCTTTTAATT AACGGAACG GGTACGCGCACA AGACCGCTAT AACGGCACA ACAGCAACA GGTCTTACTA AGAGACAACA GGGAAGGTAC AAAGACCATTG GGAACATTTG GGAACATTTG	60 120 180 240 360 420 540 600 660
50 55 60	GSFCGQDLRF Seg ID NO: Nucleic Ac: Coding sequence GCTGCCTAGG TCCGGGCCCC TTGCCCCAGG ATGTGGAAGG GAAGGAGCTGGCT GAGGATCTGGCT GAGGATCTGGCT GAGGATCTGGCT GTTGGAAAG GCATCGATT TTGCCTAAACT GTTGAAAAG GCATCGGTT TTGGCCTAA	PLINAIRDAL 502 DNA sec td Accession Dence: 181. 11 GTCTNGAAAG CCACGTTCGC TCAGGATCT TGTCAGATCT TGCAGGTCCT GACAGGCCA CAGGTGCCGA TGGCAACACT TGGCCACGA ATGGTTTGTG GAGCTGAAGG GAGTGTTAGG GAGCTGAAGG GTGGCTGAAGG	AAT quence 1 #: NM_006 669 21	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA TTGGGAGCG GACACTGAGA GTGACTCACA CACGGCAAG GAGAAAGTGG GAGAAAGTGG GTGTGCGAAC GTGGTTGCAAC	41 	51 CTCCACCCC GCTTTTAATT AACGGAACG GGTACGCGCACA AGACCGCTAT AACGGCACA ACAGCAACA GGTCTTACTA AGAGACAACA GGGAAGGTAC AAAGACCATTG GGAACATTTG GGAACATTTG	60 120 180 240 300 360 420 480 540 600 660 720
50 55 60	GSFCGQDLRF Seq ID NO: Nucleic Ac Coding sequ	PLINAIRDAL 502 DNA sec Ld Accession Gence: 181. 11 GTCTGGAAAG CCACCGTGGC TCAGAATCTT TGTCAGCTCT GCACAGCCA CAGGTGCCAA CAGGTGCCAA TGACAACTCT CAACTTCAGA TGCCACCAG GGCCACCAG GGGCACCAG GGGCACCAG GGGCACAG GGGCACAG GAGGTGCAAG	AAT puence 1 #: NM_006 669 21	31 CTCCCTCTCC GCTGGGCCTG CCCCAGGAGA TTGGGAGCG GACACTGAGA GTGACTCACA CACGGCAAG GAGAAAGTGG GAGAAAGTGG GTGTGCGAAC GTGGTTGCAAC	41 	51 CTCCACCCC GCTTTTAATT AACGGAACG GGTACGCGCACA AGACCGCTAT AACGGCACA ACAGCAACA GGTCTTACTA AGAGACAACA GGGAAGGTAC AAAGACCATTG GGAACATTTG GGAACATTTG	60 120 180 240 300 360 420 480 540 600 660 720
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50 55 60 65	GSFCGGDLEF Seq ID NO: Nucleic Ac: Coding sequ GCTGCCTAGG TCCGGCCCC TTCCGCCCAGA AGTTGGGT GCGCTAAACG GTTGGCTAAGG GCGTAACGGT TCGGCCCAAACG GTTGGCAAACG GTTGGCAAACG TTGGCCTAAACG GCCTAAACG TTGGCTGAAACG GCATCGGTT Seq ID NO: Protein Ac:	PUTNATIONAL 502 DNA sec dd Accessio ence: 181. 11 GTCTGGAAAG CCACCUTCGC TORGAACTT TOTCAGAACTT TOTCAGAACTT TOTCAGACTCT TOTCAGACTCT TOTCAGACTCT TOTCAGACTCT TOTCAGACTCT TOTCAGACTCT TOTCAGACTCT TOTCAGACTCA TAGCACACA TAGCACACA TAGCACACAC TAGCACACAC TAGCACACAC TAGCACACAC TAGCACACAC TAGCACACAC TAGCACTCACAC TAGCACAC TAGCACTCACAC TAGCACAC TAGCACTCACAC TAGCACTCACAC TAGCACTCACAC TAGCACTCACAC TAGCACTCACAC TAGCACTCACAC TAGCACTCACAC TAGCACTCACAC TAGCACACAC C TAGCACACACAC TAGCACACACAC TAGCACACACAC TAGCACACACACAC TAGCACACACACACACACAC TAGCACACACACACACACACACACACACACACACACACAC	AAT Junnee 1 #: NN_006 669 21 1 1 100305CACC GETOCTICOR GETOCTICOR GETOCTICOR GETOCTICOR GETOCTICOR GETOCTICOR GETOCTICOR GETOCTICOR AGCACAGT TEACTICOR TACATICOR AMCANGTACC AMCANGTACC AMCANGTACC AMCANGTACC AMCANGTACC TACTICOR 1 BEQUENCE 1 BEAUTICO 1	31	41 GGGGCTCCTG TGGCGGGGT GGGCGCGGGT GGCGCGCTCT GGTCGCTCTG GGAACCAGCTG GTGTAACAGG AACCAAGTC ATGAACAGG GAAAATTC GAACAAGTC GAACAACTG GAACA	51 CTCCCACCCC GCTTTTANT AACGGGAACG GGTAGGGGGAGGGGGAGGGGGAGGGGGGGGGG	60 120 240 300 420 480 540 600 720 840
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50 55 60 65 70 75	GSFCGDULFF Seq ID NO. Nuclaic Act Coding seq 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	\$20 DNA second Color (Color Color Co	ANT JUMBICS 18 1 NN_006 19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	111 111 111 111 111 111 111 111 111 11	41 10GGGGCTCCTG GGAGCTCCTG GCACAACTC GCACAACTC GCACAACTC GCACAACTC GCACACCCA GTGACACCCA GTGACACCCA GTGACACCA GTGACACCA GTGACACCA GTGACACCA GTGACACCA 41 1 VANPGAREDOV ASRIVATSEST SP 41 1 TACTTCACTA	51 CITCCCACCCC CCCCCCCCCCCCCCCCCCCCCCCCCCC	60 120 180 240 300 420 480 540 660 660 780 840
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5	AGATCCAAAG	CAAATTTTTA CACATTAGAC	AATCTCCAGG	CTTCCCAAAT	CACCTGACTT	ATAACCAAAT	540 600
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	TGATGTCCAT	GGCTTTGTGG GTCATGACCT	GAAGATACTG	TGGAGATGAG	CTTCCAGATG	ACATCATCAG	720 780
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	AAAAAAAGGA	TGATCAAAAC	ACACAGTGTT	TATGTTGGAA	TCTTTTGGAA	ATACATAATT	960 1020
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	EGGHLATYKO	LEAARKIGFH	VCAAGWMAKG	RVGYPIVKPG	PNCGPGKTGI	IDYGIRLNRS	120
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	GATTTCATGT	CTGTGCTGCT CAACTGATGA	GGATGGATGG	CTAAGGGCAG	AGTTGGATAC	CCCATTGTGA	360
45	AGCCAGGGCC	CAACTGATGA	TTTGGAAAAA	CTGGCATTAT	TGATTATGGA	ATCCGTCTCA	420
45	ATAGGAGTGA	AAGATGGGAT TCCAAAGCGA	GCCTATTGCT	ACAACCCACA	CGCAAAGGAG	TACGARGATA	480 540
	ACCAAATCTG	CTACTGGCAC	ATTAGACTCA	AGTATGGTCA	GCGTATTCAC	CTGAGTTTTT	600
	TAGATTTTGA	CCTTGAAGAT TGTCCATGGC	GACCCAGGTT	GCTTGGCTGA	TTATGTTGAA	ATATATGACA	660 720
50	TCATCAGTAC	AGGAAATGTC	ATGACCTTGA	AGTITCTAAG	TGATGCTTCA	GTGACAGCTG	780
	GAGGTTTCCA	AATCAAATAT	GTTGCAATGG	ATCCTGTATC	CAAATCCAGT	CAAGGAAAA	840 900
	ATACAAGTAC	TACTTCTACT AAGGATGATC	AAAACACACA	GTGTTTTAGC	TGGAAGATTT	TGGAACTCCT	960
	TTGATCTCAC	TGTTATTATT	AACATTTATT	TATTATTTT	CTAAATGTGA	AAGAAATACA	1020
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	TAAATATTGT	TGCAATAAAT	ATCCTTCGGA	ATTC			
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	WIIPIAPPP	LWEDTQGWGP	KOGIFHNSIW	LERAGVYHR	BARSGKYKLT	YABAKAVCBF	60 120
70	ERWDAYCYNP	LEAARKIGFH HAKECGGVFT	DPKRIFKSPG	FPNEYEDNOI	CYWHIRLKYG	ORIHLSFLDF	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDELPDDIIS	TGNVMTLKFL	SDASVTAGGP	240
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75	Seq ID NO:	508 DNA sec ld Accession	quence	044 1			
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	AAAGCCCAGG	CCCGGGCGGC	CAGACCAAGA	GGGAAGAAGC	ACAGAATTCC	TCAACTCCCA	120 180
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	100,001,000						

	TCCTGGTCCC	CTACCTGCTC	TTCATGGTCA	TTGCTGGGAT	BCCACTTTTC	TACATGGAGC	480
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-	GTGGAGACAG	CTCGGGCCTC	AACGACACTT	TTGGGACCAC	ACCIGCIGCC	GAGTACTTTG	780
	AACCTCCCCT	GCTGCACCTC	CACCAGAGCC	ATGGCATCGA	CGACCTGGGG	CCTCCGCGGT	840
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~	TAAGCACAAT	AAAAGACATC	CACAATGGAA	AAAAAAAAAG	GAATTC		
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	MSKSKCSVGL	MSSVVAPAKE	PNAVGPKEVE	LILVKEONGV	QUISSTLINE	MOT BANKET ST	120
	ETWGKKIDPL	LSVIGFAVDL VWKICPILKG	ANVWRPPYLC	VICEDOVELLA	AMAI.HVI.PSS	PATRI DWIKE	180
	PACHMEDIACE	DAHPGDSSGD	SCHNOTPOT	TPAREYERRG	VLHLHOSHGI	DDLGPPRWOL	240
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	GEVVESFLGY	MACKHSVPIG	DVANDGPGLI	FITYPEATAT	LPLSSAWAVV	PPIMLLTLGI	420
							480 540
75	GTSILFGVLI	EAIGVAWFYG	VGQFSDDIQQ	MIGGRESLIW	KTCMKTABLC	FLLFVVVVSI LAYAIAPEKD	600
13	PETAPPHICA	QFTLRHWLKV	GMATMISSUM	MARTINA	Conforma	Dittall Did	
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	Seq ID NO:	510 DNA se	quence				
00	Nucleic Ac	id Accessio	n #: NM_00	1216.1			
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~-	GCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
85	AGCCCCTGGC	TOCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG GCAGGAGGAT	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TUCCCCCGGAT	GCAGGAGGAT	180 240
	TCCCCCTTGG	GAGGAGGCTC	TTUTGGGAA	GATGACCCAC	1-000-COMOGN	GGATCTGCCC	

	ACTGARGAGG	ATTCACCCAG	AGAGGAGGAT	CCACCCGGAG	AGGAGGATCT	ACCTGGAGAG	300
	GAGGATCTAC	CTGGAGAGGA	GGATCTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
	TOTOTCAAGT	TAGAGGATCT	ACCTACTOTT	GAGGCTCCTG	GAGATCCTCA	AGAACCCCAG	420
	AATAATGCCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGCGAC	480
-5	CONCOURAGE	CCCGGGTGTC	CCCAGCCTGC	GCGGGCCGCT	TCCAGTCCCC	GGTGGATATC	540
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	ACTGCCTATG	AGCAGTTGCT	GTCTCGCTTG	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
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	GAGGCCTCCT	TCCCTGCTGG	AGTGGACAGC	AGTCCTCGGG	CTGCTGAGCC	AGTCCAGCTG	1260
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20	GTGAGCTACC	GCCCAGCAGA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGGAGAA	1440
	TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGGTA	ACTGTCCTGT	CCTGCTCATT	1500
	ATGCCACTTC	CTTTTAACTG	CCAAGAAATT	ATAAAATTT	AATATTTATA	AT	
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	MAPLCPSPWL	PLLIPAPAPA	LTVOLLLSLL	LLMPVHPORL	PRMOEDSPLG	GGSSGEDDPL	6
30	CEPOT DEPEN	SPREEDERGE	EDLPGEEDLP	GEEDLPEVKP	KSEEEGSLKL	EDLPTVEAPG	12
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	PT.I CPOLDEL	DEL'BI'BINUCH	SVQLTLPPGL	RMALGPGRBY	RALOLHLHWG	AAGRPGSEHT	24
	VECUPEDARY	WWW.STAPA	RVDEALGREG	GLAVLAAFLE	EGPEENSAYE	QLLSRLEEIA	30
	PROCESSOURCE	TOTEST, LOSD	PSRYPOYEGS	LTTPPCAOGV	INTVENOTVM	LSAKQLHTLS	36
35	DECORAGEORE	LOIMERATOR	INGRVIRASE	PAGVDSSPRA	AEPVQLNSCL	AAGDILALVF	42
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40	Coding sequ	ence: 139	78				
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	ATGGTGGGTG	AAGGACCCTA	CCTTATCTCA	GATCTGGACC	AGCGAGGCCG	GCGGAGATCC	60
45	THE COURSE AND	CATATCACCC	CAGCCTGAAG	ACCATGATCC	CAGTGCGACC	CTGTGCAAGG	120
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	TOGRCATATG	ACTCATCTGA	CACCAATGCC	AAAAGATTTC	GAGTCCTTTG	GGATGAAGAG	300
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	CCGACAGTTC	TCATTCACCA	AATCCTCCAG	CAGACTGAGA	GGACCTCTGG	GAAAGTCTGG	480
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	GCCCTTGCCT	GGGCCATCAA	CTACCGCACG	GCCATCCGGT	TGAAGGTGGC	GCTCTCCACC	600
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	GCCAAGCTCA	ATTCAGCTTT	CCGAAGGTCA	GCAATTTTGG	TGACAGACAA	GCGAGTTCAG	960
	ACAATGAATG	AGTTTCTGAC	CTGCATCAGG	CTGATCAAAA	TGTATGCCTG	GGAGAAATCT	1020
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	ACATTATCCT	GCCACATCCT	CCTGAGACGC	AAACTCACCG	CACCCGTGGC	ATTIAGIGIO	1200
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70	TTTGTGGTGA	GAAAGTTATG TTGGGAGAAT	TCGTTATCCC	GAAGCCCAGC	TOCIGOCIIG	TOCTA A ACAC	1620
<i>i</i> .0	GCAGTGTTTG	TTGGGAGAAT	CATCAGAGGA	TACAGGCCTC	ATGGATTTIC	TGC TAAAGAC	1680
	AAGGATGAAT	CTAGAAGGCT	TCTTACTTGG	CCCCAAGAAG	TOGATAGGAC	**************************************	1740
	GCCAAATACC	TGGGGAAGAT	CTTGGGAATA	TOTOGGAATG	COMPONE	ACTOR STOCK	1800
	CTCCTTGCAG	ACSTTTCACA	ACAGATGCAG	A TO CHEMICATO	CARACTCAC	AGRARACATA	1860
75	ACTTIGGCCT	AAAAGTATGA	GCAGGCATGG	MICTICATO	CAMACOCOCO	CIVITAGACCTA	1920
13	CTCTTTGGAG	TGAGCAACCT	TCACCIONIGG	CACCACACACACACACACACACACACACACACACACACAC	ACATTOGGGA	GCGGGGCCTC	1980
	CAGAAGGACC	GGGGGCAGAG	CCCCTATGGA	ACCOMMEN	COCCOCA	CTCCGACCGT	2040
	AACCICICIO	TGCTGGACGA	GCAGAGGATI	COCCEDENCE	CCC COTTO	CAACCACCTC	2100
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	CIGCGAGGAI	GCCCTGCTGA	CACACACACA	CATCCTCCT	TRATOGGGTA	CCTCCTTTCT	2400
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85	CICITCACIO	COMMOGRACIA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ATGACCTGTC	GGCCCCAGGG	CAACAGGACC	2520
0,5	A TOTAL CONTRACTOR	TOTOTOTOT	CONTRACTAGAC	NTCGGTCAGC	: ATGTGTACCA	GTGGGTGTAC	2580
	VCDCCVVCCV	TOGGCGCGG	CONCORRE	GGGGTCACCA	AAGGCTTCGT	CTTCACCAAG	2640
	NC19CHHGCH	1 1001011CM					

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	ACCACACTGA	TGGCATCCTC TCTTTGACAC	CTCTCTGCAT	GACACGGTGT	TTGATAAGAT	CTTAAAGAGC	2760 2760
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5	GCCAGCCTTG	CTGTAGGCTT	CTTCATTCTG	TTACGCATTT	TCCACAGAGG	AGTCCAGGAG	2940
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10	CGAACGCGAA	CAGAGACGCA TTCCTGAATG	AGCCAAATTC	ACCTCCGTGG	AGCTGCTCAG	GGAATACATT	3240
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	GCAGAAGTCA	GATTGTAG					
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30	MVGEGPYLIS	DLDQRGRRRS	FAERYDPSLK	TMIPVRPCAR	LAPNPVDDAG	LLSFATFSWL	60
	TRUMUKGYRO	DISTUDITION.	STYDSSDINA	KRFRVLWDEE	VARVGPEKAS	LSHVVWKFOR	120
i	TRVLMDIVAN	ILCIIMAAIG	PTVLIHQILQ	QTERTSGKVW	VGIGLCIALF	ATEFTKVFFW	180 240
	ALAWAINYRT	AIRLKVALST CAAYAFFILG	LVFENLVSFK	TLTHISVGEV	PALTERDARA	BILLUTOKOVO	300
35	PATTETTMAN	LIKMYAWEKS	PTABLGISVI	PERKLIPKAG	PVOSGNISALA	PIUSTIAIVL	360
55	TI.CCUTT.Y.DD	WI.TADUATESV	TAMENUMKES	TATLPFSTKA	MARANVSLRR	MKKILIDKSP	420
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40	KDESRRLLTW	PQEVDRTQRA IFHGNVRENI	AKYLGKILGI	CONVESCION	OFDI CHILDYC	DISTRICEPCI.	660
40	TLAIVSQQAW	SLARAVYSDR	OLVI.I.DDDI.S	PADPHACKHA	PERCIKKTLE	GKTVVLVTHO	720
	LOPE RSCORV	ILLEDGEICE	KCTHKELMEE	RGRYAKL IHN	LRGLOFKDPE	HLYNAAMVEA	780
	PKESPAEREE	DAGIIGYLLS	LPTVFLFLLM	IGSAAFSNWW	LGLWLDKGSR	MTCGPQGNRT	840
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	ASLAVGPFIL	LRIPHRGVQE	LKKVENVSRS	PWFTHITSSM	QGLGIIHAYG	RKESCITYTS	1080
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	SCTIPIDEVD	ICILSLEDLR	TKLTVIPODP	VLFVGTVRYN	LDPFESHTDE	MLWQVLERTP	1200
50	MRDTIMKT.PR	KLOARVTENG	ENFSVGEROL	LCVARALLRN	SKIILLDRAT	ASMDSKTDTL	1260
	VONTIKDAFK	GCTVLTIAHR	PMAATNCOHA	LVMENGKVIE	PDKPEVLARK	PDSAFAMLLA	1320
	AEVRL						
	Seg ID NO:	514 DNA sec	ruence				
55	Nucleic Act	id Accession	1 #: Z31560		•		
	Coding sequ	uence: 1-966	5				
		11	21	31	41	51	
	1	11	1	11	ĩ.	1	
60	CACAGCGCCC	GCATGTACAA	CATGATGGAG	ACGGAGCTGA	AGCCGCCGGG	CCCGCAGCAA	60
••	ACTTCGGGGG	GCGGCGGCGG	CAACTCCACC	GCGGCGGGCGG	CCGGCGGCAA	CCAGAAAAAC	120
	AGCCCGGACC	GCGTCAAGCG	GCCCATGAAT	GCCTTCATGG	TGTGGTCCCG	CGGGCAGCGG	180
	CGCAAGATGG	CCCAGGAGAA AACTTTTGTC	CCCCAAGATG	CACAACTCGG	AGATCAGCAA	GCCTAAGCCC	240 300
65							360
05	AAGACGCTCA	TGAAGAAGGA	TAAGTACACG	CTGCCCGGCG	GGCTGCTGGC	CCCCGGCGGC	420
							480
	ATGGACAGTT	ACGCGCACAT	GAACGGCTGG	AGCAACGGCA	GCTACAGCAT	GATGCAGGAC	540
70	CAGCTGGGCT	ACCOGCAGCA	CCCGGGCCTC	AATGCGCACG	GCGCAGCGCA	GATGCAGCCC	600 660
70	ATGCACCGCT	ACGACGTGAG CGCCCACCTA	CGCCCTGCAG	TACOUNCTOCK	AGGGCACCCC	TOCCATOCOTA	720
	ATGARCGGCT	TGGGTTCGGT	CAGCATGICC	GAGGCCAGCT	CCAGCCCCCC	TGTGGTTACC	780
	TOTAL	ACTOCAGGGG	CONTROCAG	GCCGGGGACC	TCCGGGACAT	GATCAGCATG	840
	TATCTCCCCC	GCGCCCGAGGT	GCCGGAACCC	GCCGCCCCCA	GCAGACTTCA	CATGTCCCAG	900
75	CACTACCAGA	GCGGCCCGGT	GCCCGGCACG	GCCATTAACG	GCACACTGCC	CCTCTCACAC	960
	ATGTGAGGGC	CUGACAGCGA	ACTGGAGGGG	GGAGAAATTT	TCAAAGAAAA	ACGAGGGAAA	1020
	TGGGAGGGGT AAAAA	GCAAAAGAGG	MUMUTANGAA	ACMOUNTOUR		TACGCTCAAA	7000
80	Seq ID NO:	515 Protei	n sequence	•			
	Protein Acc	cession #: 0	CAA83435				
		11	21	31	41	51	
	î	1	1	1	ĭ	Ĭ.	
85	HSARMYNMME	TELKPPGPOO	TSGGGGGNST	AAAAGGNQKN	SPDRVKRPMN	AFMVWSRGQR	60
	RKMMORNDKM	HNSRISKRIG	AEWKLLSETE	KRPFIDEAKR	LRALHMKEHP	DYKYRPRRKT	120
	KTLMKKDKYT	LPGGLLAPGG	NSMASGVGVG	AGLGAGVNOR	MDSYAHMNGW	SNGSYSMMOD	180

QLGTPQHPGI NAHGAAQMQP MHRYDVSALQ YNSMTSSQTY MHGSPTYSMS YSQQGTPGMA 240 LGSMGSVVKS BASSSPPVVT SSSHBRAPCQ AGDLRDMISM YLPGAEVPEP AAPSRLHHMSQ 300 HYGSGPPVET AINGTLPLSH M

Seq ID NO: 516 DNA sequence Nucleic Acid Accession #: U91618 Coding sequence: 29..541

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		CTGGCTTTCA					120
	AGCATTAGAA	GCAGATTTCT	TGACCAATAT	GCATACATCA	AAGATTAGTA	AAGCACATGT	180
	TCCCTCTTGG	AAGATGACTC	TGCTAAATGT	TTGCAGTCTT	GTAAATAATT	TGAACAGCCC	240
15	AGCTGAGGAA	ACAGGAGAAG	TTCATGAAGA	GGAGCTTGTT	GCAAGAAGGA	AACTTCCTAC	300
	TOCTTTAGAT	GGCTTTAGCT	TGGAAGCAAT	GTTGACAATA	TACCAGCTCC	ACAAAATCTG	360
	TCACAGCAGG	GCTTTTCAAC	ACTGGGAGTT	AATCCAGGAA	GATATTCTTG	ATACTGGAAA	420
	TGACAAAAAT	GGAAAGGAAG	AAGTCATAAA	GAGAAAAATT	CCTTATATTC	TGAAACGGCA	480
	GCTGTATGAG	AATAAACCCA	GAAGACCCTA	CATACTCAAA	AGAGATTCTT	ACTATTACTG	540
20	AGAGAATAAA	TCATTTATTT	ACATGTGATT	GTGATTCATC	ATCCCTTAAT	TAAATATCAA	600
	ATTATATTTG	TGTGAAAATG	TGACAAACAC	ACTTATCTGT	CTCTTCTACA	ATTGTGGTTT	660
	ATTGAATGTG	TTTTTCTGCA	CTAATAGAAA	TTAGACTAAG	TGTTTTCAAA	TAAATCTAAA	720
	TCTTCAAAAA	AAAAAAAAA	AAATGGGGCC	GCAATT			

Seq ID NO: 517 Protein sequence Protein Accession #: AAB50564

	1	11	21	31	41	21	
	1	I	1	1	1	3	
30	MMAGMKIQLV						60
	VCSLVNNLNS	PARETGEVHE	EELVARRKLP	TALDGFSLEA	MLTIYQLHKI	CHSRAFQHWE	120
	T TORRETT DOO	ATT PROPERTY OF THE	WOUTDUTTED	OF VENIFORDS	VITEPONCYVV		

Seq ID NO: 518 DNA sequence Nucleic Acid Accession #: NM_006536.2 Coding sequence: 109..2940

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	ATGTATGCAG	CAGGCTCAGT	GTGAGTGAAC	TGGAGGCTTC	TCTACAACAT	GACCCAAAGG	120
	AGCATTGCAG	GTCCTATTTG	CAACCTGAAG	TTTGTGACTC	TCCTGGTTGC	CTTAAGTTCA	180
	GAACTCCCAT	TCCTGGGAGC	TGGAGTACAG	CTTCAAGACA	ATGGGTATAA	TGGATTGCTC	240
	ATTICANTTA	ATCCTCAGGT	ACCTGAGAAT	CAGAACCTCA	TCTCAAACAT	TAAGGAAATG	300
;	ATAACTGAAG	CTTCATTTTA	CCTATTTAAT	GCTACCAAGA	GAAGAGTATT	TTTCAGAAAT	360
	ATAAAGATTT	TAATACCTGC	CACATGGAAA	GCTAATAATA	ACAGCAAAAT	AAAACAAGAA	420
	TCATATGAAA	AGGCAAATGT	CATAGTGACT	GACTGGTATG	GGGCACATGG	AGATGATCCA	480
	TACACCCTAC	AATACAGAGG	GTGTGGAAAA	GAGGGAAAAT	ACATTCATTT	CACACCTAAT	540
	TTCCTACTGA	ATGATAACTT	AACAGCTGGC	TACGGATCAC	GAGGCCGAGT	GTTTGTCCAT	600
)	GAATGGGCCC	ACCTCCGTTG	GGGTGTGTTC	GATGAGTATA	ACAATGACAA	ACCTTTCTAC	660
	ATABATGGGC	AAAATCAAAT	TAAAGTGACA	AGGTGTTCAT	CTGACATCAC	AGGCATTTTT	720
	GTGTGTGAAA	AAGGTCCTTG	CCCCCAAGAA	AACTGTATTA	TTAGTAAGCT	TTTTAAAGAA	780
	GGATGCACCT	TTATCTACAA	TAGCACCCAA	AATGCAACTG	CATCAATAAT	GTTCATGCAA	840
	AGTTTATCTT	CTGTGGTTGA	ATTTTGTAAT	GCAAGTACCC	ACAACCAAGA	AGCACCAAAC	900
;	CTACAGAACC	AGATGTGCAG	CCTCAGAAGT	GCATGGGATG	TAATCACAGA	CTCTGCTGAC	960
	TTTCACCACA	GCTTTCCCAT	GAATGGGACT	GAGCTTCCAC	CTCCTCCCAC	ATTCTCGCTT	1020
	GTACAGGCTG	GTGACAAAGT	GGTCTGTTTA	GTGCTGGATG	TGTCCAGCAA	GATGGCAGAG	1080
	GCTGACAGAC	TCCTTCAACT	ACAACAAGCC	GCAGAATTTT	ATTTGATGCA	GATTGTTGAA	1140
	ATTCATACCT	TOGTGGGCAT	TGCCAGTTTC	GACAGCAAAG	GAGAGATCAG	AGCCCAGCTA	1200
)	CACCAAATTA	ACAGCAATGA	TGATCGAAAG	TTGCTGGTTT	CATATCTGCC	CACCACTGTA	1260
	TCAGCTAAAA	CAGACATCAG	CATTTGTTCA	GGGCTTAAGA	AAGGATTTGA	GGTGGTTGAA	1320
	BARCTGARTG	GAAAAGCTTA	TGGCTCTGTG	ATGATATTAG	TGACCAGCGG	AGATGATAAG	1380
	CTTCTTGGCA	ATTGCTTACC	CACTGTGCTC	AGCAGTGGTT	CAACAATTCA	CTCCATTGCC	1440
	CTGGGTTCAT	CTGCAGCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500
	TTCTTTGTTC	CAGATATATC	AAACTCCAAT	AGCATGATTG	ATGCTTTCAG	TAGAATTTCC	1560
	TCTGGAACTG	GAGACATTTT	CCAGCAACAT	ATTCAGCTTG	AAAGTACAGG	TGAAAATGTC	1620
	AAACCTCACC	ATCAATTGAA	AAACACAGTG	ACTGTGGATA	ATACTGTGGG	CAACGACACT	1680
	ATGTTTCTAG	TTACGTGGCA	GGCCAGTGGT	CCTCCTGAGA	TTATATTATT	TGATCCTGAT	1740
	GGACGAAAAT	ACTACACAAA	TAATTTTATC	ACCAATCTAA	CTTTTCGGAC	AGCTAGTCTT	1800
)	TGGATTCCAG	GARCAGCTAA	GCCTGGGCAC	TGGACTTACA	CCCTGAACAA	TACCCATCAT	1860
	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGCGCCT	CCAACTCAGC	TGTGCCCCCA	1920
	GCCACTGTGG	AAGCCTTTGT	GGAAAGAGAC	ACCCTCCATT	TTCCTCATCC	TGTGATGATT	1980
	TATGCCAATG	TGAAACAGGG	ATTTTATCCC	ATTCTTAATG	CCACTGTCAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100
5	GTTATAAAAA	ATGATGGAAT	TTACTCGAGG	TATTTTTTCT	CCTTTGCTGC	AAATGGTAGA	2160
	TATAGCTTGA	AAGTGCATGT	CAATCACTCT	CCCAGCATAA	GCACCCCAGC	CCACTCTATT	2220
	CCAGGGAGTC	ATGCTATGTA	TGTACCAGGT	TACACAGCAA	ACGGTAATAT	TCAGATGAAT	2280
	GCTCCAAGGA	AATCAGTAGG	CAGAAATGAG	GAGGAGCGAA	AGTGGGGCTT	TAGCCGAGTC	2340
	AGCTCAGGAG	GCTCCTTTTC	AGTGCTGGGA	GTTCCAGCTG	GCCCCCACCC	TGATGTGTTT	2400
)	CCACCATGCA	ABATTATTGA	CCTGGAAGCT	GTAAAAGTAG	AAGAGGAATT	GACCCTATCT	2460
	TOGRERGER	CTCCAGAGAGA	CTTTGATCAG	GGCCAGGCTA	CAAGCTATGA	AATAAGAATG	2520
	AGTAAAAGTC	TACAGAATAT	CCAAGATGAC	TTTAACAATG	CTATTTTAGT	AAATACATCA	2580
	ABGCCIABATC	CTCAGCAAGC	TGGCATCAGG	GAGATATTTA	CGTTCTCACC	CCAGATTTCC	2640
	ACCIA ATCCAC	CTYCARCATCA	GCCARATGGA	GARACACATG	AAAGCCACAG	AATTTATGTT	2700
5	GCAATACGAG	CARTGGATAG	GRACTCCTTA	CAGTCTGCTG	TATCTAACAT	TGCCCAGGCG	2760
	CCTCTGTTTA	TTCCCCCCAA	TTCTGATCCT	GTACCTGCCA	GAGATTATCT	TATATTGAAA	2820
	GGAGTTTTAA	CAGCAATGGG	TTTGATAGGA	ATCATTTGCC	TTATTATAGT	TGTGACACAT	2880

		GCAGGAAAAA					2940
	ATAAATATCC	AAAGTGTCTT	CCTTCTTAGA	TATAAGACCC	ATGGCCTTCG	ACTACAAAAA	3000
		AAGTCAAATT					3060
	ATACAGATAA	GATTTTTACA	TGGTAGATCA	ACAATTCTTT	TTGGGGGTAG	ATTAGAAAAC	3120
5	CCTTACACTT	TGGCTATGAA	CAAATAATAA	AAATTATTCT	TTARAGTRAT	GTCTTTAAAG	3180
	GCAAAGGGAA	GGGTAAAGTC	GGACCAGTGT	CAAGGAAAGT	TTGTTTTATT	GAGGTGGAAA	3240
	AATAGCCCCA	AGCAGAGAAA	AGGAGGGTAG	GTCTGCATTA	TAACTGTCTG	TGTGAAGCAA	3300
	TCATTTAGTT	ACTITIGATEA	ATTTTTCTTT	TCTCCTTATC	TGTGCAGTAC	AGGTTGCTTG	3360
	TTTACATGAA	GATCATGCTA	TATTTTATAT	ATGTAGCCCC	TAATGCAAAG	CTCTTTACCT	3420
10	CTTGCTATTT	TGTTATATAT	ATTTCAGATG	ACATCTCCCT	GCTAATGCTC	AGAGATCTTT	3480
	TTTCACTGTA	AGAGGTAACC	TTTAACAATA	TGGGTATTAC	CTTTGTCTCT	TCATACCGGT	3540
	TTTATGACAA	AGGTCTATTG	AATTTATTTG	TNTGTAAGTT	TCTACTCCCA	TCAAAGCAGC	3600
	TTTCTAAGTT	TATTGCCTTG	GGTTATTATG	GAATGATAGT	TATAGCCCCN	TATAATGCCT	3660
	TACCTAGGAA						
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Seq ID NO: 519 Protein sequence Protein Accession #: NP_006527.1

						51	
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		CNLKFVTLLV					60
	IKEMITEASF	YLFNATKRRV	PPRNIKILIP	ATWKANNNSK	IKQESYEKAN	VIVTDWYGAH	120
	GDDPYTLOYR	GCGKEGKYIH	FTPNFLLNDN	LTAGYGSRGR	VPVHEWAHLR	WGVFDEYNND	180
	KPPYINGONO	IKVTRCSSDI	TGIFVCEKGP	CPOENCIISK	LPKEGCTFIY	NSTQNATASI	240
25	MFMOSLSSVV	EFCNASTHNO	EAPNLONOMC	SLRSAWDVIT	DSADFHHSFP	MNGTELPPPP	300
	TESTAVOAGOK	VVCLVLDVSS	KMAEADRLLO	LOOAABFYLM	QIVRIHTFVG	IASFDSKGEI	360
	RAOLHOINSN	DDRKLLVSYL	PTTVSAKTDI	SICSGLKKGF	EVVEKLNGKA	YGSVMILVTS	420
	GDDKLLGNCL	PTVLSSGSTI	HSIALGSSAA	PNLEELSRLT	GGLKFFVPDI	SNSNSMIDAF	480
	SRISSGTGDI	FCOHIQLEST	GENVKPHHQL	KNTVTVDNTV	GNDTMFLVTW	QASGPPEIIL	540
30	PDPDGRKYYT	NNFITNLTFR	TASLWIPGTA	KPGHWTYTLN	NTHHSLQALK	VTVTSRASNS	600
	AVPPATVEAF	VERDSLHFPH	PVMIYANVKQ	GFYPILNATV	TATVEPETGD	PVTLRLLDDG	660
	AGADVIKNDG	IYSRYFFSFA	ANGRYSLKVH	VNHSPSISTP	AHSIPGSHAM	YVPGYTANGN	720
	TOMNAPRKSV	GRNEEERKWO	PSRVSSGGSP	SVLGVPAGPH	PDVFPPCKII	DLEAVKVEEE	780
	TAT OUT DOD	DFDQGQATSY	ELDWCKCI'ON	I ODDENNATL	VNTSKRNPOO	AGIREIFTFS	840
35	POISTNOPEH	QPNGETHESH	RIYVAIRAMD	RNSLOSAVSN	IAQAPLFIPP	NSDPVPARDY	900
	LILKGVLTAM	GLIGIICLII	VVTHHTLSRK	KRADKKENGT	KLL		

Seq ID NO: 520 DNA sequence
Nucleic Acid Accession #: NM_000228.1
Coding sequence: 82..3600

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	Ī	1	1	1	1	1	
	GCTTTCAGGC	GATCTGGAGA	AAGAACGGCA	GAACACACAG	CAAGGAAAGG	TCCTTTCTGG	60
45	GGATCACCCC	ATTGGCTGAA	GATGAGACCA	TTCTTCCTCT	TGTGTTTTGC	CCTGCCTGGC	120
	CTCCTGCATG	CCCAACAAGC	CTGCTCCCGT	GGGGCCTGCT	ATCCACCTGT	TGGGGACCTG	180
	CTTGTTGGGA	GGACCCGGTT	TCTCCGAGCT	TCATCTACCT	GTGGACTGAC	CAAGCCTGAG	240
	ACCTACTGCA	CCCAGTATGG	CGAGTGGCAG	ATGAAATGCT	GCAAGTGTGA	CTCCAGGCAG	300
	CCTCACAACT	ACTACAGTCA	CCGAGTAGAG	AATGTGGCTT	CATCCTCCGG	CCCCATGCGC	360
50	TGGTGGCAGT	CCCAGAATGA	TGTGAACCCT	GTCTCTCTGC	AGCTGGACCT	GGACAGGAGA	420
	TTCCAGCTTC	AAGAAGTCAT	GATGGAGTTC	CAGGGGCCCA	TGCCCGCCGG	CATGCTGATT	480
	GAGCGCTCCT	CAGACTTCGG	TAAGACCTGG	CGAGTGTACC	AGTACCTGGC	TGCCGACTGC	540
	ACCTCCACCT	TCCCTCGGGT	CCGCCAGGGT	CGGCCTCAGA	GCTGGCAGGA	TGTTCGGTGC	600
	CAGTCCCTGC	CTCAGAGGCC	TAATGCACGC	CTAAATGGGG	GGAAGGTCCA	ACTTAACCTT	660
55	ATGGATTTAG	TGTCTGGGAT	TCCAGCAACT	CARAGTCARA	AAATTCAAGA	GGTGGGGGAG	720
	ATCACAAACT	TGAGAGTCAA	TTTCACCAGG	CTGGCCCCTG	TGCCCCAAAG	GGGCTACCAC	780
	CCTCCCAGCG	CCTACTATGC	TGTGTCCCAG	CTCCGTCTGC	AGGGGAGCTG	CTTCTGTCAC	840
	GGCCATGCTG	ATCGCTGCGC	ACCCAAGCCT	GGGGCCTCTG	CAGGCCCCTC	CACCGCTGTG	900
	CAGGTCCACG	ATGTCTGTGT	CTGCCAGCAC	AACACTGCCG	GCCCAAATTG	TGAGCGCTGT	960
60	GCACCCTTCT	ACAACAACCG	GCCCTGGAGA	CCGGCGGAGG	GCCAGGACGC	CCATGAATGC	1020
	CARAGGTGCG	ACTGCAATGG	GCACTCAGAG	ACATGTCACT	TTGACCCCCC	TGTGTTTGCC	1080
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	AACTGTGAGC	GGTGTCAGCT	GCACTATTTC	CGGAACCGGC	GCCCGGGAGC	TTCCATTCAG	1200
	GAGACCTGCA	TCTCCTGCGA	GTGTGATCCG	GATGGGGCAG	TGCCAGGGGC	TCCCTGTGAC	1260
65	CCAGTGACCG	GGCAGTGTGT	GTGCAAGGAG	CATGTGCAGG	GAGAGCGCTG	TGACCTATGC	1320
	AAGCCGGGCT	TCACTGGACT	CACCTACGCC	AACCCGCAGG	GCTGCCACCG	CTGTGACTGC	1380
	AACATCCTGG	GGTCCCGGAG	GGACATGCCG	TGTGACGAGG	AGAGTGGGCG	CTGCCTTTGT	1440
	CTGCCCAACG	TGGTGGGTCC	CAAATGTGAC	CAGTGTGCTC	CCTACCACTG	GAAGCTGGCC	1500
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70	CAACCAGTTC	ACAGGGCAGT	GCCCTGTCGG	GAAGGCTTTG	GTGGCCTGAT	GTGCAGCGCT	1620
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	TGTGACTGTG	ATTTCCGGGG	AACAGAGGGC	CCGGGCTGCG	ACAAGGCATC	AGGCCGCTGC	1740
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	CCCTACCCGG	TOTGCGTGGC	CTGCCACCCT	TGCTTCCAGA	CCTATGATGC	GGACCTCCGG	1860
75	GAGCAGGCCC	TGOGCTTTGG	TAGACTCCGC	AATGCCACCG	CCAGCCTGTG	GTCAGGGCCT	1920
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	ATCCGAGCAG	TTCTCAGCAG	CCCCGCAGTC	ACAGAGCAGG	AGGTGGCTCA	GGTGGCCAGT	2040
	GCCATCCTCT	CCCTCAGGCG	AACTCTCCAG	GGCCTGCAGC	TGGATCTGCC	CCTGGAGGAG	2100
	GAGACGTTGT	CCCTTCCGAG	AGACCTGGAG	AGTCTTGACA	GAAGCTTCAA	TGGTCTCCTT	2160
80	ACTATGTATC	AGAGGAAGAG	GGAGCAGTTT	GAAAAAATAA	GCAGTGCTGA	TCCTTCAGGA	2220
	GCCTTCCGGA	TGCTGAGCAC	AGCCTACGAG	CAGTCAGCCC	AGGCTGCTCA	GCAGGTCTCC	2280
	GACAGCTCGC	GCCTTTTGGA	CCAGCTCAGG	GACAGCCGGA	GAGAGGCAGA	GAGGCTGGTG	2340
	CGGCAGGCGG	GAGGAGGAGG	AGGCACCGGC	AGCCCCAAGC	TTGTGGCCCT	GAGGCTGGAG	2400
	ATGTCTTCGT	TGCCTGACCT	GACACCCACC	TTCAACAAGC	TCTGTGGCAA	CTCCAGGCAG	2460
85	ATGGCTTGCA	CCCCAATATC	ATGCCCTGGT	GAGCTATGTC	CCCAAGACAA	TGGCACAGCC	2520
	TOTOGCTCCC	CCTCCAGGGG	TGTCCTTCCC	AGGGCCGGTG	GGGCCTTCTT	GATGGCGGGG	2580
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		AGGAATCTGC	CTCACAGATT	CAATCCAGTG	CCCAGCGCTT	GGAGACCCAG	2700
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	CAGGTCCGGG	ACTTCCTAAC	AGACCCCGAC	ACTGATGCAG	CCACTATCCA	GGAGGTCAGC	2820
5	GAGGCCGTGC	TGGCCCTGTG	GCTGCCCACA	GACTCAGCTA	CTGTTCTGCA	GAAGATGAAT	2880 2940
3	GAGATCCAGG	CCATTGCAGC	CAGGCTCCCC	AACGIGGACT	AGGRAGGCAG	CAGACCAAGC	3000
	CATGCACTGG	AGGGCCAGGT	GGAAGATGTG	GTTGGGAACC	TGCGGCAGGG	GACAGTGGCA	3060
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10	AAGCAGCTGG	GTGACTTCTG	GACACGGATG	GAGGAGCTCC	GCCACCAAGC	CCGGCAGCAG	3240
	GGGGCAGAGG	CAGTCCAGGC	CCAGCAGCTT	GCGGAAGGTG	CCAGCGAGCA	GGCATTGAGT	3300 3360
	GCCCAAGAGG	GATTTGAGAG	AATAAAACAA	AAGTATGCTG	AGTTGAAGGA	CCGGTTGGGT	3420
	CAGAGTTCCA	TGCTGGGTGA GGGAGACCAT	CCAGGGGGGCC	CACACCATCA	BAGACATGGA	CTTCGACCTG	3480
15	CTGCCGCGCA	GCCAGGCCAT	CATGCTGCGC	TCGGCGGACC	TGACAGGACT	GGAGAAGCGT	3540
15	GTGGAGCAGA	TCCGTGACCA	CATCAATGGG	CGCGTGCTCT	ACTATGCCAC	CTGCAAGTGA	3600
	TGCTACAGCT	TCCAGCCCGT	TGCCCCACTC	ATCTGCCGCC	TTTGCTTTTG	GTTGGGGGCA	3660
	GATTGGGTTG	GAATGCTTTC	CATCTCCAGG	AGACTTTCAT	GCAGCCTAAA	GTACAGCCTG	3720
20	GACCACCCCT	GGTGTGTAGC	TAGTAAGATT	ACCCTGAGCT	GCAGCTGAGC	CTGAGCCAAT	3780 3840
20	GGGACAGTTA	CACTTGACAG	ACAAAGATGG	TGGAGATTGG	CATGUCATTO	CONCRECCE	3900
	CTCTCAAGTC	AAGGAAGCTG ACCAAGCACA	AAAA COTTAAC	AAAAGTGATG	TABABATTO	AAGCCAAATA	3960
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	MANICITIO	· ·					
25		521 Protein					
	Protein Acc	ession #: 1	NP_000219.1				
				31	41	51	
	1	11	21	31	41	21	
30	ACCOUNT OF THE	LPGLLHAQQA	CODGREVEDO	CDLLVCBTDD	LDASSTORIA	KPETYCTOYG	60
50	PROMECCEC	SROPHNYYSH	RVENVASSSG	PMRWWOSOND	VNPVSLOLDL	DRRFOLOEVM	120
	MEFOGPMPAG	MLIERSSDFG	KTWRVYOYLA	ADCTSTFPRV	ROGRPQSWQD	VRCQSLPQRP	180
	MARINGGRUO	INTADIASGI	PATOSOKIOE	VGEITNLRVN	PTRLAPVPOR	GYHPPSAYYA	240
	VSQLRLQGSC	FCHGHADRCA	PKPGASAGPS	TAVQVHDVCV	COHNTAGPNC	ERCAPFYNNR	300
35	PWRPAEGQDA	HECORCDONG	HSETCHPDPA	VFAASQGAYG	GVCDNCRDHT	EGXNCERCOL	360
	HYFRNRRPGA	SIQUETCISCE	CDPDGAVPGA	PCDPVTGQCV	CKEHVQGERC	DLCKPGFTGL	420 480
	TYANPOGCHR	PTVQPVHRAV	DMPCDEESGR	CLCLPNVVGP	RCDQCAPIHW	CDACTICTURE	540
	TECHCOPENSIO	GRCLCRPGLT	appendence	ACMBADACAY	CHPCFOTYDA	DI-REOAL-REG	600
40	PLPNATASLW	SCPCLEDRGL	ASRILDAKSK	IEOIRAVLSS	PAVTEQEVAQ	VASAILSLRR	660
-10	TLOGLOLDLP	LEESTLSLPR	DLESLDRSFN	GLLTMYQRKR	EQFEKISSAD	PSGAFRMLST	720
	AYEOSAGAAO	OVSDSSRLLD	OLRDSRREAB	RLVRQAGGGG	GTGSPKLVAL	RLEMSSLPDL	780
	TPTFNKLCGN	SROMACTRIS	CPGELCPQDN	GTACGSRCRG	VLPRAGGAFL	MAGQVAEQLR	840
4.5	GFNAQLQRTR	QMIRAAEESA	SQIQSSAQRL	ETQVSASRSQ	MBEDVRRTRL	LIQQVRDFLT	900
45	DPDTDAATIQ	EVSEAVLALW	LPTDSATVLQ	KMNEIQAIAA	RLPNVDLVLS	QTKQDIARAR	960
	RLQAEABEAR	SRAHAVEGQV SMTKQLGDFW	EDVVGNLRQG	TVALQEAQDT	MOGTSRSLRL	IQDRVAEVQQ	1020
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	MIRRADIAGE	EKRVEQIRDE	INGRYLYYAT	CK	Za a a de la calación	201111100	
50							
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	ccaing seq	dence: 84	3083				
55	1	11	21	31	41	51	
	ī	ī	Ī	1	1 :	1	
	TTTTCTTAGA	CATTAACTGC	AGACGGCTGG	CAGGATAGAA	GCAGCGGCTC	ACTTGGACTT	60
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	CTATACTCCA	CCGGGAGGAA	ACTCCAAGCT	TCCTGATCAC	ATGTCGGGCT	CTAAATGCCC	480
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	AAATTGCCTT	CAAAATTGTC	TCTCAGGAAC	CAGCAGGCAC	ACCCATGTTC	CTUCTARGCA	780
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	CAGCACGTAT	TGAAGAAAAT	ATTTTAAGTT	CIGAATTACT	TCGATTTCAA	GTAACAGATT	960
	TOGRTGRAGE	GTACACAGAT	AATTGGCTTG	CAGTATATTT	CTTTACCTCT	GGGAATGAAG	1020
	GAAATTGGTT	TGAAATACAA	ACTGATCCTA	GAACTAATGA	AGGCATCCTG	AAAGTGGTGA	1080
75	AGGCTCTAGA	TTATGAACAA	CTACAAAGCG	TGAAACTTAG	TATTGCTGTC	AAAAACAAAG	1140
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	ATCACCAC	TAACAAAGCT	GCCTCAAATG	TCAAATATOT	CATGGGACGT	AACGATGGTG	1380
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	ATTCTACTT	CATAGTTAAC	AAAACAATCA	CAGCTGAGGT	TCTGGCCATA	GATGAATACA	1500
	CGGGTAAAAC	TTCTACAGGC	ACCCTATATO	TTAGAGTACC	CGATTTCAAT	GACAATTGTC	1560
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85	TAAAGTTGCC	TGCCGTATGG	AGTATCACAA	CCCTCAATGC	TACUTOGGCC	CICUICAGAG	1740 1800
	CCCAGGAACA	GATACCTCCT TGAGATGCCA	GGAGTATACC	CACTCOCCT	GGTACTTACA	GACAACAGGG	1860
	ACAATCGGTG	1 GAGATUCCA	COCAGCTTGA	CACIGGRAGI	CIGICAGIGI	U.L.	1000

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	OKIKTOOTET	DOGGET MEDGE	TARTERINA	MDDOTETUNE	TITARULATO	QPVKLPAVWS	480
40	SHVKIVEGER	DOGILMIDOR	TABLE VERN	HICKORY MINY	TODYTOALED	DWWI.DAWWG	540
40	VYVKVPDPND	NCPTAVLERO	AVCSSSPSVV	CONTROLLING	OT ST PROCES	MCT CCTCVD	600
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	TTSPGTRYGR	PHSGRLGPAA	IGPPPRGPPP	LUCAPULLET	CDCGMGSTGG	VTGGFIPVPD	720
	GSEGTIHQWG	IEGAHPEDKE	ITNICVPPVT	ANGADIMESS	BYCINTIARG	TAVEGTSGME	780
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	LDDSFLDSLG	PKFKKLABIS	LGVDGEGKEV	QPPSKDSGYG	IESCGHPIEV	QQTGFVKCQT	900
	LSGSQGASAL	SASGSVQPAV	SIPDPLQHGN	YLVTETYSAS	GSLVQPSTAG	POPLLTQNVI	960
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	CACCCAAAM	ATOCCARCAG	CATACATTOT	TTTGGTTTTT	CTAACTTTCT	TTTAAGACCA GAAAAAAATT	1140
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Seq ID NO: 525 Protein sequence Protein Accession #: P39900

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**TPENDREND' O'ATRENAGU MENUTPLEGE KINTOLELI UYRIGANGO FILATONGO!
LAMANGUSSO IGGOARTDO ENTITUDUT INFITANTI GREGICIES DENAMPETUL
LAMANGUSSO IGGOARTDO ENTITUDUT INFITANTI GREGICIES DENAMPETUL
FINIPPIALS ERENTSON. ISSLMPTIES GLEANTEEA REQUELTOO KINLISULEE
ENTPESTIS FURNIVAKI DANFIEREY RYPFVORGY HEYDERGOM DEGUFFLITK
NOGIOPEID ANYSSINKY YPFOSROPE YDELGITK TLEASHORD 180 240 300 360 420 5

Seq ID NO: 526 DNA sequence Nucleic Acid Accession #: NM_024423.1

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20	TACACAGCCA	GGGCTGTTGC	GCTGTCTGAT	AAGAAAAGAT	CATTTACCAT	ATGGCTTTCT	360 420
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		GGAGCCTCAC					2040
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	ACCOR ACCOR	TOTAL COMPACE	TATGGGATCA	CCSSTVINASA	ATGGAGGGCA	GGAAACCATT	2340 2400 2460
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	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTGAAGAAT	CCATTAGAGG	ACACACTGGT	2560
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40							6840
40	ACTTCTGTGT	GACCTTTGAA	AGGCTACTTA	TTTCCTCTCT	TAGCTTTCTC TTAGTTAATA	ATTAAAATCA	6900
	ATGAACAATG	CCAGCCTCAT	GGGGTTGTTG	AATGATTAAA	TTAGTTAATA	TACCINGAGT	6960
	ACATAGAACA	CTGCCTGCAC	ATAGTAAAAG	AATTATAAGT	GTGAGGTAGT	TGGTAAAATT	7020
	ATGTAGTTGG	ATATACTACC	GAACAATATC	TAATCTCTTT	TTAGGGAAAT	AAAGTTTGTG	7020
40	CATATATATA	ATCCCGAAAC	ATG				
45							
45	Seq ID NO:	527 Protei	a sequence				
45	Seq ID NO:		a sequence				
45	Seq ID NO: Protein Ac	527 Protein cession #: 1	n sequence NP_077741.1				
	Seq ID NO:	527 Protei	a sequence	31	41	51	
45 50	Seq ID NO: Protein Act	527 Protein cession #: 1	n sequence NP_077741.1 21	Ĩ.	i	1	
	Seq ID NO: Protein Act	527 Protein cession #: 1	n sequence NP_077741.1 21 TLVIFSRDGE	ACKKVILNVP	SKLEADKIIG	 RVNLEECFRS	60
	Seq ID NO: Protein Acc	527 Protein cession #: 1	a sequence NP_077741.1 21 TLVIFSRDGE	ACKKVILNVP KRSPTIWLSD	SKLEADKIIG KRKOTOKEVT	RVNLEECFRS VLLEHOKKVS	120
	Seq ID NO: Protein Act 1 MARAGPRRSV ADLIRSSDPD	527 Proteincession #: 1 11 RGAVCLHLLL PRVLNDGSVY	Bequence NP_077741.1 21 TLVIFSRDGE TARAVALSDK	ACKKVILNVP KRSPTIWLSD PFPLFLOOVE	SKLEADKIIG KRKQTQKEVT SDAAONYTVP	RVNLEECFRS VLLEHQKKVS YSISGRGVDK	120 180
50	Seq ID NO: Protein Act 1 MAAAGPRRSV ADLIRSSDPD RTRHTRETVL	527 Protein cession #: 1 11 RGAVCLHLLL PRVIMDGSVY RRAKRRWAPI	n sequence NP_077741.1 21 TLVIPSRDGE TARAVALSDK PCSMQENSIG	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG	SKLEADKIIG KRKQTQKEVT SDAAQNYTVP YSADLPLPLP	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENDNH	120 180 240
	Seq ID NO: Protein Act	527 Protein cession #: 1 11 RGAVCLELLL PRVINDGSVY RRAKRRWAPI DTGNLPCTR EVLESSRPGT	a sequence NP_077741.1 21 TLVIFSRDGE TARAVALSDK PCSMQENSLG VDREEYDVFD TVGVVCATDR	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG DEPDIMHTRL	SKLEADKIIG KRKQTQKEVT SDAAQNYTVF YSADLPLPLP KYSILQQTPR	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENDNH SPGLFSVHPS	120 180 240 300
50	Seq ID NO: Protein Act i i MAAAGPRRSV ADLIRSSDF KTRHTRETVL EPLNLFYIER PVFTEAIYNF TGVITTVSHY	527 Protein cession #: 1 11 	n Bequence NP_077741.1 21 † TLVIFSRDGE TARAVALSDK PCSMQENSLG VDREEYDVFD TVGVVCATDR LIMKVQDMDG	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMHTRL QFFGLIGTST	SKLEADKIIG KRKQTQKEVT SDAAQNYTVF YSADLPLPLP KYSILQQTFR CIITVTDSND	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENDNH SPGLFSVHPS NAPTFRQNAY	120 180 240 300 360
50	Seq ID NO: Protein Act i MAAAGPRRSV ADLIRSSDPD KTRHTRETVL EPLANLFYIER PVFTEALYNP TGVITTVSHY TGVITTVSHY	527 Protein cession #: 1 11 RGAVCLBLLL FRYLANDGSVY RRAKRRWAPI DTGNLFCTRP EVLESSRPGT LDREVVDKYE VBILRIVDKYE	a sequence NP_077741.1 21 TLVIFSRDGE TARAVALSDK PCSNQENSLG VDREEYDVFD TVGVVCATDR LIMKVQDMDG	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMHTRL QFPGLIGTST VNPTILKGNE	SKLEADKIIG KRKQTQKEVT SDAAQNYTVF YSADLPLPLF KYSILQQTPR CIITVTDSND NGHFKISTDK	RVNLEECFRS VLLEHQKKVS YS ISGRGVDK IRVEDENDNH SPGLFSVHPS NAPTFRQNAY ETNEGVLSVV	120 180 240 300 360 420
50	Seq ID NO: Protein Act MAAAGPRRSV ADLIRSSDPD KIRHTRETVL EPLNLFYIER PVFTEALYNP TGVITTVSHY EAFVEENAFN	527 Protein cession #: 1 11 RGAVCLBLLL PRVLNDGSVY RRAKRWAPI DTGMLPCTRP EVLESSRPGT LDREVVDKYS VEILRIPIED	L SEQUENCE NP_077741.1 21 TLVIFSRDGE TARAVALSDK PCSMQENSLG VDREEYDVFD TVGVVCATDR LIMKVQDMDG KDLINTANWR	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMHTRL QFFGLIGTST VNPTILKGNE TALMRALVTV	SKLEADKIIG KRKQTQKEVT SDAAQNYTVF YSADLPLPLE KYSILQQTFR CIITVTDSND NGHFKISTDK HVRDLDEGPB	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENDNH SPGLFSVHPS NAPTFRQNAY ETNEGVLSVV CTPAAQYVRI	120 180 240 300 360 420 480
50 55	Seq ID NO: Protein Act MAAAGPRRSV ADLIESSDPD KTRHTESTVL EPLNLPYIER PVFTEAIYNP TGVITTVSHY EAFVEENAFN KPLNYEENAFN KPLNYEENAFN	527 Protein cession #: 1 11 RGAVCLHLLL PRVLNDGSVY RRAKRWAPI DTGNLFCTRP EVLESSRPGT LDREVVDKYS VEILRIPTED VNLEIGVNNE	n sequence NP_077741.1 21 TLVIFSRDGE TARAVALSDK PCSMGENSIG VDREEYDVFD TVGVVCATDR LIMKVQDMDG KDLINTANWR APFARDIPRV	ACKKVILNVP KRSFTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMHTRL QFPGLIGTST VNFTILKGNE TALNRALVIT	SKLEADKIIG KRKQTQKEVT SDAAQNYTVF YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENDNH SPGLFSVHPS NAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP	120 180 240 300 360 420 480 540
50 55	Seq ID NO: Protein Act MAAAGPRRSV ADLIESSDPD KTRHTESTVL EPLNLPYIER PVFTEAIYNP TGVITTVSHY EAFVEENAFN KPLNYEENAFN KPLNYEENAFN	527 Protein cession #: 1 11 RGAVCLHLLL PRVLNDGSVY RRAKRWAPI DTGNLFCTRP EVLESSRPGT LDREVVDKYS VEILRIPTED VNLEIGVNNE	n sequence NP_077741.1 21 TLVIFSRDGE TARAVALSDK PCSMGENSIG VDREEYDVFD TVGVVCATDR LIMKVQDMDG KDLINTANWR APFARDIPRV	ACKKVILNVP KRSFTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMHTRL QFPGLIGTST VNFTILKGNE TALNRALVIT	SKLEADKIIG KRKQTQKEVT SDAAQNYTVF YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENDNH SPGLFSVHPS NAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP	120 180 240 300 360 420 480 540 600
50	Seq ID NO: Protein Act MANAGPRRSV ADLIRSSDPD KTRHTRETVL EPLANLFYIER PUFTEALYMP EAFVEENAFN KPLAVEGRKI KENLAVGGKI KENLAVGGKI KRELVNITVL	527 Proteinession #: 1 11 RGAVCLHLLL PRVLNDGSVY RRAKRWAPI DTGNLFCTRP EVLESSRGT LDREVUDKYS VEILRIPIED VNLEIGWNNE MGYKAYDPEN AIDKODRSCT	a sequence nP_077741.1 21	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMEHTHL QFFGLIGTST VNFTILKGNE TALNRALVTV LEDPKGWITI NDNPPEILQE	SKLEADKIIG KRKQTQKEVT SDAAQNYTVF YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS YVVICKPKRA AGPORYTIPI	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENDNH SPGLFSVHPS NAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP YTDILAVDPD TVKDRAGOAA	120 180 240 300 360 420 480 540 600
50 55	Seq ID NO: Protein Act MANAGPRRSV ADLIRSSDPD KTRHTRETVL EPLMLPYIER PVFTEAIYNP TGVITTVSHY EAFVEENARM KPLNYESRRQ KENLAVGSKI KMELVNITVL EVUGGAPFVR	527 Proteicession #: 1 11 RGAVCLHLLL FRVLNDGSVY FRAKRRWAPI DTGHLPCTRP EVLESSRPGT LDREVVDKYS VBILRIPTED MGYKAYDPEN MGYKAYDPEN AIDKODRSCT SLPHTSPEIS SLPHTSPEIS	D BEQUENCE DE OTTO THE TOTAL TO THE TOTAL THE	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMHTRL QFFGLIGTST VNFTILKGNE TALWRALVTV LHDPKGWITI NDNPPEILQE TAARLSTYGKN	SKLEADKIIG KRKQTQKEVT SDAAQNYTVP YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS YVVICKPKMG AGPQEYTIPI	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENINH SPGLFSVHPS MAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP YTDILAVDPD TVKDRAGQAA VCTSVFRATKG	120 180 240 300 360 420 480 540 600 660 720
50 55	Seq ID NO: Protein Act MANAGPRRSV ADLIRSSDPD KTRHTRETVL EPLMLPYIER PVFTEAIYNP TGVITTVSHY EAFVEENARM KPLNYESRRQ KENLAVGSKI KMELVNITVL EVUGGAPFVR	527 Proteicession #: 1 11 RGAVCLHLLL FRVLNDGSVY FRAKRRWAPI DTGHLPCTRP EVLESSRPGT LDREVVDKYS VBILRIPTED MGYKAYDPEN MGYKAYDPEN AIDKODRSCT SLPHTSPEIS SLPHTSPEIS	D BEQUENCE DE OTTO THE TOTAL TO THE TOTAL THE	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMHTRL QFFGLIGTST VNFTILKGNE TALWRALVTV LHDPKGWITI NDNPPEILQE TAARLSTYGKN	SKLEADKIIG KRKQTQKEVT SDAAQNYTVP YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS YVVICKPKMG AGPQEYTIPI	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENINH SPGLFSVHPS MAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP YTDILAVDPD TVKDRAGQAA VCTSVFRATKG	120 180 240 300 360 420 480 540 600
50 55 60	Seq ID NO: Protein Act MANAGPRRSV ADLIRSSDPD KTRHTRETVL EPLMLPYIER PVFTEAIYNP TGVITTVSHY EAFVEENARM KPLNYESRRQ KENLAVGSKI KMELVNITVL EVUGGAPFVR	527 Proteicession #: 1 11 RGAVCLHLLL FRVLNDGSVY FRAKRRWAPI DTGHLPCTRP EVLESSRPGT LDREVVDKYS VBILRIPTED MGYKAYDPEN MGYKAYDPEN AIDKODRSCT SLPHTSPEIS SLPHTSPEIS	D BEQUENCE DE OTTO THE TOTAL TO THE TOTAL THE	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMHTRL QFFGLIGTST VNFTILKGNE TALWRALVTV LHDPKGWITI NDNPPEILQE TAARLSTYGKN	SKLEADKIIG KRKQTQKEVT SDAAQNYTVP YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS YVVICKPKMG AGPQEYTIPI	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENINH SPGLFSVHPS MAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP YTDILAVDPD TVKDRAGQAA VCTSVFRATKG	120 180 240 300 360 420 480 540 600 660 720
50 55 60	Seq ID NO: Protein Act MANAGPRRSV ADLIRSSDPD KTRHTRETVL EPLMLPYIER PVFTEAIYNP TGVITTVSHY EAFVEENARM KPLNYESRRQ KENLAVGSKI KMELVNITVL EVUGGAPFVR	527 Proteicession #: 1 11 RGAVCLHLLL FRVLNDGSVY FRAKRRWAPI DTGHLPCTRP EVLESSRPGT LDREVVDKYS VBILRIPTED MGYKAYDPEN MGYKAYDPEN AIDKODRSCT SLPHTSPEIS SLPHTSPEIS	D BEQUENCE DE OTTO THE TOTAL TO THE TOTAL THE	ACKKVILNVP KRSPTIWLSD PFPLFLQQVE LIAYASTADG DEPDTMHTRL QFFGLIGTST VNFTILKGNE TALWRALVTV LHDPKGWITI NDNPPEILQE TAARLSTYGKN	SKLEADKIIG KRKQTQKEVT SDAAQNYTVF YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS YVVICKPKRA AGPORYTIPI	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENINH SPGLFSVHPS MAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP YTDILAVDPD TVKDRAGQAA VCTSVFRATKG	120 180 240 300 360 420 480 540 600 660 720
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50 55 60	Seq ID NO: Protein Act i MAAAGPRRSV ADLIRSSDPD KTRHTRETUL EPIANLFYIER PUFTEAI YMP EMPLENAPN KENLYESH KRELVEINTUL EVERAPFYE TKLLEVNICE KREPEDLAQQ MMKGGNOTLE Seq ID NO:	527 Proteinession #:1 RGAVCLHLLL FRVLNDGSVY RRAKRRWAPI DTGNLFCTRP EVLESSRPOT LDREVVDKYS VBILRIPTED VNLEIGVNNES MGYKAYDPEN AIDKODRSCT SLPWISPEIS CTHEPYGRAT NLIISNTEAP SCRGAGHHT 528 DNA se	a Bequence nP_077741.1 21 TLVIFSRDGE TARAVALSDK PCSMQENSLG VDREEYDVFD TVGVVCATDR LIMKVQDMDG KDLINTAMMR APFADI PRV RNGNGLRYKK GTLAVNI EDV RLMSLTKVAD SRSTGVI IJGK GDDRVCSANG LDSCRGGHTE Quence	ACKVILNVP KRSPTIWLSD PFPLFLQOVE LIAYASTADG DEPDIMHTRL QPFGLLGITT VNPTILKGNE TALARALVTV LHDPRGWITI NDNPPEILGS TAARLSYQON WAILAILLGI FMIQTTNINSS VDNCRYTYSE	SKLEADKIIG KRKQTQKEVT SDAAQNYTVP YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS YVVICKPKMG AGPQEYTIPI	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENINH SPGLFSVHPS MAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP YTDILAVDPD TVKDRAGQAA VCTSVFRATKG	120 180 240 300 360 420 480 540 600 660 720
50 55 60	Seq ID NO: Protein Act	527 Proteinession #: 1 11 RGAVCLHLLL PRYLINDGSVY RRAKRWAPI DTGNLPCTR EVLESSRPGT LDREVVDKYS VSLIRIPIED VNLEIGVNNE MGYKAYDPEN AIDKODRSCT SLPMTSPEIS SCRAGHHHT 528 DNA see 528 DNA see	D SEQUENCE DE TOTAL 1.1 LIVITENCIE TRAVALSDK PCSMOENSIG UDREEYDUPD TVGVVCATDR LIMKVQDMDG KOLINTAWWR APFARDI PRV RNGNGLRYKK GTLAVNIEDU RESTUVIJGK GDDRVCSANG LDSCRGGHTE QUENCE DS CRGGHTE QUENCE D # 1 NM 00:	ACKVILNVP KRSPTIWLSD PFPLFLQOVE LIAYASTADG DEPDIMHTRL QPFGLLGITT VNPTILKGNE TALARALVTV LHDPRGWITI NDNPPEILGS TAARLSYQON WAILAILLGI FMIQTTNINSS VDNCRYTYSE	SKLEADKIIG KRKQTQKEVT SDAAQNYTVP YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS YVVICKPKMG AGPQEYTIPI	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENINH SPGLFSVHPS MAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP YTDILAVDPD TVKDRAGQAA VCTSVFRATKG	120 180 240 300 360 420 480 540 600 660 720
50 55 60 65	Seq ID NO: Protein Act	527 Proteinession #:1 RGAVCLHLLL FRVLNDGSVY RRAKRRWAPI DTGNLFCTRP EVLESSRPOT LDREVVDKYS VBILRIPTED VNLEIGVNNES MGYKAYDPEN AIDKODRSCT SLPWISPEIS CTHEPYGRAT NLIISNTEAP SCRGAGHHT 528 DNA se	D SEQUENCE DE TOTAL 1.1 LIVITENCIE TRAVALSDK PCSMOENSIG UDREEYDUPD TVGVVCATDR LIMKVQDMDG KOLINTAWWR APFARDI PRV RNGNGLRYKK GTLAVNIEDU RESTUVIJGK GDDRVCSANG LDSCRGGHTE QUENCE DS CRGGHTE QUENCE D # 1 NM 00:	ACKVILNVP KRSPTIWLSD PFPLFLQOVE LIAYASTADG DEPDIMHTRL QPFGLLGITT VNPTILKGNE TALARALVTV LHDPRGWITI NDNPPEILGS TAARLSYQON WAILAILLGI FMIQTTNINSS VDNCRYTYSE	SKLEADKIIG KRKQTQKEVT SDAAQNYTVP YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS YVVICKPKMG AGPQEYTIPI	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENINH SPGLFSVHPS MAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP YTDILAVDPD TVKDRAGQAA VCTSVFRATKG	120 180 240 300 360 420 480 540 600 660 720
50 55 60 65	Seq ID NO: Protein Act I MAAAGPRRSV ADLINSSDPD KTRITRETVL EPLANFY IER POVICTY CONTROL FLAVEENNAP KELVNITY CONTROL KENLANGSKI KHELVNITY TKILKUNICE KENPECHAPI TKILKUNICE KEPPECHAPI KEPPECHAPI KEPPECHAPI KEPPECHAPI KEPPECHAPI Seq ID NO: Nucleic Ac Coding seq	527 Proteinession #: 1 11 RGAVCLHLLL PRVINDGSVY RRAKRWAPI DUTGNIPCTR EVLESSRDGS DUTGNIPCTR EVLESSRDGS DUTGNIPCTR EVLESSRDGS DUTGNIPCTR EVLESSRDGS DUTGNIPCTR EVLESSRDGS EVLESS	D SEQUENCE NP_077741.1 21 1 TLVIFSROGE TARAVALSHK PCSWGENSIG TLIMKYONDO TLIMKYONDO TLIMKYONDO TLIMKYONDO ROBERTOUTO TLIMKYONDO TLIMK	ACKKVILAVP KRSPTIWLSO PFPLFLQOVE LIAVASTADG DEPOTMETRL QFFGLIGTST VNFTILKGNE TALKRALVTV LEIDPRGWITI LEIDPRGWITI HONPPEILQE TAARALSYONN WAILALLGI FMTQTTNNSS VDNCRYTYSE	SKLEADKIIG KRKQTQKEVT SDAAQNYTVP YSADLPLPL KYSILQOTPR CIITVTDSND NGHPKISTDK HVRDLDEGPB DEISGSITTS JVVICKPKNG AGFQEYTTEI ALLPSVLIFI QGFCCTMGSG WESPTQPRLG	RVNLEECFRS VLLEHQKKVS YSISGRGVDK IRVEDENINH SPGLFSVHPS MAPTFRQNAY ETNEGVLSVV CTPAAQYVRI KILDREVETP YTDILAVDPD TVKDRAGQAA VCTSVFRATKG	120 180 240 300 360 420 480 540 600 660 720
50 55 60	Seq ID NO: Protein Act	527 Proteinession #: 1 11 RGAVCLHLLL PRYLINDGSVY RRAKRWAPI DTGNLPCTR EVLESSRPGT LDREVVDKYS VSLIRIPIED VNLEIGVNNE MGYKAYDPEN AIDKODRSCT SLPMTSPEIS SCRAGHHHT 528 DNA see 528 DNA see	D SEQUENCE DE TOTAL 1.1 LIVITENCIE TRAVALSDK PCSMOENSIG UDREEYDUPD TVGVVCATDR LIMKVQDMDG KOLINTAWWR APFARDI PRV RNGNGLRYKK GTLAVNIEDU RESTUVIJGK GDDRVCSANG LDSCRGGHTE QUENCE DS CRGGHTE QUENCE D # 1 NM 00:	ACKVILNVP KRSPTIWLSD PFPLFLQOVE LIAYASTADG DEPDIMHTRL QPFGLLGIT VNPTILKGNE TALARALVTV LHDPRGWITI NDNPPEILGS TAARLSYQON WAILAILLGI FMIQTTNINSS VDNCRYTYSE	SKLEADKIIG KRKQTQKEVT SDAAQNYTVP YSADLPLPLP KYSILQQTPR CIITVTDSND NGHFKISTDK HVRDLDEGPB DEISGSIITS YVVICKPKMG AGPQEYTIPI	RVNILBECFRS VLLEHQKYCS VLLEHQKYCS VSISGRGVDK IRVEDENDHH SPGLIFSVHPS ETNEGVLSVV CTPAQCYVRI KILDREVETP TYDILAVDT TYDILAVDT VKURAGQAA VCGVPGAKCA MKNGGQETIE EESIRGHTG	120 180 240 300 360 420 480 540 600 660 720
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	AGGGGTTTTA GGCAATATTG	CTTTGAGGAC	CAGTGTAGTC	AAGGGAAAAC	ATGAGTTAAA	AAGAAAAGCA	6300
	GGCAATATTG	CAACCATAAA	CONCENTRA	CCTTCACACT	CARTCUTTTC	CCCATGCAGG	6360
	ACTOTOCTOC	CCTACAAACG	TTANGACTGA	TCATTTCAAA	AATCTATTAG	CTATATCAAA	6420
5	AGCCTTACAT	TTTAATATAG	GTTGAACCAA	AATTTCAATT	CCAGTAACTT	CTATTGTAAC	6480
	CATCATTTT	CTOTATOTOT	TOTAGDATOT	TOATTGGATT	TTTGTTTGTA	ATAGTAAAAT	6540
	ACCGGATACA	TTTCACGTGT GGACACTAGA	CCTTCAGTAT	TGATTTGGTT	GAATATTGGG	TCATAATGGT	6600
	TGAGAAGCAT	GGACACTAGA	GCCAGAATGC	TTGGATATGA	ATCCTGGATC	TGTCACTTAC	6660 6720
10	TTCTGTGTGA	CCTTTGAAAG	GCTACTTATT	TOUTUTUTA	ACTTANTATA	CCTABACTAC	6780
10	MARCANIGCC	CCCCCACAC	ACTABANCAS	TTATAACTCT	GAGGTAGTTG	GTAAAATTAT	6840
	GTAGTTGGAT	GCCTGCACAT ATACTACCGA	ACAATATCTA	ATCTCTTTTT	AGGGAAATAA	AGTTTGTGCA	6900
	TATATATAAT	CCCGAAACAT	G				
15	Seq ID NO:	529 Proteir	sequence				
	Protein Acc	cession #: h	IP_001932.1				
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20	MANAGERESU	RGAVCLHLLL	TLVIPSRDGE	ACKKVILNVP	SKLEADKIIG	RVNLEECFRS	60
	ADLIBSSDPD	FRVLNDGSVY	TARAVALSDK	KRSFTIWLSD	KRKQTQKEVT	VLLEHOKKVS	120
	KTDHTRETUI.	PRAKERWART	PCSMOENSLG	PFPLFLOOVE	SDAACNYTVF	YSISGRGVDK	180
	BPLNLFYIER	DIGNLECTRP	VDREEYDVFD	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
	PVFTEALYNP	EVLESSRPGT LDREVVDKYS VEILRIPIED	TVGVVCATDR	DEPOTMETRL	KYSILQQTPR	SPGLFSVHPS	300
25	TGVITTVSHY	LDREVVDKYS	LIMKVQDMDG	QFFGLIGTST	CIITVIDSND	NAPTFRQNAY	360
	EAFVERNAFN	VEILRIPIED	KDLINTANWR	VNPTILKGNE	NGHPKISTOK	ETNEGVLSVV	420
							480 540
	KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	THODKGMITI	DEISGSTITS	KILDREVETP	600
30	KNELYNITVL	AIDKDDRSCT SLPNTSPEIS	GTLAVNIEDV	MONPPETER	PORTECKNING	TUTURADED	660
30	EPVHGAPFYP	CTHPTQCRAT	CDOMOUTECK	WATERTICE	ALT. POINT.TT.	VCGUEGATEG	720
							780
	MARCONOTT.E	OCDGAGUUUT	LDSCROGHTE	VDNCRYTYSE	WHSPTOPRIG	EKLHRCNONE	840
	DRMPRODYVI	SCRGAGHHHT TYNYEGRGSP	AGSYGCCSEK	QEEDGLDFLN	NLEPKFITLA	BACTER	
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	Seq ID NO:	530 DNA 8ec	Ineuce				
	Nucleic Ac:	id Accession	1 #: NM_016	583.2			
40	Coding sequ	uence: 72	342				
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	1	11	21	31	11	i	
	001000000	AGAGAGAGGA	CACCAGGACA	GCTGCTGAGA	CCTCTAAGAA	GTCCAGATAC	60
							120
45	CCATGGCCCA	GTTTGGAGGC GCCCTTGAGT	CTGCCCGTGC	CCCTGGACCA	GACCCTGCCC	TTGAATGTGA	180
	ATCCAGCCCT	GCCCTTGAGT	CCCACAGGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
							300
	TGAAGCCTGG	AGGAGGTACT TGGCCTGAAC TGTGCAGAGC	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGA	AAAGTGACGT	360
	CAGTGATTCC	TGGCCTGAAC	AACATCATTG	ACATAAAGGT	CACTGACCCC	CAGCTGCTGG	420 480
50	AACTTGGCCT	TGTGCAGAGC	CCTGATGGCC	ACCGTCTCTA	TGTCACCATC	CCTCTCGGCA	540
	TARAGCTCCA	AGTGAATACG TGCAGAAATC	CCCCTGGTCG	GIGCAAGICT	CONCREGATO	CACCTGGTGCC	600
	TGGACATCAC	CACCCATTCC	Traccicion	GAGATAAGCA	TOTOCTTOAT	GGACTTGGCC	660
	TIGGIGACIG	TON ACCOUNT	CTGGRAGCC	TCACAGGGAT	CTTGBATAAA	GTCCTGCCTG	720
55	*CCCTCCCCAT	CCCCAACCTC	TOCCCTCTCC	TCAATGAGGT	TCTCAGAGGC	GTCCTGCCTG TTGGACATCA	780
55	CCCTCCTCCA	TCACATTGTT	AACATGCTGA	TCCACGGACT	ACAGTTTGTC	ATCAAGGTCT	840
							900
	GCCCATGTGC	TGGAAGATGA	CACAGTTGCC	TTCTCTCCGA	GGAACCTGCC	CCCTCTCCTT	960
	TCCCACCAGG	CCTCTCTAAC	ATCCCATGTG	CCTCACCTAA	TAAAATGGCT	CCTCTCCTT	1020
60	ААААААААА	AAAAAAAAA	AAAAAAAA				
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	MPCTGGLIVE	YGLLAQTMAO	FGGLPVPLDO	TLPLNVNPAL	PLSPTGLAGS	LTNALSNOLL	60
	SCGLLGILEN	LPLLDILKPG	GGTSGGLLGG	LLCKVTSVIP	GLNNIIDIKV	LTNALSNGLL TDPQLLELGL	120
							180
70	THSPGSLQIS	LLDGLGPLPI	QGLLDSLTGI	TNKATABITAÖ	GNVCPLVNEV	LRGLDITLVK	240
	DIVNMLIHGL	OLAIKA					
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75	Nucleic Ac	id Accessio	n #: NM 00-	4363.1			
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	1	11	21	31	41	51	
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80	CTCAGGGCAG	AGGGAGGAAG	GACAGCAGAC	CAGACAGTCA	CAGCAGCCTT	GACAAAACGT	60
							120
	TCTCCCTCGG	CCCCTCCCCA	CAGATGGTGC	ATCCCCTGGC	AGAGGCTCCT	GCTCACAGCC	180
	TCACTTCTAA	CCTTCTGGAA	CCCGCCCACC	ACTGCCAAGC	TCACTATTGA	GCTCACAGCC ATCCACGCCG CCAGCATCTT	240
0.5	TTCAATGTCG	CAGAGGGGAA	GGAGGTGCTT	CTACTTGTCC	ACAATCTGCC	CCAGCATCTT	300 360
85	TTTGGCTACA	GCTGGTACAR	AGGTGAAAGA	GTGGATGGCA	ACCUTCAAAT	TATAGGATAT GATAATATAC CTACACCCTA	360 420
	GTAATAGGAA	CTCAACAAGC	TACCCCAGGG	CCCGCATACA	GIGGICUAGA	GATAATATAC	420
	CCCAATGCAT	CCCTGCTGAT	CCAGAACATC	. ALCUNUMATO	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	CANCACCCIA	400

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	CACGTCATAA GAGCTGCCCA	AGTCAGATCT	TGTGAATGAA	GAAGCAACTG	GCCAGTTCCG	GGTATACCCG	540 600
	GIGGCCTTCA	CCTCTGAACC	TGAGACTCAG	GACGCAACCT	ACCTGTGGTG	GGTAAACAAT	660
_	CAGAGCCTCC	CCCCCACTCC	CAGGCTGCAG	CTGTCCAATG	GCAACAGGAC	CCTCACTCTA	720
5	TTCAATGTCA GCCAGGCGCA	CAAGAAATGA	CACAGCAAGC	TACAAATGTG	AAACCCAGAA	CCCAGTGAGT	780 840
	TOCCOTOTAA	ACACATCTTA	CAGATCAGGG	GAAAATCTGA	ACCTCTCCTG	CCACGCAGCC	900
	TOTALOCCAC	CTCCACAGTA	CTCTTGGTTT	GTCAATGGGA	CTTTCCAGCA	ATCCACCCAA	960 1020
10	GAGCTCTTTA AACTCAGACA	TCCCCAACAT	CACTGTGAAT	AATAGTGGAT	CCTATACGTG	TOCAGGCCCAT	1020
10	CCCAAACCCT	TCATCACCAG	CAACAACTCC	AACCCCGTGG	AGGATGAGGA	TGCTGTAGCC	1140
	TTAACCTGTG	AACCTGAGAT	TCAGAACACA	ACCTACCTGT	GGTGGGTAAA	TAATCAGAGC	1200 1260
	CTCCCGGTCA GTCACAAGGA	GTCCCAGGCT	ACCCTATGAG	TOTOGRAPOO	GGACCCTCAC	AAGTGTTGAC	1320
15	CACAGOGACC	CAGTCATCCT	GAATGTCCTC	TATGGCCCAG	ACGACCCCAC	CATTTCCCCC	1380
	TCATACACCT	ATTACCGTCC	AGGGGTGAAC	CTCAGCCTCT	CCTGCCATGC	AGCCTCTAAC	1440
	CCACCTGCAC	AGTATTCTTG	GAAGAACAGC	GGACTCTATA	CCTGCCAGGC	CAATAACTCA	1560
	GCCAGTGGCC	ACAGCAGGAC	TACAGTCAAG	ACAATCACAG	TCTCTGCGGA	GCTGCCCAAG	1620
20	CCCTCCATCC	CCNGCAACAA	CTCCAAACCC	GTGGAGGACA	AGGATGCTGT	GGCCTTCACC	1680
	GTCAGTCCCA	GGCTGCAGCT	GTCCAATGGC	AACAGGACCC	TCACTCTATT	CAATGTCACA	1800
	BOAR ATGACG	CARGAGICCTA	TGTATGTGGA	ATCCAGAACT	CAGTGAGTGC	AAACCGCAGT	1860 1920
25	GACCCAGTCA	CCCTGGATGT	CCTCTATGGG GAACCTCAAC	CCGGACACCC	CCATCATTTC	TARCCCAGAC	1920
23	CCCCACTATT	CTTGGCGTAT	CAATGGGATA	CCGCAGCAAC	ACACACAAGT	TCTCTTTATC	2040
	CCCABBATCA	AATAAATOO	TAACGGGACC	TATGCCTGTT	TTGTCTCTAA	CTTGGCTACT	2100
	GGCCGCAATA	ATTCCATAGT	CAAGAGCATC CGGCATCATG	ACAGTCTCTG	TOGTTGGGGT	TCTCCTGGT	2220
30	TAGCAGCCCT	COTOTAGTTT	CTTCATTTCA	GGAAGACTGA	CAGTTGTTTT	GCTTCTTCCT	2280
	TABACCATTT	GCBACAGCTA	CAGTCTAAAA	TIGCTICITI	ACCAAGGATA	TTTACAGAAA	2340
	AGACTCTGAC	CAGAGATCGA	GACCATCCTA CTTGGTGGCG	CCCAACATCG	GTCCCAGTTA	CTCGGGAGGC	2460
							2520
35	ACTGCACTCC	AGTCTGGCAA	CAGAGCAAGA	CTCCATCTCA	AAAAGAAAAG	AAAAGAAGAC	2580 2640
	TCTGACCTGT	ACTOTTGAAT	ACAAGTTTCT	AAACTGTCCA	CCAAGATCAA	GCAGAGAAAA	2700
	TAATTAATTT	CATGGGACTA	CAGCTTCATG AATGAACTAA	TGAGGATTGC	TGATTCTTTA	AATGTCTTGT	2760
40			TTTTTTCTTT AAATTGAGAC				2820
40	AGACTTGGGA	AACTATTCAT	GAATATTTAT	ATTGTATGGT	AATATAGTTA	TTGCACAAGT	2940
	TCAATAAAAA	TCTGCTCTTT	GTATAACAGA	AAAA			
	Seg ID NO:	533 Protei	n sequence				
45	Seq ID NO: Protein Acc	533 Protein ession #: 1	n sequence NP_004354.1				
45	Seq ID NO: Protein Acc	533 Protein ession #: 1	n sequence NP_004354.1 21	31	41	. 51	
45	Protein Acc	ession #: 1	NP_004354.1	1	1	1	60
-	Protein Acc	ession #: 1 11 WCIPWQRLLL PRYNGNPOIT	NP_004354.1 21 TASLLTFWNP	 PTTAKLTIES PGPAYSGREI	TPFNVAEGKE IYPNASLLIO	VLLLVHNLPQ NIIQNDTGFY	60 120
45 50	Protein Acc	ession #: 1 11	NP_004354.1 21 TASLLTFWNP GYVIGTQQAT VDELPKESIS	PTTAKLTIES PGPAYSGREI SENSKPVEDK	TPFNVAEGKE IYPNASLLIQ DAVAFTCEPE	VLLLVHNLPQ NIIQNDTGFY TODATYLWWV	120 180
-	Protein Acc	11 WCIPWQRLLL ERVDGNRQII MEEATGQFRV LOLSNGNRTL	NP_004354.1 21 TASLLTFWNP GYVIGTQQAT YPELPKPSIS TLFNVTRNDT	PTTAKLTIES PGPAYSGREI SMNSKPVEDK ASYKCETONP	TPFNVAEGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI	VLLLVHNLPQ NIIQNDTGPY TQDATYLWWV LNVLYGPDAP	120 180 240
50	Protein Acc	11	NP_004354.1 21 TASILITEWNP GYVIGTQQAT YPELPKPSIS TLFNVTRNDT AASNPPAQYS BPPKPFITSN	PTTAKLTIES PGPAYSGREI SMNSKPVEDK ASYKCETQNP WFVNGTFQQS NSNPVEDEDA	TPFNVAEGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ	VILLVHNLPQ NIIQNDTGFY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWVNN	120 180 240 300 360
-	Protein Acc 1 MESPSAPPHR HLFGYSWYKG TLHVIKSDLV NNQSLPVSPR TISPLNTSYR AHNSDTGLMR	11	NP_004354.1 21 TASILLTFWNP GYVIGTQQAT YPELPKPSIS TLFNVTRNDT AASMPPAQYS EPPKPFITSM	PTTAKLTIES PGPAYSGREI SENSKPVEDK ASYKCETONP WFVNGTFOQS NSNPVEDEDA YECGIONELS	TPFNVAEGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILM	VILLVHNLPQ NIIQNDTGFY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWVNN VLYGPDDPTI	120 180 240 300 360 420
50	Protein Acc 1 MESPSAPPHR HLFGYSWYKG TLHVIKSDLV NNQSLPVSPL AHNSDTGLNR QSLPVSPRLQ QSLPVSPRLQ	11	NP_004354.1 21 TASLLTFWNP GYVIGTQQAT YPELPKPSIS TLFNVTRNDT AASNPPAQYS EPPKPFITSN LSVTRNDVGP	PTTAKLTIES PGPAYSGREI SENSKPVEDK ASYKCETQNP WFVNGTFQQS NSNPVEDEDA YECGIQNELS IDGNIOOHTO	TPFNVAEGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILM ELFISNITEK	VLLLVHNLPQ NIIQNDTGFY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWVNN VLYGPDDPTI VSGLYTCQAN	120 180 240 300 360 420 480
50	Protein Acci MESPSAPPHR HLFGYSWYKG TLHVIKSDLV NNQSLPVSPR TISPLNTSYR AHNSDTGLAR QSLPVSPRLQ SPSYTYYRPG NSASGHSRTT LPVCPDLOLS	11	NP_004354.1 21 TASILITEWNP GYVIGTQQAT YPELPKPSIS TLFMNTRNDT AASNPPAQYS EPPKPFITSN LSYTRNDVGP SNPPAQYSWL PKPSISSNNS VTRNDARAYV	PTTAKLTIES PGPAYSGREI PGPAYSGREI SMNSKPVEDK ASYKCETQNP WFVNGTFQQS NSNPVEDEDA YECGIQNELS IDGNIQQHTQ KFVEDKDAVA CGIONSVSAN	TPFNVAEGKE TYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILN ELPISNITEK PTCEPEAQNT RSDPVTLDVL	ULLLVHNLPQ WILQNDTGPY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWWNN VLYGPDDPTI NSGLYTCQAN TYLWWVNGQS YGPDTPIISP	120 180 240 300 360 420 480 540
50	Protein Acc	11 WCIFWQRLLL ERVDGNRQII NEEATGQFRV LQLSNGNRTLL SGEMINISCE TTVTTITVYA LSNDNRTLTI VNLSLSCHAA VKTITVSAEL NGNRTLTIFN	NP_004354.1 21 TASLLTFWNP GYVIGTQQAT TPELPKPSIS TLFNVTRNDT AASNPPAQYS EPPKPPITSN LSVTRNDVGP SNPPAQYSWL PKPSISSNNS VTRNDARAYV PSPOYSWRIN	PTTAKLTIES PGPAYSGREI SMNSKPVEDK ASYKCETQNP WFVNGTFQQS NSNPVEDEDA YECGIQNELS IDGNIQQHTQ KFVEDKDAVA CGIQNSVSAN GIPOOBTOVL	TPPNVABGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILM ELFISNITEK FTCEPEAQNT RSDPVILDVL RSDPVILDVL RSLRITPNNN	ULLLVHNLPQ WILQNDTGPY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWWNN VLYGPDDPTI NSGLYTCQAN TYLWWVNGQS YGPDTPIISP	120 180 240 300 360 420 480 540
50	Protein Acc	11 WCIFWQRLLL ERVDGNRQII NEEATGQFRV LQLSNGNRTLL SGEMINISCE TTVTTITVYA LSNDNRTLTI VNLSLSCHAA VKTITVSAEL NGNRTLTIFN	NP_004354.1 21 TASILITEWNP GYVIGTQQAT YPELPKPSIS TLFMNTRNDT AASNPPAQYS EPPKPFITSN LSYTRNDVGP SNPPAQYSWL PKPSISSNNS VTRNDARAYV	PTTAKLTIES PGPAYSGREI SMNSKPVEDK ASYKCETQNP WFVNGTFQQS NSNPVEDEDA YECGIQNELS IDGNIQQHTQ KFVEDKDAVA CGIQNSVSAN GIPOOBTOVL	TPPNVABGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILM ELFISNITEK FTCEPEAQNT RSDPVILDVL RSDPVILDVL RSLRITPNNN	ULLLVHNLPQ WILQNDTGPY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWWNN VLYGPDDPTI NSGLYTCQAN TYLWWVNGQS YGPDTPIISP	120 180 240 300 360 420 480 540
50	Protein Acc 1 MESPSAPPHR HLFGYSWYKG TLHVIKSDLV NNOSLPUSPY ANNSDTGLMS ANNSDTGLMS QSLPVSPRLQ SPSYTYYRG NSASGHSRTT LPVSPRLQLS PDSSYLSGAN ATGRNNSIVK	11	NP_004354.1 21 TASILITHMP GYVIGTOQAT YPELPKRSIS TLFNVTRUDT ENPROYSE ENP	PTTAKLTIES PGPAYSGREI SMISKPVEDK ASYKCETONP WYVMGTPQQS MSNPVEDEDA YECGIQNELS KPVEDKDAVA CGIQNSVSAM GIPQQETQVL IMIGVLVGVA	TPPNVABGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILM ELFISNITEK FTCEPEAQNT RSDPVILDVL RSDPVILDVL RSLRITPNNN	ULLLVHNLPQ WILQNDTGPY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWWNN VLYGPDDPTI NSGLYTCQAN TYLWWVNGQS YGPDTPIISP	120 180 240 300 360 420 480 540
50	Protein Act	11 CARPER CONTROL OF	P_004354.1 21 TASLLTFWNP GYVIGTQAAT YPELPKPSIS TLFNVTRIDTS EPPKPPITSN LSVTRNDVSP ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPRYSM E	PTTAKLTIES PGPAYSGREI SMISKPVEDK ASYKCETONP WYVMGTPQQS MSNPVEDEDA YECGIQNELS KPVEDKDAVA CGIQNSVSAM GIPQQETQVL IMIGVLVGVA	TPPNVABGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILM ELFISNITEK FTCEPEAQNT RSDPVILDVL RSDPVILDVL RSLRITPNNN	ULLLVHNLPQ WILQNDTGPY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWWNN VLYGPDDPTI NSGLYTCQAN TYLWWVNGQS YGPDTPIISP	120 180 240 300 360 420 480 540
50	Protein Act	11	PP_004354.1 21 TASLLTFWNP GYVIGTQQAT YPELPKPSIS TLFNVTRIDT AASHPAQYS EPPKPPITS LSVTRNDVGP PKPSISSENS VTRNDVGP PKPSISSENS VTRNDARAYV TRNDARAYV QUENCE quence n #: NM_006 793	PTTAKLTIES PGPAYSGREI SMISKPVEDK ASYKCETONP WPVNGTPOOS YECCIQNBLS IDGNIQOHTO KPVEDKDAVA CGIQNSVSAN GIPQOLTQVL IMIGVLVGVA	TPFNVAEGKE TPFNVAEGKE TYPMASILIQ DAVAFTCEPE VSARRSDSV TQELFIPNIT VALICEPEIQ VDRSDPVILM ELFISNITEK FTCEPEAQNT RSDPVILDVL PIAKITPNNN LI	VILLVENLPQ VILLVENLPQ VILLVENTPY VICTOR VILLVENTY VICTOR VINES VINES VILLVENTY VILLVEN	120 180 240 300 360 420 480 540
50 55 60	Protein Acc 1	11 CARPER CONTROL OF	P_004354.1 21 TASLLTFWNP GYVIGTQAAT YPELPKPSIS TLFNVTRIDTS EPPKPPITSN LSVTRNDVSP ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPPRYSM ENPRYSM E	PTTAKLTIES PGPAYSGREI SMISKPVEDK ASYKCETONP WYVMGTPQQS MSNPVEDEDA YECGIQNELS KPVEDKDAVA CGIQNSVSAM GIPQQETQVL IMIGVLVGVA	TPPNVABGKE IYPNASLLIQ DAVAFTCEPE VSARRSDSVI TQELFIPNIT VALTCEPEIQ VDHSDPVILM ELFISNITEK FTCEPEAQNT RSDPVILDVL RSDPVILDVL RSLRITPNNN	ULLLVHNLPQ WILQNDTGPY TQDATYLWWV LNVLYGPDAP VNNSGSYTCQ NTTYLWWWNN VLYGPDDPTI NSGLYTCQAN TYLWWVNGQS YGPDTPIISP	120 180 240 300 360 420 480 540
50 55 60	Protein Acc I MESPSAPPHR HLFGYSWYKG TLHVIKSDLV NNQSLPVSPRL QSLPVSPRLQ SPSYTYRPG NSASGHSRTT LFVSPRLQLS PDSSYLSGAN ATGRNNSTVK Seq ID NO: Nucleic Ac: Coding sequ	11 WITHORNELL ERVOGNRGII MERATGOPRV LQLSNGNRTL LSNGNRTLI VNLSLSCHAA VKTITVSAEL NGRRTLTIVNLSCHAA SITVSAEC NGRRTLTIF SITVSAEC NGRRTLTIF SITVSAEC NGRRTLTIF SITVSAEC SITVSAEC SITVSAECT SITVSAEC LNLSCHSASN SITVSAECT SI	PP_004354.1 21 TASILITEMPE GYVIGTQQAT YPELPKPSIS TLFENTRIDT AASHPPAQYS EPPKPFITSN LSYTRIDTOS NIPPRQYSWL YKPSISHNIN PKFSISHNIN PGLSAGATVG quence n #: NM_004 793 21	PTTAKLTIES POPAYSGREI SENSKPYEDK ASYKCETONP WFVNGTFOOS NSNPVEDEDA YECGIONELS CGIONELS CGIONGU	TPENVAEGKE IYPNASLLIQ DAVAPTCEPE VSARRSDSVI TQELPIPNIT VALTCEPEIQ VDHSDPVILM ELFISNITEK PTCEPEAQNT LIVE PIAKITPNNN LI 41	VILLVENLEDQ VILLVENLEDQ VILLVENLEDQ VILLVENLEDQ VILLVENLEDQ VINTYLWAVN VLYQPDDPTI VSGLYTCQAN TYLWYNGQ TYACPVSNL	120 180 240 300 360 420 480 540
50 55 60 65	Protein Acc I MESPSAPPHR HLFGYSWYKG TLHVIKSDLV NNQSLPVSPRL QSLPVSPRLQ SPSYTYRPG NSASGBRIT LFVSPRLQLS PDSSYLSGAN ATGRNNSTVK Seq ID NO: Nucleic Ac: Coding seq	11 10 MCIPMQRLLL ERVDGNRQII MCIPMQRLLL ERVDGNRQII NEEATGGFRV LQLSNGNRTL LGSENINISCH LGNNRTLTI VALLSCHAA VKTITVSAH LSNCHITLIP NUNLSICHAA VKTITVSAH LNICHAAS SITVSAGTS 534 DNA Se dd Accessio Lence: 11. 11 ATGCGAAAG ATTATUGGT	NP_004354.1 21 1 TASLLIFWNP GYVIGTQQAT YPELPKPSIS TLFNVTRNDUGP EPPKPFITSN LSVTRNDUGP SNPPAQYSML PKPSISBNNS VTRNDARATV PSPGYSMLIN PSPGYSMLIN PCLESAGATV QUENCE #! NM_000 793 21 ACAACTCAAC GTTHYSGCAT	PTTAKLTIES PGPAYSGREI SPINSKPYEDK ASYKCETONP WFVNGTFQQS NSNPVEDEDA YECGIQNELS IDGNIQQHIC KPVEDKDAVA GIQNSVSAN GIPQOETQVL IMIGULVGVA 31 1 TGTTQGTTGC TGCCCTGACT	TPENVAEGKE IYPNASLLIQ DAVAPTCEPE VSARRSDSVI TQELPIPNIT VALTCEPEIQ VDRSDPVILN ELFISNITER FTCEPEAQNT LI LI LI LI LI LI LI LI LI LI LI LI LI	VILLUVINLEQ VILLUV	120 180 240 300 360 420 480 540 600 660
50 55 60	Protein Acc I MESPSAPPHR HLFGYSWYKG TLHVIKSDLV NNGSLPVSPR TI SFLATSTYR GOSLPVSPRILG SPSYTYYKRG SNSAGRISHT LPVSPRILGLS PDSSYLSGAN ATGRNNSTVK Seq ID NO: Nucleic Acc Coding sequ I AATCCCGGACA TGGAAATGTG	11 MCIPMORILL MCIPMORILL MCIPMORILL MCIPMORILL MCIPMORILL MCIPMORICH MCIPMORICH MCIPMORICH MCIPMORICH MCIPMORITH	PP_004354.1 21 TASLLTFWNP GYVIGTQQAT YPELPKRBIS YPELPKRBIS RPPKPTISN LASHPPAQYS RPPKPPITSN LSVTENDUP SNPPAQYSHL YKPSISSNIS YTRIDARAYV PSPQYSMIN PGLARGATVG quence n #: NM_004 793 21 ACAACTCAAC	PTTAKLTIES FORAYSGREI SMNSKPVEDK ASYKCETONP WPYNOTFOR NSNPVEDEDA YECCIONELS KEPTENDAVA GICONSTSAN GICONTOL MIGULYGVA 31 1 TOTTOOTTGC TSEAGCACCCTGACT TSBAGGGCCCCTGACT TSBAGGGCCCCCTGACT TSBAGGGCCCCCGACT	TPPNVAEGKE IYPNASLLIQ DAVAPTERE VSARRSDSVI TQELPIPNIT TQELPIPNIT ELPISNITEK PTCEPEQONT ELPISNITEK PTCEPEQONT LI I TTCCAGGGCC GCGQAGTGCA	VILLVENLEPQ VILLVE	120 180 240 300 360 420 480 540 660 660
50 55 60 65	Protein Acc 1 MESBSAPPHR M	ression #: 1 1	NP_004154.1 21 TASILITHNIP TASILITHNIP TYPELPRING TYP	PTTARLITIES FORAYSGREI SWINSKYEEN SWINSKYEEN ASYKCETONE WYVNOTFOQS NSNEVEDEDA CHICANO GICONSVSAN GIPQGETQVL IMIGVLVGVA 31 1 TOTTCOTTGC TSCACCTGACC CTGCCCTGACC CTGCCCTCTC CTCTACTGGCG	TPPNVAEGKE IYPNASLLIQ DAVAFTERE IYPNASLLIQ DAVAFTERE VSARRSDSVI TOGELFIBVI TVALTCEPEIQ VDRSDPVILN ELFISNITEK FTCEPEAGNT RSDEVILOVL PIAKITPNNN LI 1 1 TTCCAGGGCC GCGAGTUCA AGCAACGATG AGCAACGATG TGCCTGTCTG TGTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	VILLIVENLED VILLIV	120 180 240 300 360 420 480 540 600 660
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50 55 60 65 70	Protein Act LESPSAPPHR HLPOYSHYMG HLPOYSHYMG HLPOYSHYMG HLPOYSHYMG HLPOYSHYMG ADBITH HLPOYSHYMG SPRITTHRA GRIPHSPRIL PUPSPRILIS POSSYLGGAN ATCHESIS ATCHES	ression #: 1 1	NE_004154.1 TABLILTEWIP GYVIGTOON FYEELERSIS TLENVIENDT AARSPEAONS EPPERPITS LEVENTENDT PRESISENS VERDIAGATV PSEOTSKEIN GUING QUENCE A NI NM_00 ACACTCAAC GYTGGGGGAT ACCCACTGCT TYTGTGGCAT CCACGAAAAT ACCCACTGCT TYTGTGGCAT ACCCACTGCT CCACGAAAAT ACCCACTGCT TYTGTGGCAT ACCCACTGCT CCACGAAAAT CCCACTGCT CCACGAAAAT ACCCACTGCT CCACGAAAAT ACCCACTGCT CCACGAAAT ACCCACTGCT CCACGAAAAT CCCACTGCT CCACGAAAAT ACCCACTGCT CCACGAAAAT ACCCACTGCT CCACGAAAAT ACCCACTGCT CCACGAAAT ACCCACTGCT CCACGAAAT ACCCACTGCT CCACGAAAT ACCCACTGCT CCACGAAAT ACCCACTGCT CCACGAAAT ACCCACTGCT CCACGAAAT ACCCACTCACTCACT CCACGAAAT ACCCACTCACT CCACGAAAT ACCACTCACT CCACGAAAT ACCCACTCACT CCACGAAAT ACCCA	PTTAKUTIES POPAYSGREI SYNSKYPEKA ASYKCETONE WYNKOTFOGS NSNVPUEEDA VENCGIONELS LDONIQGHTQ KEYPEKDANA CGIONSVSAN GIONSVSAN GIONSVSAN GIONOMINA SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	TPPNVABGKE IYPNVABGKE IYPNVABGKE IYPNVABGKE VAARRAGSVI TOGEFIPNI VALICEPEID V	VILLUMILPO NIIGNITGET TOPATTLAMN LBULYGPDAP UNINGSTTCO NITTLAMNAN VLYGPDAPI NGGLYTCOAN TTLAMNANG VLYGPDAPI STAMNANG TCHAMNAN TCHAMNANG TCHAMNAN AGAPTCOAN TCHAMNANG TCHAMNAN AGAPTCOAN TCHAMNANG TCHAMNAN TCHAMNANA TCHAMNANA ACTITATCA CTCCAAACAA ACTITATCA CTCCAAACAA ACTITATCA	120 180 240 300 360 420 480 540 600 660
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50 55 60 65 70	Protein Act MESPSAPPHR	HERSON #: 1 11 MILTENGRILL HEVENGNROII HERYOGNROII HERYOGNROII HERYOGNROII LOLSNRHIL LOLSNRHIL LOLSNRHIL LONGNRIL LINGNRIL LI	NE_DOISS.1. 21 ITASILITENEM GYVIGTOON TYPEDERSIS TLENVIRENT TENVIRENT TENVIRENT ENTERPROPER LSVTENDARAY PRESISENS VYENDRARY	PTTAKUTIES POPAYSGREI SYNSKYPEN ASYNCETONE WYNKITPOLS YECGIONEU KYVERIONAV GIFOGETONE KYVERIONAV GIFOGETONE INIGUINEU STATE TOTTOGTTGC TGCCTTGAT TGCAGCCAC GAGGTACCA GAGGTACCA GAGGTACCA CANACCTGG GAGGTACCA	TPPNVABGKE IYPNVABGKE IYPNVABGKE IYPNVABGKE VARARSDSVI TOGLPIPNI VALICEPEL VARACEPEL VALICEPEL V	VILLUMINEO MILONTORY TO CONTROL OF THE CONTROL OF T	120 120 240 300 420 420 480 600 660 120 120 1240 300 300 420 480 660
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5	MAKDNSTVRC IGIFVGICLF FLKQMLERYQ DADYPWPRQC LCHTFWVLLG	CLSVLGIVGI NNSPPNNDDQ CVMNNLKEPL	IIGCCGIALT MKSSRKILLA WKNNGVTKTW NLEACKLGVP	YFILMFIVYA DRLMLQDNCC	FEVASCITAA GVNGPSDWQK	TORDFFTPNL YTSAFRTENN	120 180 240
10	Nucleic Aci	536 DNA sec d Accession ence: 120.	#: NM_0026	38.1			
10	1	11	21	31	41	51	
15	GCTGGACTGC TGAGGGCCAG AGGCAGCTGT TCAATGGACA CGCAAGAGCC	AAGGAATTAT ATAAAGATTG CAGCTTCTTG CACGGGAGTT AGATCCCGTT AGTCAAAGGT	CCCTTGTAAA GTATGGCCTT ATCGTGGTGG CCTGTTAAAG AAAGGACAAG CCAGTCTCCA CCCCTAACC	TACCACAGAC AGCTCTTAGC TGTTCCTCAT GTCAAGACAC TTTCAGTTAA CTAAGCCTGG	CAAACACCTT CGCTGGGACG TGTCAAAGGC AGGTCAAGAT CTCCTGCCCC	CCTGACACCA CTGGTTCTAG CGTGTTCCAT AAAGTCAAAG ATTATCTTGA	60 120 180 240 300 360
20	TCAAGAAGTG CGGTCCTTGC TGCTGCCCTT	TGCACCTGTG CCCCTTCCCA	TCTTGCGGGA CCGTCCCCAG CACTGTCCAT TTTCCAATAA	AGCTACAGGC TCTTCCTCCC			480 540 600
25	Seq ID NO: Protein Acc	537 Protein ession #: 1	n sequence P_002629.1				•
	1	11	21	31	41	51	
30	1	1	 EAAVTGVPVK		. [Hammeodelle	60
30	AQEPVKGPVS	TKPGSCPIIL	IRCAMLNPPN	RCLEDIDCPG	IKKCCEGSCG	MACEVEO	60
	Seq ID NO:	538 DNA sec	quence n.∦: NM_001				
35	Coding seq	id Accession Lence: 71:	2560				
	1	11	21	31	41	51	
	AAAGGGGCAA	GAGCTGAGCG	GAACACCGGC	CCGCCGTCGC	GGCAGCTGCT	TCACCCCTCT	60
40	CTCTGCAGCC	ATGGGGCTCC	CTCGTGGACC	TCTCGCGTCT	CTCCTCCTTC	TCCAGGTTTG	120
	CTGGCTGCAG	TGCGCGGCCT	CCGAGCCGTG AGCAGGAGCC	CCGGGCGGTC	TTCAGGGAGG	CTGAAGTGAC	180 240
	CTTGGAGGCG	CAAGAGCCAG	CTCTGTTTAG	CACTGATAAT	GATGACTTCA	CTGTGCGGAA	300
	TGGCGAGACA	GTCCAGGAAA	GAAGGTCACT	GAAGGAAAGG	AATCCATTGA	AGATCTTCCC	360
45	ATCCAAACGT	ATCTTACGAA	GACACAAGAG	AGATTGGGTG	GTTGCTCCAA	TATCTGTCCC	420
	AGACACCARG	AAGGGTCCCT	TCCCCCAGAG GCATCACGGG	GCCGGGGGGCA	GACAGCCCCC	CTGAGGGTGT	540
	CTTCGCTGTA	GAGAAGGAGA	CAGGCTGGTT	GTTGTTGAAT	AAGCCACTGG	ACCGGGAGGA	600
50	GATTGCCAAG	TATGAGCTCT	TTGGCCACGC	TGTGTCAGAG	AATGGTGCCT	CAGTGGAGGA	660 720
30	CCCCATGAAC	CACCCATCA	TCTTAGAGGG	ACTOCTACCA	GGTACTTCTG	TGATGCAGGT	780
	GACAGCCACG	GATGAGGATG	ATGCCATCTA	CACCTACAAT	GGGGTGGTTG	CTTACTCCAT	840
	CCATAGCCAA	GAACCAAAGG	ACCCACACGA	CCTCATGTTC	ACCATTCACC	GGAGCACAGG	900 960
55	CACCATCAGC	GTCATCTCCA	GTGGCCTGGA ATGGGGACGG	CCGGGAAAAA	ACCICACTOR	CACACTGAC	1020
33	CATCCTTCAT	GCCAATGACA	ATGCTCCCAT	GTTTGACCCC	CAGAAGTACG	AGGCCCATGT	1080
	GCCTGAGAAT	GCAGTGGGCC	ATGAGGTGCA	GAGGCTGACG	GTCACTGATC	TGGACGCCCC	1140
	CAACTCACCA	GCGTGGCGTG	CCACCTACCT AGAGCAACCA	TATCATGGGC	GGTGACGACG	DOCCUTTOGA	1200 1260
60	TACCATCACC	AAAAACCAGC	ACACCCTGTA	CGTTGAAGTG	ACCAACGAGG	CCCCTTTTGT	1320
	GCTGAAGCTC	CCAACCTCCA	CAGCCACCAT	AGTGGTCCAC	GTGGAGGATG	TGAATGAGGC	1380
	ACCTGTGTTT	GTCCCACCCT	CAGAAGTCGT	TGAGGTCCAG	BAGGGCATCC	CCACTGGGGA	1440 1500
	CATCCTGAGA	GACCCAGCAG	GGTGGCTAGC	CATGGACCCA	GACAGTGGGC	AGGTCACAGC	1560
65	TOTGGGCACC	CTCGACCGTG	AGGATGAGCA	GTTTGTGAGG	AACAACATCT	ATGAAGTCAT	1620 1680
	GGTCTTGGCC	ATGGACAATG	GAAGCCCTCC	CACCACTGGC	COTCAGATCA	CCATCTGCAA	1740
	CCAAAGCCCT	GTGCGCCAGG	TGCTGAACAT	CACGGACAAG	GACCTGTCTC	CCCACACCTC	1800
70		GCCCAGCTCA		AGACATCTAC	TGGACGGCAG	AGGTCAACGA CATATGACGT	1860 1920
70	GCACCTTTCT	ACAGIGGICI	ATGGCAACAA	AGAGCAGCTG	ACGGTGATCA	GGGCCACTGT	1980
	GTGCGACTGC	CATGGCCATG	TCGAAACCTG	CCCTGGACCC	TGGAAGGGAG	GTTTCATCCT	2040
	CCCTGTGCTG	GGGGCTGTCC	TGGCTCTGCT	GTTCCTCCTG	CTGGTGCTGC	TTTTGTTGGT	2100 2160
75.	GAGAAAGAAG	CGGAAGATCA	AGGAGCCCCT	CGAAGAGGAC	CAGGACTATG	ACATCACCCA	2220
	GCTCCACCGA	GGTCTGGAGG	CCAGGCCGGA	GGTGGTTCTC	CGCAATGACG	TGGCACCAAC	2280
	CATCATCCCG	ACACCCATGT	ACCGTCCTCG	GCCAGCCAAC	CCAGATGAAA	TOGGCAACTT	2340
	CTTGGTGTTC	GACTATGAGG	GCAGCGGCTC	CGACGCOGCG	TCCCTGAGCT	CCCTCACCTC	2460
80	CTCCGCCTCC	GACCAAGACC	AAGATTACGA	TTATCTGAAC	GAGTGGGGCA	GCCGCTTCAA	2520
	GAAGCTGGCA	GACATGTACG	GTGGCGGGGA	GGACGACTAG	GCGGCCTGCC	TGCAGGGCTG	2580 2640
	GACTTCGGAG	CTTGTCAGGA	AGTGGCCCTA	GCAACTTGGC	GGAGACAGGC	TATGAGTCTG	2700
	ACCITTAGAGT	GGTTGCTTCC	TTAGCCTTTC	AGGATGGAGG	AATGTGGGCA	GTTTGACTTC	2760
85	AGCACTGAAA	ACCTCTCCAC	CTGGGCCAGG	GTTGCCTCAG	AGGCCAAGTT	TCCAGAAGCC	2820
	TCTTACCTGC	CGTAAAATGC	TCAACCCTGT	GICCIGGGCC	TOGGCCTGCT	GTGACTGACC ACTTAATTTT	2880 2940
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-	GTTGCGTTGC	TATAGATGAA	GGGTGAGGAC	AATCGTGTAT	ATGTACTAGA	ACTTTTTTAT	3180
5	TAAAGAAACT	TTTCCCAGAA	AAAAA				
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	MGLPRGPLAS	PPPFOACATO	CAASEPCRAV	PREAEVILEA	GGAEQEPGQA	LGKVPMGCPG	60
	ORDALPSTON	DOFTVRNGET	VOERRSLKER	NPLKIFPSKR	ILRRHKRDWV	VAPISVPENG	120 180
15	KGPFPQRLNQ	LKSNKDRDTK NGASVEDPMN	IPYSITGPGA	DSPPEGVPAV	EKETGWLLLN	CTCUMOUTAT	240
13							300
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	DMT-TVT-AGWA	GDDGDHFTIT	THPESNOGIL	TTRKGLDFEA	KNOHTLYVEV	TNEAPPVLKL	420
20	PTSTATIVVH	VEDVNEAPVF DSGQVTAVGT	VPPSKVVEVQ	EGIPTGEPVC	VYTAEDPDKE	TOTLLITLID	540
20							600
	TVVLSLKKPL	KODTYDVHLS	LEDHGNKEOL	TVIRATVCDC	HGHVETCPGP	WKGGFILPVL	660
	GAVLALLFLL	LVLLLLVRKK	RKIKEPLLLP	EDDTRDNVFY	YGEEGGGEED	QDYDITQLHR	720
25						APPYDTLLVF	780
25	DYEGGGDAA	SLSSLTSSAS	DODODADATW	BWGSRPKKLA	DMIGGGEDD		
	. Seq ID NO:	540 DNA sec	quence .				
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	ATGAGGCTCC	AAAGACCCCG	ACAGGCCCCG	GCGGGTGGGA	GGCGCGCGCC	ARGGTTCCAG	60 120
35							180
55	CTGCTCGCCT	TGCTGCTGGT	CGTGGCCCTA	CCGCGGGTGT	GGACAGACGC	CAACCTGACT	240
							300
	TGTCATGTTT	GTGAGAGAGA ACTGCGTTAT	AAACACTTTC	GAGTGCCAGA	ACCCAAGGAG	CATCOTTCCC	360 420
40							480
70	CTCCTGGAAG	AGCCCATGCC	CTTCTTTTAC	CTCAAGTGTT	GTAAAATTCG	CTACTGCAAT	540
	TTAGAGGGGC	CACCTATCAA	CTCATCAGTG	TTCAAAGAAT	ATGCTGGGAG	CATGGGTGAG	600 660
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GCCGGGTTTC CITTUTTOMA ATROGAMANTA TARAGOGCICA TOC
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75
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Protein Accession #: NP 002382.1
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Seg ID NO: 548 DNA sequence

Nucleic Acid Accession #: NM_006783.1 Coding sequence: 1..786

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		549 Protein								
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	Nucleic Ac:	id Accession	n.#: NM_002	571.1						
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00	IMKAPARDD	PINOCETRAL	KFUFKHUNID	шимунын	***					
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)	- COCCERCION	COACCATOG	GGCTTCCCAG	GCTGGTCTGC	GCCTTCTTGC	60			
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45	1	11	21 	1	1	Ī	60
45	1 GLPRLVCAFL	11 LAACCCCPRV	21 AGVPGEAEQP	APELVEVEVG	STALLKOGLS ALTOUTPODE	QSQGNLSHVD RIFLCOGKRP	60 120
	1 GLPRLVCAFL WFSVHKEKRT RSOEYRIOLR	11 - LAACCCCPRV LIFRURQGQG VYKAPEEPNI	21 AGVPGEAEQP QSEPGEYEQR OVNPLGIPVN	APELVEVEVG LSLQDRGATL SKEPEEVATC	STALLKCGLS ALTQVTPQDE VGRNGYPIPQ	QSQGNLSHVD RIFLCQGKRP VIWYKNGRPL	120 180
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	I 	11 LAACCCCPRV LIFRVRQQG VYKAPEPNI SSQTVESSGL VMLEVEPVGM KEHSGRYBCQ DLEFQWLREE WMAPKERKVW	21 AGVPGEAEQP QSEPGEYEQR QVMPLGIPVM YTLQSILKAQ LKEGDRVEIR AWNLDTMISL TDQVLERGPV VKENMVLNLS SNDLGKNTSI	APELVEVEVG LSLQDRGATL SKEPEEVATC LVKEDKDAQF CLADGNPPPH LSEPQELLVN LQLHDLKRBA CEASGHPRPT LFLELVNLTT	STALLKOGLS ALTQVTPQDE VGRNGYPIPQ VCELNYRLPS FSISKQNPST YVSDVRVSPA GGGYRCVASV ISMNVNGTAS LTPDSNTTTG	QSQGNLSHVD RIFICQGKRP VIWYKNGRPL QSHMKESREV REAESETTND APERQEGSSL PSIPGLNRTQ EQDQDPQRVL LSTSTASPHT	120 180 240 300 360 420 480 540
50	I 	LAACCCCPRV LIFRURQGQG VYKAPEPNI SSQTVESSGL VWLEVEPUGM KEHSGRYBCQ DLEFQWLREE WMAPKERKVW LLETGVECTA LPEPESRGVV	21 AGVFGEAEQP GSBFGEYEQR QWBPLGIPVN YTLQSILKAQ LKEGDRVEIR AWNLDTMISL TDQVLERGPV VKENMVLNLS SNDLGKNTSI IVAVIVCILV	APELVEVEVG LSLQDRGATL SKEPEEVATC LVKEDKDAQF CLADGNPPPH LSEPQELLVN LQLHDLKREA CRASGHPRPT LFLELVNLTT LAVLGAVLYF	STALLKOGLS ALTQVTPQDE VGRNGYPIPQ YCELNYRLPS FSISKQNPST TVSBVRVSPA GGGYRCVASV ISNNVNGTAS LTPDSNTTTG LYKKKLPCR	QSQGNLSHVD RIFICQGKRP VIWYKNGRPL QSHMKESREV REAESETTND APERQEGSSL PSIPGLNRTQ EQDQDPQRVL LSTSTASPHT	120 180 240 300 360 420 480
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50 55	GLPRLVCAFL WFSVKKEKRT RSQEYRIQLR KEEKRVHIQ KEEKRVHIQ KITHVAFPAR TLITCBAESSQ LVKLALFGFP STLWLVTPE RAMSTSTERK PSRKTELVVE Seq ID NO:	11	21 AGVFGEAEOP GSERGEYEOR QVNPLGIPVN YTLOSILKAQ LKEGGRVEIR AWNLDTMISL LKEGGRVEIR AWNLDTMISL IVOLVICLIA IVALVICLIA GLLQGSSGDK Quence	APELVEVEVG LSLQDRGATL SKEPEEVATC LVKEDKDAQF CLADGNPPPH LSEPQELLVN LQLHBLKREA CEASGHPRPT LFLEVNLTT LAVLGAVLYF RAPGDQGEKY	STALLKOGLS ALTQVTPQDE VGRNGYPIPQ YCELNYRLPS FSISKQNPST TVSBVRVSPA GGGYRCVASV ISNNVNGTAS LTPDSNTTTG LYKKKLPCR	QSQGNLSHVD RIFICQGKRP VIWYKNGRPL QSHMKESREV REAESETTND APERQEGSSL PSIPGLNRTQ EQDQDPQRVL LSTSTASPHT	120 180 240 300 360 420 480 540
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50 55	GLPRLVCAFL WFSVEKERT RSDEYRICLE RSDEYRICLE KMERNRYHIC TVPVPYFTEK NGVLVLEPAR TLITCRAESSQ LVKLAIFGPP RAMSTSTERK PSRKTELVVE Seq ID NOI NUCLELA AC	11	21 AGVPGEAEQP QSEPGEYEQR QVENEGIEVE YTLOSILKAQ LKEGGRVEIR AWNLDMISL TDQVLERGPV VKERMVLMIS TDQVLERGPV GULQGSSGDK GLLQGSSGDK Quence n #: NM_00: .2639	APELVEVEVG LSIQDRAATL SKEPEEVATC LVKEDKDAQF CLAUGNEPPH LGEPELLVN LQLKDLKKBA CEASGHPRPT LAVLGAVLYF RAPGDQGEKY	STALLKCGLS ALIQUTPQDE VGRNGYPIPQ VGRNGYPIPQ FSISKQNPST VSSDVRVSPA GGGYRCVASV ISMNVNGTAS LTPDSNTTIG LYKKGKLPCR IDLRH	QSQGNLSHVD RIFLCQGKRP VIFYXNGRPL GNHMKESREV REASESTIND APERQESSL PSIPGLMRTQ EQOQDEGRVL LSTSTASPHT RSGKQEITLP	120 180 240 300 360 420 480 540
50 55 60	GLPRLVCAPL WFSVHKEKRT RSOEYRIQLR REERNRVHIQ TVPVFYFTEK MGYLVLEPAR TLICEASSQ LVMLALTGPP STLWLVTPE RANSTSTERK PSKKTELVVE Seq ID NO: Nucleic Ac Coding seq	LIACCCCPRV LIPEURQGG VYKAPEENI SSQTVESSGL WILEVEFYOM KEHSGR YECQ DLEFOMLREE WMAFKERKVW LLETGVECTA LPEPESRGVV VKSDKLPPEM 554 DNA se tid Accessio uence: 165.	21	APELVEVEVG LSIQDRGATL SKEPEEVATC LVKEDKDAQF CLAUGUNEPPH LSEPCELLVN LQLHDLKRBA CEASGHPRPT LAVLGAVLYF RAPGDQGEKY	STALLKCGLS ALIQVTPQDE VGRNGYPIPQ VGRNGYPIPQ VGELNYRLPS FSISKQNPST VYSDVRVSPA GGGYRCVASV ISMINNGTAS LYPENTITG LYPKGKLPCR IDLRH	GSCGNLSHVD RIFLCQGKRP VIHYMOREN CHINKESRBV REAEESTTHD APERQESSL PSIFGLMRTQ EQOQDEQRVL LSTSTASPHT RSGKQBITLP	120 180 240 300 360 420 480 540 600
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                                                     ATGAGGACCA GOGAGGAAA TATGTCATGT ATCCCATAGC TGTGAGTGGC GATCACGAGA
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                                                        TROASTITAT GGAATCTACC ARCTGTTTAG GGCCCTGATT TGCTGGGCAG TTTTTCTGTA
TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCT AGAAAATCA
CTATTGGTAG GGATGGTGG CTCATGCCTG TAATCCCAGC ACTTGGAGAG GCTGAGGTTG
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35
                                                        CGCCACTACA CTCCAGCCTG GGTGACAGAG TGAGATCTGC CTC
                                                        Seq ID NO: 555 Protein sequence
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	MROSLLFLTS	VVPPVLAPRP	PDDPGFGPHQ	REEKLOSELS	DYDILSLSNI	QQHSVRKRDL	6
	OTSTHURTLL	TFSALKRHFK	LYLTSSTERF	SONFKVVVVD	GKNESEYTAK	WQDFFTGHVV	12
45	GEPDSRVLAR	IRDDDVIIRI	NTDGAEYNIE	PLWRPVNDTK	DKRMLVYKSE	DIKNVSRLQS	18
	PKVCGYTKVD	NEELLPKGLV	DREPPBELVH	RVKRRADFDF	MKNTCKLLVV	ADHRFYRYMG	24
	PORESTTTNY	LIELIDRYDD	IYRNTSWDNA	GFKGYGIOIE	OIRILKSPOE	VKPGEKHYNM	30
	AKSYPNEEKD	AWDVKMLLEQ	FSFDIAEEAS	KVCLAHLFTY	QDPDMGTLGL	AYVGSPRANS	36
	HOGUCPKAYY	SPYCKKNIYL	NSGLTSTKNY	GKTILTKEAD	LVTTHELGHN	FGAEHDPDGL	42
50	AECAPNEDOG	GKYVMYPIAV	SCOHENNKMF	SNCSKQSIYK	TIESKAQECF	QERSNKVCGN	48
	SPVDEGERCO	PGIMYLNNDT	CCNSDCTLKE	GVOCSDRNSP	CCRNCOFETA	QKKCQEAINA	54
	TCKGVSYCTG	NSSECPPPGN	ARNOTYCLDL	GKCKDGKCIF	PCEREOOLES	CACNETONSC	60
	INCCENT.9GP	CVPYVDAEOK	NUFLERGREC	TYGECDMNGK	CEKRYODVIE	RFWDFIDOLS	66
	INTEGERIAD	NIVGSVLVFS	LIPWIPPSIL	VHCADKKTDK	OYESLSLEHP	SNVEMLSSMD	72
55	CACUDITED	PAPOTPGRLO	DARVIPSAPA	APKLIDHORMD	TIOEDPSTDS	HMDEDGFEKD	78
-		SFEDLTDHFV					

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	1	11	21 	31 	41	51	
	TOTALGOCTIGG	CGGTAGAATC	TTCCCAGTAG	GCGGCGCGGG	AGGAAAAGAG	GATTGAGGGG	60
65	CTAGGCCGGG	COGATCCCGT	CCTCCCCCGA	TGTGAGCAGT	TTTCCGAAAC	CCCGTCAGGC	120
	GAAGGCTGCC	CAGAGAGGTG	GAGTCGGTAG	CGGGGCCGGG	AACATGAGGC	AGTCTCTCCT	180
	ATTCCTGACC	AGCGTGGTTC	CTTTCGTGCT	GGCGCCGCGA	CCTCCGGATG	ACCCGGGCTT	240
	CGGCCCCCAC	CAGAGACTCG	AGAAGCTTGA	TTCTTTGCTC	TCAGACTACG	ATATTCTCTC	300
	TTTATCTAAT	ATCCAGCAGC	ATTCGGTAAG	AAAAAGAGAT	CTACAGACTT	CARCACATGT	360
70	AGAAACACTA	CTAACTTTTT	CAGCTTTGAA	AAGGCATTTT	AAATTATACC	TGACATCAAG	420
	TACTGAACGT	TTTTCACAAA	ATTTCAAGGT	CCTCCTCCTC	GATGGTAAAA	ACGAAAGCGA	480
	GTACACTGTA	AAATGGCAGG	ACTTCTTCAC	TGGACACGTG	GTTGGTGAGC	CTGACTCTAG	540
	GGTTCTAGCC	CACATAAGAG	ATGATGATGT	TATAATCAGA	ATCAACACAG	ATGGGGCCGA	600
	ATATAACATA	GAGCCACTTT	GGAGATTTGT	TAATGATACC	AAAGACAAAA	GAATGTTAGT	660
75	TTATAAATCT	GAAGATATCA	AGAATGTTTC	ACGTTTGCAG	TCTCCAAAAG	TGTGTGGTTA	720
	TTTAAAAGTG	GATAATGAAG	AGTTGCTCCC	AAAAGGGTTA	GTAGACAGAG	AACCACCTGA	780
	AGAGCTTGTT	CATCGAGTGA	AAAGAAGAGC	TGACCCAGAT	CCCATGAAGA	ACACGTGTAA	840
	ATTATTGGTG	GTAGCAGATC	ATCCCTTCTA	CAGATACATG	GGCAGAGGGG	AAGAGAGTAC	900
	AACTACAAAT	TACTTAATAG	AGCTAATTGA	CAGAGTTGAT	GACATCTATC	GGAACACTTC	960
80	ATGGGATAAT	GCAGGTTTTA	AAGGCTATGG	AATACAGATA	GAGCAGATTC	GCATTCTCAA	1020
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23							

Seq ID NO: 557 Protein sequence Protein Accession #: NP_068604.1

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Seq ID NO: 558 DNA sequence Nucleic Acid Accession #: NM_004994.1 Coding sequence: 20..2143

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		559 Protein eesion #: 1					
15	Procein Acc	seasion a: 1	4P_004985.1				
13		11	21	31	41	51	
	t	Ť.	î^	1	7.	ĭ	
	MET MODE VEN	LIMECCEAN	PROROSTLVL	PRODURTMENT	DROLAFEVIA	PVGVTPVARM	60
	DODESKS! CDV	PEATOCCE AN	DETTIELDSAT	LEAMPTPROG	VPDLCPPOTE	BGDI-KWHHHN	120
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			NYDTDDRPGP				300
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45 50	Seq ID NO: Protein Acc	561 Prote cession #: 1	in sequence NP_000204.1	CTTTGTTCTG	41	51 	60
	Seq ID NO: Protein Acc	561 Protectes in the second se	in sequence NP_000204.1 21 SLSGTLANRC	31 KKAPVKSCTE	41 CVRVDKDCAY MSPOGLEVEL	51 CTDEMFRDRR RPGEERHFEL	60
	Seq ID NO: Protein Acc 1 MAGGRPSPWA CNTQAELLAA RUFEPLESPV	561 Protectes of the control of the	in sequence NP_000204.1 21 SLSGTLANRC ESSPQITEET SMSDDLDNLK	31 KKAPVKSCTE QUDTTLERSQ KMGQMLARVL	41 CVRVDKDCAY MSPQGLRVRL SQUTSDYTIG	51 CTDEMFRDRR RPGEERHFEL FGKFVDKVSV	60 120 180
50	Seq ID NO: Protein Acc 1 MAGPRPSPWA CNTQAELLAA EVFEPLESPV	561 Prote cession #: 1 11 RLLLAALISV GCQRESIVVM DLYIIMDFSN MYRDWPNSDPP	in sequence NP_000204.1 21 SLSGTLANRC ESSPQITEET SMSDDLONIKE ESSPQINISLT	31 - KKAPVKSCTE QIDITLERSQ KMGQNLARVL	41 CVRVDKDCAY MSPQGLRVRL SQLITSDYTIG OGER ISGNLD	51 CTDEMFRDRR RPGBERHFEL FGKFVDKVSV APEXGFDAIL	60 120 180 240
	Seq ID NO: Protein Acc 1 MAGPRPSPWA CNTQAELLAA EVFEPLESPV PQTDMRPEKL OTAVCTRDIG	561 Protectession #: 1 11 RILLAALISV GCQRESIVVM DLYILMOFSN KEPWFNSDPP WRPDSTHLLV	in sequence NP_000204.1 21 SLSGTLANRC ESSPQITEET SMSDDLONLK PSPKNVISLT PSTESAFHYE	31 - KKAPVKSCTE QIDTTLRRSQ KMGQNLARVL EDVDEFRNKL ADGANVLAGI	41 CVRVDKDCAY MSPQGLRVRL SQUTSDYTIG QGERISGNLD MSRNDERCHL	51 CTDEMFRDRR RPGEERHFEL FGKFVDKVSV APEGGFDAIL DTTGTYTQYR	60 120 180 240 300
50	Seq ID NO: Protein Acc 1 MAGPRPSPWA CNTQAELLAA EVFEPLESPV PQTDMRPEKL QTAVCTRDIG TONVPSNYTL	561 Protecession #: 1 11 RILLAALISV GCQRESIVVM DLYILMDFSN KEPWPNSDPP WRPDSTHLLV VRILAKHNII	in sequence NP_000204.1 21 SLSGTLANRC ESSPQITEET SMSDDLDNLK PSPRNVISLT FSTESAFHYE	31 - KKAPVKSCTE QIDITLERSQ KMGQNLARVL EDVDEFRNKL ADGANVLAGI SYYEKLETYF	41 CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL PUSSLGVLQE	51 CTDEMFRDRR RPGEERHFEL FGKFVDKVSV APEXGFDAIL DTTGTYTQYR DSSNIVELLE	60 120 180 240 300 360
50	Seq ID NO: Protein Acc 1 MAGPRPSPWA CNTQAELLAA EVFEPLESPV PQTDWRPEKL QTAVCTRDIG TQDYPSVPTL	561 Protectession #: 1 11 RLLLAALISV GCQRESIVVM DLYILMOFSN KEPWPNSDPP WRPDSTHLLV VRLLAKHNII DTDMINERDG	in sequence NP_000204.1 21 SLSGTLANRC ESSPQITEET SMSDDLONLK PSPRNVISLT FSTESAFHYE PIFAVINYSY LETEVISKMP	31 	41 CVRVDKDCAY MSPQGLRVRL SQUTSDYTIG QGERISGNLD MSRNDERCHL PVSSLGVLQE	51 CTDEMFRDRR RPGERHFBL FGKFVDKVSV APEXSFDAIL DTTGTYTQYR DSSNIVELLE CLRALENVDG	60 120 180 240 300 360 420
50	Seq ID NO: Protein Acc 1 	561 Prote 11 RLLLAALISV GCQRESIVVM DLYILMOPSN KEPWPNSDPP WRPDSTHLLV VRLLAKHILL DIRALDSPRG VANIALISSRG	in sequence NP_000204.1 21 SLSGTLANRC ESSPQITEST SMSDDLDNLK FSFRNVISLT FSTERSHEVE PIFAVINYSY LRTEVTSKNP	31 - KKAPVKSCTB CIDTTLRISG CIDTTLRISG CHGONLARVL EDVDEPRINL ADGANVLAGI SYYEKLHTYF QKTRTGSFIL	41 CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG GGBRISGRIG MSRNDERGL PVSSLGVLQE RRGEVGIVQV KEVRSARCSP	51 CTDEMFRDRR RPGBERHFEL FGKFVDKVSV APEXGFDAIL DITGTYTQYR DSSNIVELLE QLRALERVDG MCDPVCGOCV	60 120, 180, 240, 300, 420, 480
50 55	Seq ID NO: Protein Acc 1 MAGPRPSPWA CNTQAELLAA EVPEPLESPV POTDWRPERL QTAVCTRDIG TODYSSVPTL EAFWIRSNL THVOLIPEDQ CSEGWSGOTC	561 Prote ression #: 1 11 RLLLAALISV GCQRESIVVM DLYILMOFSN KEPWFNSDPP WRPDSTHLLV VRLLAKHNII DIRALDSPRG KGNIHLKPSF NCSTGSLEDI	in sequence NP_000204.1 21 SLSGTLANNC ESSPOITEST SMSDDLDMLK FSFRNVISLT FSTESAPTHYS PIFSAPTHYS LRTEVTSKNP SDGLKMDAGI OPCLREGESK	31	41 	51 	60 120 180 240 300 360 420
50	Seq ID NO: Protein Acc 1 MAGPRPSPWA CNTQAELLAA EVPEPLESPV POTDWRPERL QTAVCTRDIG TODYSSVPTL EAFWIRSNL THVOLIPEDQ CSEGWSGOTC	561 Prote ression #: 1 11 RLLLAALISV GCQRESIVVM DLYILMOFSN KEPWFNSDPP WRPDSTHLLV VRLLAKHNII DIRALDSPRG KGNIHLKPSF NCSTGSLEDI	in sequence NP_000204.1 21 SLSGTLANNC ESSPOITEST SMSDDLDMLK FSFRNVISLT FSTESAPTHYS PIFSAPTHYS LRTEVTSKNP SDGLKMDAGI OPCLREGESK	31	41 	51 	60 120 180 240 300 360 420 480 540 600
50 55	TACTG Seq ID NO: Protein Acc 1 MAGPRPSPHA CNTQAELLAA EVFEDLESPY GYDVMFPEL GTAVCTRDIG TQDYSSVPTL EAFNRIRSNL THVCQLPEDQ CSEGWSGTC CCCPTSGFL CKCRQSLYT LKRAESVYT LKRAESVYT	561 Prote ression #: 1 11 RLLLAALISV GCQRESIVVM DLYILMOFSN KEPWFNSDPP WRPDSTHILLV VRLLAKHNII DIRALDSFRILL GRNTHLKPSF NCSTGSLSDI CNDEGRCSMG DTICEINYSA CSPROEDDDC	in sequence nP_000204.1 21	31 KAPVKSCTE QIDTILRRSQ RMGQNLARVIL EDVDEPRINLI ADGANVLAGI SYYEKLHTYP QKTRTGSFRI ICDVCTCELQ PCSGRGEQCQ PSCDCPLENA SCVQQQANGT	41 CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGBRISGHLD MSRNDERCHL PVSSLGVLQE RRGEVGIVQE KEVRSARCSP GHCVCYGERR TCIDSNGGIC GEKKGRTCES	51 	60 120 180 240 300 360 420 480 540 600 660
50 55	Seq ID NO: Protein Acc 1 NAGPRPSFWA CMTOAELLAA EVFEDLESPY QTDWRPSFVETL GTAVCTRDIG TODYSSVETL EAFWRIESNL THYOQLFEDQ CSEGWSGTC FOCEPTSGFL CKCHQOSLY LKRAEEVYVR	561 Prote cession #: 1 11 11 RLLLAALISV GCQRESIVVM DLYILMDFSN KEPMENSDPP WRPDSTHLLV VRLLAKHNII DIRALDSFRG KGNIHLKFSF KGNIHLKFSF KGNIHLKFSF COMMON COMMON COM	in sequence NP_000204.1 21 21 SLSGTLANRC ESSPGITEST SMSDDLDNLS. FSPROVISLT PSTESAPHYE PIFAVTNYSY LATEVYSING LOPCLREGEDK QCYCEPGHTG TYSYTMEGGG TYSYTMEGGG TALLIDCOM	31 KKAPVKSCTE QIDTITURESQ (IDTITURESQ (IDTITURESQ (IDTITURESQ (INFOCE) (IDVICE) (I	41 CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG GGERISGNLD MSRNDERCIL PVSSLGVLQE RRGEVGITQV KEVRSARCSF GHCVCYGEGR TCIDSNGGIC GEKKGRTCE KKKDCPPGS	51 CTDEMFRDRR FORERHFEL FGKFVDKYSV APEGGFDAIL DTTGTYTQYR DSSNIVELLE QLRALBINDG NGBFVCGQCV ONGROCKCGCT ONFKVRWIDE FWHIJPLILL SDHLIDTHLL	60 120 180 240 300 420 480 540 660 720
50 55 60	TACTG Seq ID NO: Protein Acc 1 1 MAGPRPSPNA CNTQAELLAA EVFEDLESPY GYDVMFPEL GTAVCTRDIG TQDYSSVPTL EAFNRISSNL THVCQLPEDQ CSEGWSGTC CCCPTSGFL CKRAESVYT LKRAESVYT LK	561 Prote cession #: ! 11	in sequence NP_000204.1 21 SLSOTLANRC ESSPQITEET SMSDDLONIL FSTRENFHYE FSTRENFHYE LRIEVTSKNP SDGLKMDAGI QPCLREGEDK QVCEPGHTG LHPGLCEDLA CVSTREELBOA CLALLPCCB DGPATHASSI	31	41 CVRVDEDCAY MSPQGLRVEL SQLINSDYTIG GGERISGNLD MSRNDERCHL KEVRSARCSP GHCVCYGEGR TCIDSNGGIC GEKKGRTCES HYMLRENLMA SIRLIARLCTE	51 CTDEMFRDRR RPGEERHFEL FGKFVDKVSV APEGGFDALL DTTGTYTQYR RGDEVCGQCV YEGQFCEYDN MRGGHCEGGR CNFRVMVDE FWMLIPLLLL SDHLDTPMLR HLLKPDTPREC	60 120 240 300 360 420 480 540 660 720 780
50 55	TACTG Seq ID NO: protein Acc 1	561 Prote cession #: 1 11 RILLLAALISV GCQRESIVVM DLYILMOPSN KEPWENSDPP WRPDSTHLLV VRLLAKENII DIRALDSPSI CMDRGRCSMG KGN HILKPSP DCSTGSLSDI CMDRGRCSMG CSFROEDDC LCWRYCACR RKVITNNMGR KRYSTON	in sequence NP_000204.1 21	31 	41 CVEVDEDCAY WSPGGLEVEL SQLITSDYTIG GERISGHLD WSRINDERGHL WSRINDERGHL WSRINDERGHL WSRINGLY KEVRSARCSP GHCVCYGER TCIDSNGGIC GEKKGRTCES HKKKOCPPGS STYMLERILMA SIRLARLCTE HTIVIDTULMA	51 CTDEMFRDRR RPGERRHFEL FGKFVDLVSV APEGGFDAIL GLRALERIVDG GGDFVCOGCV MGRGHCKCGR CNFEVINVDE FWHIJPLLIL BUHLDFLIL HLLKFUTRBC	60 120 180 240 300 420 480 600 600 720 780 840
50 55 60	TACTG Seq ID NO: Protein Acc 1 MAGPRESHA CNTOALLAA EVFEBLESPY POTDMRPERLI GTAVCTRDIG TODYSVETL THVOQLEEDQ CSEGMSQTC PCCPRESOFL LKCAREVVVR ACLACE LOPACHECODY ACLACE ACC ACC ACC ACC ACC ACC ACC ACC ACC	561 Prote- cession #: 1 11 RILLLAALISV GCQRESIVVM DLYIIMDFSN KEPMPNSDFP WRPDSTHLLV VRLLAKHLU VRLLAKHLU VRLLAKHLU DIRALDSFRG KGNIHLKPSF NCSTGSLSDI CNDEGRCSMG DTICEINYSG ENDEGRCSMG CTFRDEDDDC LCWKYCACCK KWKYTNNMGR LNEWYRQISG	in sequence NP_000204.1 21 SLSOTLANRC ESSPQITEET SMSDDLDNILL FSTESAPHYE PIFAVINYSY LRIEVTSKNP SDGLEMDAGI QPCLREGEDK CVCEPGGTG IHPGLCEDLA CVCEPGGTG ACLALLPCCM PGFATHAASI VHKLQQTKFR VILTADODAR	11	41 CVRVDEDCAY MSPQGLRVEL SQLTSDYTIG QGBISGNLD MSRNDERCHL PVSSLGVIQE RGEVGIVQV GEKKRTCES GHCVCYGERR HCKNCOPPGS HYMLRENLMA SLRLARLCTE HTIUDTVLMA	51 	60 120 180 240 360 420 480 540 660 720 840 900
50 55 60	TACTG Seq ID NO: protein Acc 1	561 Prote cession #: 1 11 RILLLAALISV GCQRESIVVM DLYILMOPSN KEPHENSDPP WRPDSTHLLV VRLLAKENII DIRALDSPII DIRALDSPII DIRALDSPII DIRALDSPII CMBRGCSMG GSPREDDDC LCWKYCACK RIKVINNIGA RIKVINN	in sequence NP_000204.1 21 SLSOTLANRC ESSPOITEST SMSDDLDHLK PSPRNVISLT FSTESSPHTP FSTESSPHTP FSTESSPHTP GPCLREGEDK QCVCEPGHTG TPSTESSPHTP TPSTESSPHTP TPSTESSPHTP TPSTESSPHTP TPSTESSPHTP TPSTESSPHTP TSTESSPHTP 11	41 CVRVDKDCAY MSPQQLRVRL SQLTSDYTIG QGERISGNLO WSRNDERGIL PVSSLGVLQE KEVRSARCSP GHCVCYGEGR TCIDSNGGICE KKKGCP PGS KYMLERILMA SIRLARLCTE HTTUDTVLMA LVDVRVPLPI VSRGDVAPP	51 CTDEMFRDRR RPGERRIBEL FGKFVDKVSV APEGGFDAIL GLRALERIVDG GGDFVCOQCV MGRGHCKGGR CNFEVKNVDE FWHLIPLLLL SDHLIDTHAL HLLKFDTRBC RPSAKPALL RPEDDDEKQL RPSURDDLEV RPSURDDLEV RPSURDDLEV RPSURDDLEV RPSURDDLEV RPSURDDLEV RPSURDDLEV RPSURDDLEV RPSURDDLEV RPSURDULDGLE RPEDDLEV RPSURDDLEV RPSURDLEV RPSURDDLEV RPSURDDLEV RPSURDLEV RPSURDDLEV RPSURDDLEV RPSURDL	60 120 180 240 360 420 540 600 720 780 900 900 1020	
50 55 60 65	Seq ID NO: Protein Acc I MORPEPHA AUTOAELLAA BUFELLESPY EVELLESPY EVELLESPY EVELLESPY EXPERIESPY	561 Prote- cession #: 1 LLLAALISV GOORSIVM DLYILMDESN KEPPHNSDPP WRPDSTHLLV VRLLAKHIV DIRALDSRNG KONIHLKPSP NCSTGSLSDI CINDEGRESM DIICEINYSA CSPREEDDDC LCWKYCACCK KWKYTNNOGR KNKVINNOGR KNCORNOGR	in sequence sp_000204.1 21 SISSTILANRC SESSPOITEET SESSPOITE SESSPOITEET SES	31	41 CRVDKDCAY MSPQGLAVEL SQLTSDYTIC GGER ISGNLD MSRNDERGEI PVSSLGVILG FRGEGVITYOW KEVRSARCSP GRICVCTORGE GRICVCTORGE HKKKOCEPOS HKKROCEPOS HKK	51 CTDEMPEDER PROGERRIPEL PGKEVDLYSV APEGGFDAIL DITGTYTOYR ROBEVCOQCV YEQQFCEYDIN MIRGRICKGR CNFEVRHVDE FWMITPILLL SDELDTPHILL SDELDTPHILL REPEDDEKOL PWRITPILL REPEDDEKOL REPEDDEKOL ROMEROVERPIL ROMEROL REPEDDEKOL ROMERO	60 120 240 300 420 480 540 600 720 7840 900 1020 1080
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50 55 60 65	Seq ID NO: Protein Act 1 NAOPAPSPM NAOPAPSPM NAOPAPSPM NAOPAPSPM NAOPAPSPM NAOPAPSPM NAOPAPSPM NAOPAPSPM NAOPAPSM NAOPASM	S61 Prote cession 8: 1 11 ILLIAALISV GCCRESIVVE KREWNENDE KREWNENDE KREWNENDE KRILAKKOIL UTRALOSPRO KKNIHLKPE CEBRORCSMO CESPROEDDO LOWKYCACK KRIVTINNEN CHISTORIA THOLKVARV TATLERRLWS GTAQCREST TATLERRLWS GTAQCREST TATLERRLWS GTAQCREST TATLERRLWS GTAQCREST TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV TATLERRLWS GTAQCREST HOLKVARV HOLKV	in sequence sp_00204.1 21 21 SLEGITLANIC SASSPPITE ER SMEDILIANIC SMEDILIANIC SMEDILIANIC SMEDILIANIC SMEDILIANIC SMEDILIANIC SMEDILIANIC SMEDILIANIC SMEDILIANIC FORESAPHYE PERPAYTHYSI LATE-UTSOP LA	31	41 CVRVDKDCAY HISPOCLAVEL SQUTSDYTTO QGER ISGNIJ MERNDERCHL MERNDERCHL MERNDERCHL MERNDERCHL MERNDERCHL MERNDERCH MERKDCOPPES LYMLERHAM SELLARLCTE MERKDCOPPES LYMLERHAM SELLARLCTE MERKDCOPPES LYMLERHAM MERNDERCHAM MERNDE	51 CTOSHEPIDER REGUESHIPSLI FIGKEPUDIVSV APPSGEPALI DTTGTYTOVR GUSHIVELLE GUSHAUSHO GUSHIVELLE GUSHAUSHO MORGFUCGCC VFEXIFIX STRUCK FINANTOS FINANTOS FINANTOS GUSHAUSH GUSH GUSHAUSH GUSH GUSHAUSH GUSH GUSH GUSH GUSH GUSH GUSH GUSH G	60 120 240 300 480 540 600 780 840 900 1020 1140 1260
50 55 60 65	TACTO Seq ID NO: Protein Ac: I	S61 Prote- cession #: 1 II RLLIAALISV GOQRESIVM DLYILKOPSN KERPHYNDEP WRPDSTILLV VRLLAKENII DIRALDSPRG KORNILLVEP WRPDSTILLV GORNESISOL OTICELNYA CUSPROBEDDOC LICKYCACCE RKKVINNMOR LICKYCACCE KRKVINNMOR LIKEYYRQIS FIDLAVAPOY TATLCRELLW GTAQCHROTIV SOCHOUTEN SOCHOU	in sequence sp_000204.1 21 21 SLSGTLANNC ESSPOITEST SMSDDLDNIA FORSARHIVE FOR	31 KGAPVKSCTE GUDTLURSG, KWGOLLARU, KWGOLLARU, EVDEFERM, ADANVLAG, SYYEKLHTYP GGGGGGCO, FSCGCPLSMA SCYQCQAMOTA ADGENERAL ADGE	41 CVRVDRDCAY MSPQGLAVRL SQLTSDYTIO OGERISONLO MSRADERCHL POSIGIVIQU GERISONLO GERIS	51	60 120 180 240 360 480 660 780 960 960 1020 1080 11200 1230
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50 55 60 65 70	SEQ ID NO: Protein Act I MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGPRIPHA MAGRRIPHA	S61 Prote- cession #: 1 II RLLLAALISV GOQRESIVON DLYILMOPSN KEPHYNDEP WRPDSTHLLV VRLLAKSHIL DIRALDSPRG KKNHILMSP NCSTGSLSSI COMBORCOSS FROM	in sequence sp_000204.1 21 21 SLSGTLANNC SESFOTIEST SMSDDLDNIA FFTESAPHYE FFT	31	41 CVRVDKDCAY MSPOGLEVEL SQLTSDYTIO GGERISGRIU MSRADERCHL MS	51 TITLEHFEDER ROSERVEY TITLEHFEDER ROSERVEY ROSERVEY APROGRAMMY APROGRAMMY APROGRAMMY ARRIVED A	60 120 180 240 300 420 480 540 660 780 900 900 1020 1140 1200 1320 1380 1440
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	SRALDPAGNE	SAYPPNOVEC	GCGSGLPGKN YSCVGLSREA	COGTSPPVVS	CYNASDHVYK	GCFDGNVTLT	180
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70	LPPPEPTTVA	STISVITSIS	APVRPTSTTK PHNKGCVAPT	PMPAPTSQTP	ROGVEHEASK	DESPRETGGA	300
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	TTGCGCAAGT	GCCTGCGCTC	GGCCCAGCGC	TACATGCTCC	CTGACCTCAA	CGAGGTGCTG	360 420
85	CCCCCCCC CCC	NACNACCCC	CALLACALACACA CONTRACTOR OF THE PROPERTY OF TH	TOGGOGGENGEN	ACTTCCATGA	GGCAGGCGAG	480
	GGTGAGACGG	AGGCCAGCCT	GCAGGAGGGC	ATGGACCGTC	TGCGGGATGT	GGTGCGGGCC GTACACGGCC	540 600
	AGCACCTTCT	CUTGCATCAT	GCAGAAGTGG	GUAGUCAAGO	. GUIAGGI CAT	G. MCMCGGCC	900

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	VVDGNROEDA	YMLDI PHEVL GGKREVMYTA	GGTEQAGFFV	WRSNPHEAGE	GETEASLQEG	MDRVRDVVRA	180
	STESCIMOKW	GGKREVMYTA	FKALGDSVDY	IQVCDSDTVL	DPACTIEMLR	VLEEDPQVGG	240 300
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	CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA GAGATAGGAA GATATCAAAGGA GATATCAAAG	AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA	GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT TGGAGTCGAA	GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAA TTGTTTGAGG AGTGTTAGTC	ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTTGAGGA TTGGGACAGA GTTTTTGAGGA GTTTTGGGACAGA	ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCCAAA AGAAAATTTG GCAGGCTGCT	300 360 420 480 540 600 660 720 780
50 55	CTTGTTGAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAAA GGAAAAGGA GATATCCAAG GTTTCCAAG TTAGATCCAT	AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA TCTACTGTT	GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT TGGAGTCGTA GAACCTTCTG	GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAA TGTTTGAGG AGTGTTAGTC CCAAACTCAA	ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA GTTTTGGGACAGA GTTTTGGGACAGTA CTGACAAGTA	ACREGGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC	300 360 420 480 540 600 660 720 780 840
	CITGTIGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA GAGATGCAAA GGATACCAT AATGGCTCAT AATGGCTCAT ACAGTTAGCA	AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA TCATACTGTT TGACATCTCT TGACATCTCT TCTCTGAAAG	GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG TCCCTGCAC CCAGTGGGC	GGAGCACTGA TCTCCTATGA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAA TTGTTTGAGG AGTGTTAGTC CCAAACTCAA GACACGTTG GTTTTTTTTGTG	ACTACAGACA ATCARANANA ATATTGATGA GGGATARANC ATCTCACTAR AGGARACATT ARGGACARAA GTTTTGAGGA GTTTTGAGGA GTTTTGGGAA GTTTTGGGAA CTGACARGTA ACTGGATTGA ACTGGATTGA	ACREGRAMA TTGGGRAMG AGATCTTACA ATCATTGGRA TGACTACCGT TCACTGGGRA ATTTCCACTT AGCAGTCARA AGAANATTTG GCAGGCTGCT TTACATTTAC TTTTAMAGAT AATGCAACAA	300 360 420 480 540 660 720 780 840 900
	CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAAATA GAGATGCAAA GGATACCAA GTTTCAAAG TTAGATCCAT ACAGTTAGCA TCTGGTTATGA TCTGGTTATGA	AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TCTACTGCTT AGTTAAGAGC CGATTATTGA TCATACTGTT TGACATCTCC TCTCTGAAAG	GTCCTATACA CCCAAAACAA GAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCGGAC TTIATCCATT TGGAGTCGGA GAACCTTCTG TCCCTGCACA CCAGTTGGCT GGACTAGCT GGACTAGCT TGGACTTGCT TGGACTTGCT TCCCTGCACA CCAGTTGGCT TGGACTTGCT TGGACTTGCT TGGACTTAGCT TGGACTTAGCT TGGACTTAGCT TGGACTAGCT TGGACTACTTA	GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAA TTGTTTGAGG AGTGTTAGTC CCAAACTCAA GACACAGTTG GTTTTTTTTTGAG GTTTTTTTTTT	ACTACAGACA ATCANANAA ATATTGATGA GGGATANAAC ATCTCACTAA AGATAACTTT AAGGACANAA TTGGGACAGA CTGCAAGTA ACTGGATTTTGGGAA ACTGGATTGTTAGGA ACTGGATTGTAAGTA ACTGGATTGTAAGTA ACTGGATTGTTAGGAA TTGGAAGTA ACTGGATTGTTAGGAA TTGGAAGTA ACTGGATTGTTAC	ACREGARANA TTGGGRAANG AGATCTTACA ATCATTGGRA ATGATTACCOFT TCACTGGGGA ATTTCCACTT AGCAGTCANA AGANANTTG GCAGGCTGCT TTACATTTAC TTTANAGAT AATGCAACAA ACRGTACANA	300 360 420 480 540 660 720 780 840 900 960
55	CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA GGATTCCAAT GGATTCCAAT AATGGCTCAT ACAGTTAGCA TCTGGTTATG TCTCTAGAT TCTTAGAT TCTTAGAT TCTTAGAT TCTTAGAT TCTTAGAT	AGATTOGCTG CATGTAATAG TIGAATCTTAA TICATAACAC GAGTTTCAGA TITACTGCTT TAGTTAAGAGC CGATTATTGA TIGACATCTCC TICATGCTGAAAG TICATGCTGAT TICATGCTGA	GTCCTATACA GCAAAACAA GAACTTAAA TGGGAAAACA AATGGTGTT TGGATCAGAG TTATGCGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG GCACTACTCA CCAGTTGGCT GGACTACTTA CCAGTTGGCT GGACTACTTA CTCATTACACT	GGAGCACTGA TCTCCTATCA TCTCGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CAATTTCAA TTGTTTGAGG AGTGTTAGTC CCAAACTCAA GACACGTTG GTTTTTTGTG GTAAACCAATT GGAAACGAAT GGAAACGAAT GGAAACGAAT	ACTACAGACA ATTATGATCA GGATTAAAAC ATCTCACTAA AGATAACTT AAGGACAAAA GTTTTGAGGA CTGACAAGA CTGACAAGA ACTGACAAGA ACTGATTATGAGA ACTGACAAGTA ACTGAGATTATAAGA ACTGAATTATAAA ACTGAATTATAAAACTTTAACAAGACA AGATTCATAA AGATTCATAA	ACAGAGAAAA TIGGGGAAAG ATCATTGGA TIGACTACCAT TIGACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG TITACATTTAC TITACATTTAC TITACATTTAC TITACATTTAC ATTTACATTTAC ATTTACATTTAC ATTTACATTTAC AGCAGTACAAA ACAGTACAAA ACAGTACAAA AGCAGTTTOT	300 360 420 480 540 660 720 780 840 900
	CTIGTIGARE ANATATCCAA ANATATCCAA ANACATTCA ANCACATTCA GTAAGGAA ANATGCAATA GGAAAAGGAA GGAATACGAA TTAGAATCCAAT AATGGCTCAT ACAGTTAGCA TCTGGTTATG TCTCTAGAC AGTTCAGAAC AGTTCAGAAC	AGATTAGCTG CATGTAATAG TGAATCTTAA TTCATAACAG AGTTTCAGA TGTCATCTGA TGTCATCTGA TGTCATCTGA TCACTGCT TCACACTGCT TGACATCTCC TCTCTGAAAG TCATCTGCAAAA AGGTCTTTTCAGAAAATTTTC CAGAAAATGTT TCCAGGTGTT	GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAACTT TGGATCAGAG TGATCCGAG TTTATCCATT TGGATCAGAG GAACCTTCTA GAACCTTCTA CCCAGTTGGCT GGACTACTTA CTCATACACT TCAGGGCTGAC TCAGGGCTGAC TCAGGGCTGAC TCAGGGCTGAC TCAGGGCTGAC TCAGGGCTGAC TCAGGGCTGAC TCAGGGCTGAC TTATATATACC	GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTTCAG AGTGTTAGTC CCAAACTCAA GACACAGTTG GTTTTTTTTTT	ACTACAGACA ATATGATGA ATATGATGA ATATGATGA AGGATAAAATA AGGATAACTT AGGACAAAA GTTTTGAGGA CTGACAGAAA ACTGACAGAAA ACTGACAGAAA ACTGACAGAAA ACTGACAGAAA ACTGACAGAAA ACTGACAGATA ACTGACAGATA AGATTCTTAC AGATCATGA ATACCAGCCT AGTTGCGGA	ACAGARANA TTGGCGAAG AGATCTTACA ATCATTGGAA ATCATTGGAA ATTCATGACTACCGT TCACTGGGGG AGAAATTTG GCAGGCTGCT TTACATTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG ACAGTACAAG ACAGTACAAG TCTTTTATACA TCTTTTTTACA	300 360 420 480 540 660 720 780 840 900 960 1020 1140 1200
55	CTTGTGAAG CAAGTAAATG AAACATTCA ACACATTCA ACACGGGG AAATGCAATA GGAAAAGGA GGATTCAAGA GTTAGATCCAT AATGGCTCAT AATGGCTCAT ACTGGTTAGC TCTGGTTATG TTCTCTAGGA TGGGAAGAG TGGGAAGAG TGGGAAGAG CAGTTGGGAA	AGATTOGCTO CONTRACTOR TGAATAGG TGAATCTAA TCATAACAG GGOTTCAGA TGTCATCAGA TGTCATCAGA TCATCATGA TCATCATGAT TCATCATCATGAT TCATCATGAT TCATCATCATCAT TCATCATCATCATCAT TCATCATCATCATCAT TCATCATCATCATCAT TCATCATCATCATCAT TCATCATCATCATCAT TCATCATCATCATCATCAT TCATCATCATCATCATCATCAT TCATCATCATCATCATCATCAT TCATCATCATCATCATCATCAT TCATCATCATCATCATCATCAT TCATCATCATCATCATCATCATCATCATCATCATCATCAT	GTCTATACA GRAACTAAA GRAACTTAAA TGGGAAACA AATGGTGTTT TGGATCGGAC TTTATCCATT TGGAGTCGAA GRACCTTCTG TCCCTGCACA CCAGTTGGCT GGACTACATT TCAGGCTGACA TTATACACT TCAGGCTGAC TTATAGACT TATAGATC TATAGACT TATAGACC TATAGACT TATAGACCA TATAGACAC AACCAAGCAT	GGACACTGA TTTCAGGGTT TTCAGGGTT GTGGANATTA ANAGCAACCA CATAGTTTAG GGATTTTCAG AGTGTTAGT AGTGTTAGT AGTGTTAGT AGACCAGTTG GTAAACCAATT GGAAACCAATT GGAAACAATT AGAAACAATT AGAATTAGAA AAATTTAGAA	ACTACAGACA ATCACAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA CTTGAGGACTTT GGGACAGTA ACTGACAGTA ACTGACAGTA ACTGACTTT AGGATTGT TTGAGGACAAA AGTTCTTAC AGATTCATGA ATACCAGCCT AGATTGCAGCT AGGTTTGCAGT	ACAGAGAAAA AGATTTACA AGACTTACA ATCATTAGAA TGACTACOGT TCACTTAGGAA ATTACCACT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAAAGAT AATGCAACA AGCAGTTCAT TCTTTTACAGTTTACA TCTTTTACCAG TCTAGTTACAG TCAGAGCTTT	300 360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140
55	CTTGTGAAG AAATATCCAA CAAGTAAATG AACACATTCAA GTCAGCGGGG AAATGCAATAA GGAAAAGGGA GAATTCAAAG TTAGATCCAT AATGGCTCAT AATGGCTCAT ACAGTTAGCA TCTGGTTATG TTCTCTAGAC AGTTCAGAA CGGAAGAGC AGTTCAGAA CGGAAGAGC CAGTTGGATGGAT GGTCATTATG TTGCATTATG TTGCATTATG TTGCATTATG TTGCATTATG TTGCATTATG TTGCATTATG	AGATTOGCTO CATGRAPATAG TGAATCATAA TCATAACAG GAGTTTCAGA TGTAATCAGA TGTAATCAGA TGTAATCAGA TCATATGAG TCATATGAG TCATATGAG TCATATGAG TCATACTGAT TGACATCTCC TCTCTGAAAG TCATGCTGAT AGGTGTTTC CAGAAAATGT CTCAGATGGT CAGAAAATGT CAGAATAATTT TGAATAATTATTG GAGAGGACCA TCAATAATTATTG TCTTTATATAGG TCATTATATTTT TC	GTCTATACA GRAACTTARA GRAACTTARA GRAACTTARA TGGGARACA TGGGATCACA TGATCGGAC TTTATCCAT TGGATCGGAC GCACTTCTG TCCCTGCACA GCACTACTTA TCCATTCTG TCCATGCACT TCAGGCTGAC TTATGATACC AACCAAGCAT GCTACACAG GAACATCACAG GCTACCAAA AACAAGCAT AAAATACAGC	GGAGCACTGA TTTCAGGGTT TCTCGTATAA TTTCAGGGTT GTGGAANTTA AAAGCAAGCA CGATTTTCAA TTGTTTGAG AGTGTTAGT CCAAACTCAA GCACAGTTG GAAAGCAATT GAAAACAATT GGAAAGGAAT ATGATTGAG CCAGAGAAT ATGATTGAG ATGAGTTATGA ATGAGTTATGA ATGAGTTATGA ATGAGTTATGA ATGAGTTATGA ATGAGTTATGA ATGAGTTATGA	ACTACAGACA ATCATANANA ATATTGATUA GGGATANANA ATATTGATUA GGGATANANA ATCTCACTAA AGRATAACTIT TTGAGGA GTTTTGAGGA GTTTTGAGGA CTGACAGTA ACTGGATTGT ACTGGATTGT ACTGGATTGT ACTGGATTGT AGTTTTTGAGAA ATTCTTGAGAGCA AGATTTGTAGAGT TTCTGAGAGCA AGATTTGTAGAGT TTCTGAGAGCA TTCTTGAGAT TTCTGAGAGCA TTCTTCAGAT TTGTGAGT TTGTTGAGT TTGTTGAGT TTGTGAGT TTGTTGAGAT TTGTTGAGAT TTGTTGAGAT TTGTTGAGAT TTGTTGAGAT TTGTGAGACAT TTGTGAGACAT	ACAGAGAAAA AGACTTACA ATCATTGGAA TGACTACOGT TCACTOGGAA AGACTACOGT TCACTOGGAA AGAAAATTTG GCAGGTCAAA AGAAAATTTA TTACATTTAAAGAT AATGCAAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA TCTTTTACCAGT TCAAGACTTA AGTACAAC AGTACAAG TCAAGACTTACA AGTACAAG AGAGTTTTTACAGAG TCAAGACTTACAG AGTACAGAG AGTA	300 360 420 480 540 600 720 780 840 900 960 1020 1140 1200 1260 1380
55	CHTGTGAAG AAATATCCAA CAAGTAAATG AACACATTCA TCAGCGGGG AAATGCAATA GGAAAAGGGA GGATTCAAAG TTAGATCAAA TCTGGTTATC TCTCTAGAC AGTTCAGAA TCTCTTCAGAC AGTTCAGAA GGTCATTCGTATT TGGGAAAGAC CAGTTGGATG TGGGAAAGAC AGTTCAGAAC AGTCACTAATG	AGATTOGCTO CATGRAATAG GAATCTTAA TTCATAACAG GAGTTTCAGA TCTACTAGA TCTACTAGA TCTACTAGA TCTACTAGA TCACTAGA TCACTAGA TCACTAGA TCACTAGA TCACTAGA TCATCTGT TCACTAGAAA TCATCTGT TCAGAAAA TCATGAGAAAATTT CCTAGAAAATTT TCATTATATGG TCAATAATTT TCATTATATTG TTAATAGT TTGACTTTT TTGATTATATTG TTGATTATTT	GTCCTATACA GANACTANA GANACTANA TOGGNANACA NATGGTGTTT TGGATCAGAG TTTATCCATT TGGATCAGAG GACCTTCTA TGGATCAGAG CCAGTTAGCAT TCAGTCAGAC CCAGTTAGCT TCAGTCACA CTATACACT TCAGTCTAC CTATACACT CCAGTCACA ACCAAGCAT ANATACAGC CCCTAGATTA	GGAGCACTGA TTCCAGATT TCTCCTATCA TTCCAGGATT ANAGCAGCA CATAGTTTAG CGATTTCAA AGTTTTAG AGTGTTTAGG CCAAACTCAA GACACCAG GACACCAG GACACCAG GACACCAG GACACCAG GACACCAG AGACCAG AGACCAG AGACCAG AGACCAG ATTGTTTTAGG CCAGAGAATT GGAAAGGAAG AATGTTTAGG AATGTTTAGG AATGATTAGG AATGATTAGG AATGATTAGG AATGATTAGG AATGAGACTAG ATTGGAAACGA ATGAGACTAG ATTGGAAACGA	ACTACAGACA ATCANANAN ATTATAGTOM GGGATAANAC ATCTCACTAM AGGATAANC ATCTCACTAM GGGATAANAC ATCTCACTAM AGGATAACTT AAGGACAANA GTTTTGAGGA CTTGACGAAGTA ACTGGATGGT TTGAGGATGAT ACTGGATGGT TTGAGAAGTA AGGATTCTTAC AGGATTCTTAC AGGATTGT ATACCAGCCT AGGATTGCAGA ATACCAGCCT TTGTCAGAT TTGTCAGAT TTGTCAGAT TTGTCAGAT TTGTCAGAT TTGTCAGAT ATACCAGCAT AGGATTGCAGAT ATACTAGAT ATACTAGAT ATACTAGAT ATACTAGAT ATACTAGAT AGGATATATAT AAGANATATAT	ACAGAGAAAA AGAACTTACA ATCATTGGAA AGAACTACAG TCACTGGGA ATTITCACTTG AGCAGTCAAA AGAAAATTTA GCAGCTACA TTACATTAC TTACATTAC ATTITAAAGAT TCATTACAACA ACAGTACAA ACAGTACAA ACAGTACAAG AGCAGTTTOT TCTTGTTACA TCTTGTTACA AGTAGACCAT AGTAGACCAT AGCAGTACTAG CCTACTGAT CCTACTGAT CAAGGAGGAG	300 360 420 480 540 600 720 780 900 900 1020 1140 1200 1260 1320 1320
55	CHTGTGAAG AAATATCCAA AAAGTAAATG AACACATTCA GTCAGCGGGG AAATGCAAT GAGATGCAAT GAGATGCAAT GAGATGCAAT AATGCTCAT ACAGTTAGG TCTCTAGAG TCTCTAGAG TGTCTAGAG TGGGAAGAG CAGTTGGGAT GGGAAGAG AATCCTGAAC ACAGTAGGAAG AATCCTGAAC ACAGTAGGAAG AATCCCTGAAC ACAGTAGAAC AC ACAGTAGAAC ACAGTAGAAC ACAGTAGAAC ACAGTAGAAC ACAGTAGAAC ACAGTA	AGATTOGCTO CONTRACTOR CATORATAGE CAGATTTCAGA TCTACTAGA TCTACTAGA TCTACTGCTT AGTTTAAAAGC CAGATTATAGA TCATACTGCT TGACATCTC TCTCTGAAAG TCATACTGT TCAT	GTCCTATACA GARACTARAA GARACTARAA TGGGARAACA AATGGTGTTT TGGATCAGAG TGATCCGGAC TTTATCCATT TGGAGTCGAA GARCCTTCTA GAGCTGTGCT TCCCTGCACA CCAGTTGGCT TCAGGCTGAC TTATACACT TCAGGCTGAC TATAGACT TATAGACC GCTAGACT GCTACCCAAT AACAAGCCA GCTACCCAAT GCTACCCAAT GCTACCCAAT AAAATACAGC CCCTGAATTA	GGAGCACTGA TCTCCTATCA TCTCCTATCA TCTCCAGGATT ANAGCAAGCA CATAGTTTCAA TGTTTCAA TGTTTTCAA TGTTTTAGTC CCAAACTCAA GACACGATG GCAACTTTTTTTTTT	ACTACAGACA ATCANANAN ATCATAGATA ATATTGATTA AGGATANANA ATATTGATTA AGGATACATT AGGACARA ATTTGAGGA ATTTGAGGA ATTTGAGGA ATTTGAGGA ATTGGACAGA ATTTGAGGA ACTGGATTTT ACTGGATTTT ACTGGATTTT AGTTTTTAGGA AGTTTTTAGAGA ATTACTTGAGAGC AGATTTGAGAT ATTCCAGT TTCTGAGAGC AGTTTTCAGT TTCTGAGAGC AGTTTTCAGT TTCTTCAGAT TTGTTCAGAT TTGTTCAGAT TTGTTCAGAT TTGTTGAGAT TTGTTGAGAT TTGTTGAGAT TTGTTGAGAT TTGTTGAGAT TTGTTGAGAT TTGTTGAGAT TTGTTGAGAT	ACAGAGAANA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACAG TCACTGGGA ATTTCCACTT TCACTGGGGA ATTTCCACTT TTACATAGAT AGAANATTTG GCAGGGTGCT TTACATTACA TTTTAAAGAT AATGCACAA AGCAGTTTGT TCTTGTTACA TCTTGTACCAG TCTTGTACAG TCTTGTACAG TCTTGTACAG TCTTGTACAG TCTTGTACAG TCTTGTTACA TCTTGTTACA TCTTGTTACA TCTTGTTACA TCTTGTTACA TCTTGTTACA TCTTGTTACA TCTTGTTACA TCTTGTTACA TCTTGTTACA TCTTGTTACA TCAGGGAGGAG CAGGGGAGGAG CAGGGGAGGAG CAGGGGAGGAG CAGGGGAGGAG CAGGGGAGGAG CAGGGTTACA	300 360 420 480 540 660 720 780 840 900 1020 1080 11200 1200 1200 1320 1380 1440 1560
55	CTISTIGANG ANATATCCAN ANATATCCAN ANATACATTCAN ANATGCANTA ANATGCANTA ANATGCANTA ANATGCANTA ANATGCAT ANATGCAT ANATGCAT TICTAGAG TITCTAGAG TICTGAGAC TOGGAAGAG CAGTITGGAT GGAGCANTA ATGCCTANT GGACTANTA ANTCCTGANA ANATGCANTACA ANATGCANTACA ANATGCANTACA ANATGCANATCA ANATG	AGATTOGCTO CATGRAATAG GAATCTTAA TCATAACAG GATTTCAGA TCATACTGCT AGTTACAGA TCATACTGCT AGTTACAGA TCATACTGCT TCATCATATGA TCATACTGCT TCATCATGAT TCATCATTTGA TCATCATTTGA TCATCATTTGA TCATCATTGA TCATCATTGA TCATCATGAT TCATCATGAT TCATCATGAT TCATCATGAT TCATCATTGA TCATATATGG TTGATCATTTAATGG TTGATCATTTAATGG TTGATCATTTAATGG GAAAAAGGA AATGAAGGAA AATGAAGGAA AATGAAGGAA AATGAAGGAA ATGAAGGAA ATGAAGAAGAA ATGAAGAA ATGAAAGAA ATGAAAA ATGAAAGAA ATGAAAA ATGAAAGAA ATGAAAA ATGAAAGAA ATGAAAA ATGAAAA ATGAAAAA ATGAAAAA ATGAAAA ATGAAAAA ATGAAAAAA ATGAAAAAA ATGAAAAAAA ATGAAAAAAAA	GTCTATACA GCAAAACAA GAAACTAAAA GAAACTAAAA TGGGAAAACA AATGGTGTTT TGGATCGAGG TGATGCGGAC TTATCCATT TGGACTGAA GAACCTTCTA TCCATTCATT TCCATTCATT TCCATTTACACT TCCATTACACT TCAGGCTTGAC TCATTACACT TCAGGCTTGAC TTATGATACAC GCTACACAA AACCAAGCAT GCTACCAAT AAAATACAGC CCCTGAATTA AGAAGGCGT ACCCCAGATT AGAAGAGCGCT ACCCCAGATT AGAAGACCAAACAAACAAGCAA GCAACCAAGCAT AGAAGAGCGCT ACCCCAGATT AGAAGACCAAACAACAAACAAACAAACAAACAAAATACAGCAA TATGAACAACAAACAAAACA	GGAGCACTGA TCTCCTATCA TCTCCTATCA TCTCCAGGATTA AAAGCAAGCA CATAGTTTAA AAAGCAAGCA CATAGTTTACA TCTGTTTAGATCA AGGTTTAGTC CAAAACTCAA GACACAGTT GGAAACACTA GGAAAGAATA TGAAAGAATA ATGAATTGAA ATGAAGAATA ATGAATTGAA ATGAACTATA ATGAACTAA ATGAACTAAA ATGAACTAAA ATGAACTAAA ATGAACTAAA ATGAACTAAA ATGAACTAAA ATGAACTAAA ATGAACTAA ATGAACTAA ATGAACTAA ATGAACTAA ATGAACTAA ATGAACAACTAA ATGACACAA ATGACAACAA ATGACAACAAA ATGACAACAAA ATGACAACAAA ATGACAACAAA ATGACAACAAAAAAAAAA	ACTACAGACA ATCANANAN ATTATAGATA ATATTGATGA GGGATAANAC ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAA ATCTCACTAC ATTTCACGAA ATTTCACGAA ATTTCACGAA ATTCATTCACAA ATTCACTACCA ATTTTCACGAT ATCTCACGAT ATCTCACTACAA AGGAAATAAT ATCTCACTACAA AGGAAATAAT AGGACAACAA AGGAAATAAT AGGACAACAA AGGAAACTAA AGGAACTAA AGGAAACTAA AGGAACTAA AGGAACTAA AGGAACTAACTAA AGGAACTAA AGGAACTAA AGGAAA	ACAGAGAANA TTGGGGAAAG AGATCTTACA AGATCTTACA ATCATTGGAA TGACTACAG TCACTGGAG ATTTCCACTT TCACTGGGGA ATTTCCACTT TTACATTTAC TTTTANAGAT ANTAGTACAGT ANTAGTACAGT TTTTANAGAT ANTAGTACAGA AGAGTTTGT TCTTGTTACA TCTTGTACAG TCAGGGGGGGC TCAGGGGGGGC AGTGGCTACA CCAGGGGGGGG CCAGGGGGGGG CCAGGGGGGGGG	300 360 420 480 540 660 720 960 1020 1140 1260 1320 1320 1340 1500 1500
55 60 65	CTIGTIGANG AMATATCCAA ANAGTAAATG ANACACATTCA GTCAGGGGAG AMAGCACATTCA GTCAGGGGAG GATTCAAAA GGAATGCAAA AGGATGCAAA AGGATGCAAA ATTCAGAAC ACTTCAGAC ACTTCAGAC ACTTCAGAC ACTTCAGAC ACTTCAGAC ACTTCAGAC ACTTCAGAC ACTTCAGAC ACTTCAGAC AATTCAAAAA AACCAAATCA AACGAAATCA AAGAAATACA AAGAAATACA AAGAAATACA AAGAAAATCA AAGAAATCA AAGAATCA AAGAAATCA AAGAATCA AGATTOGCTO CATGRANGA GARACCTTAA TCATAACA GAGTTTCAGA TCATACACA TCATACACA TCATACACA TCATACACA TCATACACA TCATACACA TCATACACA TCATACTACA TCATACACA A TCATACACA TCATACACACA TCATACACACA TCATACACACA TCATACACACA TCATACACACA TCATACACACA TCATACACACAC	GTCCTATACA GAACTTAAA GAACTTAAA TGGGAAAACA AATGGTGTT TGGATCAGAG TGATGGGGT TGATGGGGT TGATGGGT TGATGGGT TGATGGGT TGATGGGT TGATGGT TCCATGAGAG GAACTTATA TCAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGT TCAGAGT TAGATATAC AACCAAGAT AAAATACAGC CCCTGAATTA AGAAGGGGT GCCCCTGAATTA AGAAGGGGT ACCCCAGATT AGAAGGGT ACCCCAGATT AGAAGGGGT ACCCCAGAT AGAACGAT ACCCCAGATT	GGAGCACTGA TCTCCTATCA TCTCCTATCA TCTCCAGGTT AGAGCAGCA TCTCAGGTT AGAGCAGCA CATAGCTTTA AAAGCAACCA CATAGCTTACA GCACCAGCAG AGACCAGCTG CAAAACCAGTTG CAAACCAGTTG CAACCACCAACCAA TCTGCACCACCAA TCTGCACCACCAA TCCCCCAACCAA TCCCCCAACCAA TCCCCCAACCAA	ACTACAGACA ATCANANAN ATCANANAN ATTATAGTA ATCATTANTO AGGATANAC ATCTCACTA AGGATANAC ATCTCACTA AGGATACAT AGGATAGAC TTGAGGA TTGAGGA TTGAGGA TTGAGAAGTA ACTTCTACA AGATTCATCA ACTATTCATCA AGATTCATCA ATCATTCATCA ATCATTCATCA ATCATTCAT	ACAGAGANAA ACAGAGAAA AGAACTTACA ATCATTGGAA TGACTACAG TCACTGGAG ATTITCOACTT TCACTGGGGA ATTITCOACTT TTACATTAC TTACATTAC TTACATTAC TTACATTAC ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAGAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGGAG ACTACAGAG TACAGAG	300 360 420 480 540 660 720 840 900 1020 1140 1200 1320 1380 1440 1500 1560 1680	
55	CTITTGAME ANATATCCAA CAMSTANATO ANACACATTCA GTCAGCGGGG ANATGCAATA ANAGCATTCA GTCAGCGGGG GTAGCATTCA GTCAGCGGGG GTAGCATTCA ANATGCATTA ANATGCATCA TCTGAGAC TCTGGTTATG TCTCTAGAC TGGGAAGAC TGGGAAGAC TGGGAAGAC TGGAAGAC TGGAAGAC ACGAAGTCA ACGAAGTCA AATCCTGAAC AATCCTGAAC AATCCTGAAC AATCCTGAAC AATCCAAATCA AATCCAAATCA AATCCAAATCA AATCCAAATCA AACGAAATCA AACGAAACA AACGAAATCA AACGAAATCA AACGAAACA AACGAAATCA AACGAAACA AACCAAACA C	AGATTOGCTO CATGRAATAG TGAATATAG TGAATATAGA TGAATATAGA GAGTTTAGA TGTAATAGA TGTAATAGA TGTAATAGA TGTAATAGA TGTAATAGA TGTAATAGA TGAATAGA TTAATAG TTAATAGA TTAATA	GYCCTATROA CCCCAAACAN GAAACTTRAA THOGGAAACA ATOGGAAACA ATOGGAACAC THOGGAACACA THOGGAACACA THOGGACACAC GAACCTTCO GACCACAC GAACCTCO GACCACAC GAACCTTCO GACCACAC CCCGTGACCAC CCCGTGACCAC CCCGACACAC GCTACCACAC CCCGACACAC AACCAACACAC CACACACACACACACACACACACACACA	GGAGCACTOR TITCAGGAGTA TITCAGGAGTA TITCAGGAGTA TAGAGTAGAGTA AAAGCAACA CATAGTTTCAA TITCAGGAGTA AAAGCAACA CATAGTTTCAA TITCAGAGTA AAAGCAACA CATAGTTTCAA TITCTAGAG CATAGTTTCAA TITTTCAAC GACAACATCAA GACACATCAA CATAGTAGAACTCAA TAGAGTATTAG GACACAACAA TAGAGTATAG ATTGGGAACACA TTGCACAACA TCGCCAACAA TCGCCAACAA TCGCCAACAA TCGCCAACAA TCGCCAACAA TCGCCAACAA TCGCCAACAA TCGCCAACAA TCGCCAACAA TCGCCAACAA TCGCCAACAA TCCCCAACAA TCGCCAACAA TCGCCCAACAA TCGCCCCAACAA TCGCCCAACAA TCGCCCAACAA TCGCCCAACAA TCGCCCAACAA TCGCCCCAACAA TCGCCCAACAA TCGCCCAACAA TCGCCCAACAA TCGCCCAACAA TCGCCCCAACAA TCGCCCAACAA TCGCCCAACAA TCGCCCCAACAA TCGCCCCAACAA TCGCCCCAACAA TCGCCCCAACAA TCGCCCCCAACAA TCGCCCCCCAACAA TCGCCCCCCCAACAA TCGCCCCCCCAACAA TCGCCCCCCCCCAACAA TCGCCCCCCCCCC	ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACTACAGACA ACCAGTACA ACCAGCACA CCAGCAC ACCAC ACCACAC ACCAC AC	ACAGAGANAA AGARCTTACA AGARCTTACA AGARCTTACA ATCATTGGA ATCATTGGA TCACTGGAG ATTTCACATT AGCAGTCAAA AGANATTTA GCAGGTGCAT ATTACATTTAC TTTACATTTAC TTTACATTTAC TTTACATTTAC TTTTACAGAT TCATGTTACA ATCATGACA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTA	300 360 420 480 540 660 660 720 780 900 960 1130 1200 1320 1320 1380 1440 1500 1560 1680 1680 1740
55 60 65	CTTGTTGAMG AMATATCCAM CAMGATAATCA AMACCATTCA GTCAGCGGGG AMATGCGAT GGAANGGGGA GGATTCAMG GGATTCAMG GTTAGGTCAT AGGGTCAT AGGGTCAT AGGGTTGAG AGTTCAGAG TTCTGAGAG AGTTCAGAG AGGGTCATTCAG AGGGTCATTCAG AGGGTCATCAG AGGGTCACAG AGGGTCATCAG AGGGTCATCAG AGGGTCATCAG AGGGTCATCAG AGGGTCATCAG AGGGTCACAG AGGTCACAG AGGGTCACAG AGGGTCACAG AGGGTCACAG AGGGTCACAG AGGGTCACAG A	AGATTOGCTO CATOGATAG CATOGATAG CATAGATAG CATAGATAG CATAGATAG CATAGATAGAG CATAGATAGAG CATAGAG C	GYCCTATACA CYCCATATACA GANGTTHAA TIGGRANACA ATGGITOTT TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCGAA TIGGRATCAA TIGGRATCGAA TIGGRATCAA	GGAICACTAN TOTOCIANCA TITCAGGGTT TOTOCIANCA TITCAGGGTT TOTOCIANCA TOTOCIANCA TOTOCIANCA GAIGAGGAAGCA CATAGTTTIAN GAIGAGGAAGCA CATAGTTTAGT CANAACTAA GAICACATTAG GAICACATTAG CANAACTAA GAICACATTAG CANAACTAA TOTOCIANCA TOCOCIANCA TOCOC	ACTACAGACA ATTATANTA GGGATAMAN ATATTATANTA GGGATAMAN ATATTANTA AGGGATAMAN ATATTANTA AGGGATAMAN ATATTANTA AGGGATAMAN ATATTANTA AGGGATAMAN ATATTANTA AGGGATAMAN ATATTANTA ATTATANTA ACAGRANAN TITGGGGNANG TITGGGGNANG AGAITTACA ATCATTGGA TIACTACOT TOACTGGGGA TIACTACOT TOACTGGGGA TIACTACOT TOACTGGGGA AGCACTCAA AGCACTCAA AGCACTCAA AGCACTCAA ACAGTCAA TITGGACCAG TOACAGAG 300 360 420 480 540 660 670 780 960 1080 1140 1260 1380 1440 1560 1560 1680 1740 1860		
55 60 65 70	CTTGTTGAMG ANTATCCAM CAMGATATCA CAMGATATCA CAMGATATCA GRACACATTCA GRACACATTCA GRACACATTCA GRACACATTCA CAMGATACA CAMATACA CAMGATACA CAMATACA CAMGATACA CAMATACA CAMGATACA AGATTOSCIA GAGTITATA TGATCTIA TTGATACAG GAGTITTAA TGATCTIA TTGATACAG GAGTITTAA TGATACAG GAGTITTAA TGATACAG GAGTITTAA TGATACAG TGATACTOT TGACACTCIC TGACACTC TGACACTCIC TGACACTC TG	GYCCTATRCA CCCCAAACAA GAACATTAA TOGGGAAAGA TOGGGAAAGA TOGGGAAGAG TOGAGGGA TOGAGGGA GAACATTAA TOGGGGAGA TOGAGGGA TOGAGGGA TOGAGGA TOGAGGGA TOGA	GGAGCACTAN TOTOCCATACO TOTOCCA	ACTACAGACA ATTACAGACA ATTACACAC ATTACA	ACRAGRAMA TOGGGIAMAG AGACTETA TOGGGIAMAG AGACTETA TOGGCIAMAG TOGACTAGAG TOGACTAGAG ACRACTICA ACCACTICAA ACCACT	300 360 420 480 600 720 780 900 1020 1140 1260 1320 1440 1560 1620 1620 1740 1860 1740 1860 1920	
55 60 65	CTTGTTGABG ANTATICAL ANATATICAL ANATATICAL ANATATICAL ANATATICAL ANATATICAL ANATOMICAL ANATOMICAL ANATOMICAL ACAGITAGON TITTGABAG GATTICARAG ATTICARAG ATTICARAG AGTICARAG AGGARAT AACAGATAT CAGATAT AACAGATAT AACAGATAT AACAGATAT AACAGATAT AACAGAT AGATTOGCTO CATTETATATO TOCHTACAS TOC	GYCCTATRACA CCCCAAACS GAACTTATA TOGGATAGA TOGGATAGA TOGGATCAGA TOGGATCAGA TOGATCAGA TOCAGAGA TOCAGAGA TOCAGAGA TOGATCAGAGA TOCAGAGAA TOCAGAGAA TOCTTAAAT GACTACAGAG TOGATCAGAGA TOCTTAAAT GACTACAGAG TOGATCAGAGAG TOGATCAGAGAG TOGATCAGAGAG TOCAGAGAG TOGATCAGAGAG TOCAGAGAG TOGATCAGAGAG TOCAGAGAG CAGAGAG CAGAGAG CAGAGAG CAGAGAG CAGAGAG CAGAGAG TOCAGAG TOCA	GGAGCACTAN TTOCCACACA TTOCCACACA TTOCCACACA TTOCCACACA TTOCCACACA TTOCCACACA TTOCCACACA TTOCCACACA TTOCCACACA TTOCCACACA TTOCCACACA TRISTITIAN	ACTACAGACA ATTACAGACA A ATTACAGACA ATTACAGACA ATTACAGACA ATTACAGACA ATTACAGACA ATTACAGACA ATTACAGAC	ACRAGRAMA TOGGGIAMA AGNOTIVA TOGGGIAMA AGNOTIVA TOGGGIAMA TOGGGIAMA TOGGGIAMA TOGGGIAMA TOGGGIAMA ATTICACTO TOGGGIAMA ATTICACTO TOGGGIAMA ATTICACTO TOGGGIAMA ATTICACTO TOGGGIAMA ATTICACTO TOGGGIAMA ATTICACTO TOGGGIAMA TOGGIAMA TOGGGIAMA	300 360 420 480 600 720 840 960 1020 1140 1140 11320 11380 1140 11500 11500 11620 11	
55 60 65 70	CTIGTICANG ANTATICAN CAMPANATA CAMPA	AGATTOCICA TO GORGANGO AND TO TO CATOLOGY AND	GYCCTATACA CYCCATATACA CYCCATACA GANACTINA TYGGRANAGC ATTGGATAGA ATTGGATAGA ATTGGATAGA ATTGGATAGA TYGAATTGGAT TYGAATTGGAT GANACCA CAGTTTGGAT CYCATACA TYGAATTGGAT ANAATTCACC CYCATACAT ANAATTCACC ATTGGAT GACTAACCA ATCCTTAAAT GACTTCTCAG ATCCTTAAAT GACTTCTCAG ATCCTTAAAT GACTTCTCAG ATCCTTAAAT GACTTCTCAG ATCCTTAAAT GACTTCTCAG ATCCTTAAAT GACTTCTCAG ATCCTTAAAT GACTTCTCAG ATCCTTAAAT GACTTCTCAG ATCCTTAAAT GACTTCTCAG ATCCTTAAAT GACTTCTCAG ATCCTTAAAT TYCATACAC TYCATACAC TYCATA	GGAGCACTAN TOTOCCATACO TOTOCCA	ACTACAGACA ACTACAGACA ACTACAGACA AGATTAATA AGATTAATAATAA AGGACATAA AGATTAATAA AGGACATAA AGATTAATAA AGGACATAA AGATTAATAA ACTACAA ACTACAA AGATTAATAA ACTACAA AGATTAATAA ACTACAA AGATTAATAA ACTACAA AGATTAATAA ATTACAAACA AGATTAATAA ATTACAAACA AGATTAATAA ATTACAAACAT AGATTAATAA ACTACAACAA ACTACAA ACTACAAA ACTACAAA ACTACAAA ACTACAAA ACTACAA ACTACAAA ACTACAAAA ACTACAAA ACTACAAAAA ACTACAAAAA ACTACAAAAAA ACTACAAAAAAAA	ACAGGANAA TYGGGANAA TYGGGANAA TYGGGANAA TYGGGANAA TYGGGANAA TYGGATAGA TYGGATAGA TYGGATAGA TYGACTAGA TYGACTAGA TYGACTAGA TYGACTAGA TYGACTAGA TYGACTAGA TYGACTTGAA TYGA	300 360 420 480 600 600 720 780 900 1020 1140 1260 1320 140 1560 1560 1560 1680 1740 1860 1860 1980 2040
55 60 65 70	CTIGTICANG ANTATICAN ANATATICAN ANATATICAN ANATATICAN ANATATICAN ANATATICAN ANATATICAN ANATATICAN ANATATICAN GRANAGGA GRANAGGA GRANAGGA GRANAGGA GRANAGGA TIRAGA TITCATAGA ANTICATAGA CHARTICAA ANTICATAGA CHARTICAA ANTICATAGA CHARTICAA ANTICATAGA CHARTICAA ANTICATAGA CHARTICAA CHARTI	AGATTOGCTO CATOGATAN TOGATO TOGATO TOGATOTANA TOGATOTAN	GYCCTATRACA CCCAAAACAA AAATCACAA AAATCACAAA AAATCACAAA AAATCACAA AAATCACAAA AAAA	GGAGCACTAN TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOGOT TOCKOG	ACTACOGACA ACTACOGACA	ACRAGRAMA TOGOGNAMA ATCATTOGAT TOGOGNAMA ATCATTOGAT TOACTAGAT TOACTAGAT ACCATTOGAT TOACATTAGAT TOTTAGAT TOTTAGAT TOTTAGAT TOTTAGAT TOTTAGAT TOTTAGAT TOTTAGAT TOTTAGAT TOACATTAGAT TOAC	300 360 420 480 600 720 840 900 900 1020 1180 1200 1200 1320 1380 1560 1560 1560 1780 1580 1780 1890 1890 199
55 60 65 70 75	CTIGTTGARG ANTATICAS CARGATAGA CARGATAGA ANTATICAS CARGATAGA CARGATAGA ANTATICAS ANTAT	AGATTOGCTO CATTETANAM TOGATCTTAA GATTATOGCTO CATTETANAM TOGATCTTAA TOGATCTTAA TOGATCTTAA TOTAATOGCT CAGATTATCAA TOGATCTTAA	GRICCIATROCA CCCARAICAN ANTOGRITTIAN ANTOGRITTIAN ANTOGRITTIAN ANTOGRITTIAN TOGRICCIAN TOGRICCIAN TOGRICCIAN TOGRICCIAN TOGRICCIAN TOCORRIGORY GRACE GRACE TORROCA TOR	GGAGCACTAN TOTOCCATOR	ACTACAGACA ATTACAGACA ATTACAGACA ATTACAGACA AGATACACACACACACACACACACACACACACACACACAC	ACAGRANAA TYGGGGAMAG ATGATTGGAA ATGATTGGAA ATGATTGGAA ATGATTGGAA ATGATTGGAA ATGATTGGAA ATGATTGGAA TYGATTGGAA TYGATTGGAA ATGATTGGAA ATGATTGGAA AGAAAATTGGAA AGAAAATTGGAA AGAAAATTGA CAGAGGTGAA ACAGATTTAA ACAGATTTAA CAGAGTTTAA ACAGATTTAA CAGAGTTTAA ACAGATTTAA CAGAGTTTAA ACAGATTTAA CAGAGTTTAA ACAGATTTAA ACAGATTTAA ACAGATTTAA ACAGATTTAA ACAGATTTAA ACAGATTTAA ACAGATTTAA ACAGATTTAA ACAGATTAA ACAGATTTAA ACAGATTAA 300 420 480 540 660 720 960 960 1020 1260 1260 1380 1140 1500 1500 1500 1500 1500 1620 1620 1620 1920 1920 1920 1920 1920 1920 1920 19	
55 60 65 70	CTIGTTCHAGA ANTATICCHAG ANTATICHAG	AGATTOGCTO CATTGTANTAG GARATTOGCTO GARATTAGA G	GTCCTATACA GTAGCTTANA GANCTTANA ANAGOTOTT TOGATCANA TOGA	GGAGGACTAR TOTOCCATOGA TOTOCCATOGAC TOTOCCATOGAC CATAGATTAA TOTOCCATOCA CATAGATTAA TOTOCCATOCA GAAGGACA GAAGGACA GAAGGACA GAAGGACA CATAGATTAA CATAGACA CATAGACA TOTOCATOCA GAAGGACA TOTOCATOCA CATAGACA TOTOCATOCA CATAGACA TOTOCATOCA CATAGACA TOTOCATOCA CATAGACA TOTOCATOCA TOTOCATOCA CATAGACA ACTACAGACA	ACCAGAGNAA TOGGGAGAGA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTOGAA ATCATTAC ATTTOGACTAT AAATCAACA AAATCAACA AAATCAACA AAATCAACA CAGAGATTAT CTATATTAC TTTTAACATTTAC TTTTAACATTTAC TTTTTAACATTTAC TTTTTAACATTTAC TTTTTAACATTTAC TCAGAGAGAA CAGAGAGAGAA CAGAGAGAA ATCACACAACAA AAATCACACAA AAATCACAACAA AAATCACAACAA AAATCACAACAA AAATCACAACAA AAATCACAACAA AAATCACAACAAA AAATCACAACAAA AAATCACAACAAA AAAATCACAACAAAAAAAA	300 360 420 480 600 720 840 900 900 1020 1180 1200 1200 1320 1380 1560 1560 1560 1780 1580 1780 1890 1890 199	
55 60 65 70 75	CTIGTTCHAGA ANTATCAM CAMPANATO CAMPA	AGATTOGCTO CONTRIBUTA TOGATCTIAA GOTTICAA	GTCCTATACA CCCAAAACAA ANTOGOTOTT TOGATCAGAA TOTACCAGAA ANTOGOTOTACAA TOTACCAGAA TOTACAGAA TOTACCAGAA TOTA	GGAGGACTERN TOTOCIATION TOTOCI	ACTACHGACA ACTACHGACA	ACMARRAMA TYGGGGMANA TYGGGGMANA TYGGGGMANA TYGGGGMANA TYGGGGMANA TYGGGGMAN TYGGGGMAN TYGGGGMAN TYGGGGMAN TYGGGGMAN TYGGGGMAN TYGGGGMAN TYGGGMAN TYG	300 420 480 540 660 660 780 780 900 1020 1140 11260 11380 1140 1150 1150 1150 1150 1150 1150 115
55 60 65 70 75	CTIGTTORAGE ANTATICANA	AGATTOGCTO CATOTACHAGA GATTICATA GATTACACA GATTICATA GATTACACA GATTICATA GATTACACA CAGATACACA CAGAT	GTCCTATACA CCCAAACAA TOGGAAAACA TOGGAAAACA TOGGAAACAA TOGGAAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA	GRAGICATOR TOTOCCATOR TOTOCCATOR TOTOCCATOR AND TOTOCCATOR GRAGICATOR GRACICATOR GRAGICATOR GRACICATOR GRAGICATOR GRAGICA	ACTACAGACA ACTACAGACA	ACCAGAGANA ACCATAGA ATCATTAGA ATCATT	300 420 480 540 660 720 780 960 960 1080 1020 1080 11200 112
55 60 65 70 75	CTIGTTORAGE ANTATICANA	AGATTOGCTO CATOTACHAGA GATTICATA GATTACACA GATTICATA GATTACACA GATTICATA GATTACACA CAGATACACA CAGAT	GTCCTATACA CCCAAACAA TOGGAAAACA TOGGAAAACA TOGGAAACAA TOGGAAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA TOGGAACAACAA	GRAGICATOR TOTOCCATOR TOTOCCATOR TOTOCCATOR AND TOTOCCATOR GRAGICATOR GRACICATOR GRAGICATOR GRACICATOR GRAGICATOR GRAGICA	ACTACAGACA ACTACAGACA	ACCAGAGANA ACCATAGA ATCATTAGA ATCATT	300, 420, 480, 540, 660, 660, 660, 660, 660, 660, 660, 6
55 60 65 70 75 80	CTIGTTCHAGA ANTATICONA	AGATTOGCTO CATORAPANA GOATTAACAA GOATTACAAA GOATTACAAA GOATTACAAAA GOATTACAAAAA GOATTACAAAAA GOATTACAAAAA GOATTACAAAAAA GOATTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GTCCTATRACA CCCAAACAA TAGGIUTT TGAATCAGA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACA TAGGIAATACAAA TAGGIAATACAA TAGGIAATACAA TAGGIAATACAA T	GRAGICACTOR TOTOCCANACA ANAGCANGO ANAGCANGO CORANTTANA ANAGCANGO CORANTTANA CORANTANA CORANTTANA CO	ACTACAGACA ACTACAGACA	ACCAGEMANA TOTALOGIA ACCATOGIA ACCAT	300 420 480 540 660 660 780 900 1020 1020 1140 1260 1380 1440 1560 1560 1560 1740 1800 1800 1920 2040 2162 2280 2280 2340 2460 2580

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	WO 02	/086443	TOTAL COMPANY	ACTACTCATG	CTCCTTCACA	GACCICTICGAA	2820
	AGCCTTGCTC TTTGGTAGTG	AATCTGGTGT	TCTTTATAAA	ACCCTTATGT	TTTCTCAAGT	TGAACCACCC	2880
							2940
5	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3000 3060
,	CCTAAGTCTT	CUTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	COMOL MOCCO	* * TOTAL CONTROL	ACCORPANT	CATACTCAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACCT	GTTTCTGTAG TCTAAAAGTG	CTGAATTTAC	ATATACAACA TOGANATGAG	3240 3300
10	ACTGARCTGC	GTGATGATAA	TTTCAATGAG	ATGGTTTACC AATGCGTCTT	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
							3480 3540
	GATCATGAGA	CTGGTGACAC	TTCGCTTAAA	AACTTTTCAG CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
15	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA CTACAACCTT GTGCCCAGTG	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAC	TGAAGTATTG	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3720 3780
	GACACCTTGC	TTAAAACTGT	TCTTCCAGCT	TTGCATCTCA	ATCCAATATT	TTCTGCTTCA	3780
	AGTGAAAACA	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
20	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	CCAGTTTTTG ATTTCCTATG	CAAGTGAGAA	ATATGAACCA	3960
							4020 4080
	TTGTTCCAAA	CTGTTTTATC	AATTGATGAA	CAGGCCCATC CCATTAAATA AGTTCTGTTA	CACTAATAAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAAC	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
25	ATTCCAACAG	TTGCTTCTGA	TACATTTGTA	TCTACTGATC CACAGAGATG	ATTCTGTTCC	TATAGGAAAT	4260 4320
							4320
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
	AGAGGTAGTG	ATGGCTTATC	CATTCATAAG	GATGATGATG TGTATGTCAT CACGAAAACA	GCTCATCCTA	TAGAGAATCA	4500
30	CAGGAAAAGG	TAATGAATGA	TTCAGACACC	CACGAAAACA	GTCTTATGGA	TCAGAATAAT	4560 4620
				GAAGAAGATA CCTGGTAAAT			4680
	TOCCARARGO	ACA ATTIATTIC	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
25	COTTOTO AGE	CTGBATCTBA	AGCATGGGCA	GTTCTGACAA	GTGATGAAGA	AAGTGGATCA	4800 4860
35				AATGAGACTT CTGGCAGCAG			4920
	GGATTCCCAC	AGTCCCCAAC	ATCATCTGTT	ACTAGCGAGA GAGTCTCGTA	ACTCAGAAGT	GTTCCACGTT	4980
	TCAGAGGCAG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
40	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT TGCACACTTT TATCTTTCCA TGCAGATTTA CCAGGAAGTG	5100 5160
40	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
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							5340 5400
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-,5							5520
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC CCTCGTGGAG GTACGGGAAC	5580 5640
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	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	5820 5880
	ACACAGTATC	ACTACACGCA	AGCCTATGCC	ANGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5940
	CACTGCAGTG	CTGGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TGTTGTCGTC TATGTTGCAG	6000
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	CTCCTCATTC	CTGGACCAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GCTCCTGAGC	6240
	CACTCAAATA	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGGAAAAG	6300
60	AATCGAACTT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TTGGCATTTC	ATCCCTGAGT GAGCAATGAA	6360 6420
	TTCATCATTA	CCCAGCACCAC	TCTCCTTCAT	ACCATCAAGG	ATTTCTGGAG	GATGATATGG	6480
	GACCATAATG	CCCAACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	GATGATATGG AGAAGATGAA	6540
CE							6600 6660
65	ATGGCTGAAG	CACACAAATG	TCIATCTAAT	GAGGAAAAAA	ACTITICACTO	GGACTITATC TCCTAAATGG	6720
							6780
	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA CGTGGATGTT	6840
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75	GACAGTAACT	TAGGCAGGAA	AGGATTCTGC	CCCAAATTT	ATATCATTAA	CCCATCACCT CAATGTGTGC	7260
,,,							7320
	TATTTCTAAG	AATGGAATTG	TGGTATTTT	TTCTGTATTG	ATTITIAACAG	AUUATTICAA	7380 7440
	CONTRACTOR	TACCABTTAT	CACCTTTCCT	KATATAAADA '	CTTTTAATAC	CAAATTTTTA	7440
80	AAATAAAACA	CTCTTCCATA	. TGATATTCA	CATTTTACAA	CTGCAGTATI	CACCTAAAGT	7560
							7620 7680
	TTTATAATTC	TAGATTTTT	TATTTTACTA	CTGAGTCAAG	ACCAGTT	CTGTGTAATT	7680
85	GAAATACCTI	CATTTTGAA	GAAGTTTTT	TGAGAATAAC	ACCTTACCA	ACATTGTTCA AAAAAAAAAA	7860
	AATGGTTTT	ATCCAAGGAI AAAAAAAAA	TTGCAAAAA	TAAATATAAA	ATTGCCATTA	AAAAAAAA	7920
	ANDOUGH						

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Seq ID NO: 573 Protein sequence:

	Procern Acc	GPPION #1 1	on sequence	•			
5	1	11	21	31	41	51	
-	ī	Ī	i	1	1	1	
	MD TT. YD DT. AC	IQLLCVCRLD	WANGYYROOR	KINERIGWSY	TGALNOKNWG	KKYPTCNSPK	60
	OSPINITIEDI.	TOVNVNLKKL	KPOGWDKTSL	ENTFIHNTCK	TVEINLTNDY	RVSGGVSEMV	120
	PENCETTERN	GKCNMSSDGS	PHST-EGOKED	LEMOTYCPDA	DRESSFEEAV	KGKGKLRALS	180
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	TOVERTURAL	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	COLDGEDOTK	360
	HERITOGYOD	LGAILNNLLP	NMSYVLOIVA	ICTNGLYGKY	SDOLIVDMPT	DNPELDLPPE	420
	t tomppttyp	BEEGKDIEEG	ATUMPORNSA	TNOTEKKEPO	ISTITHYNRI	GTKYNEAKTN	480
15	PEDTROPERS	GKGDVPNTSL	NSTSOPVTKL	ATEKDISLTS	OTVTELPPHT	VEGTSASLND	540
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	ENTROCYTES	SENPETITYD	VI.TDESARNA	SEDSTESSES	RSLKDPSMEG	NVWFPSSTDI	660
	TAOPHVGGGP	ESPLOTNYTE	TRYDESEKTT	KSPSAGPVMS	OGPSVTDLEM	PHYSTFAYFP	720
	TELEFOURTE	SSROODLVST	WWW.	PVYNGETPLO	PSYSSEVEPL	VTPLLLDNOI	780
20	LAPTPRACES	DSALHATPVF	PSVDVSFEST	LSSYDGAPLE	PESSASESSE	LFRHLHTVSO	840
	TI DOUTGATE	SDKVPLHASL	BATCHOLDER	PSCAOYSDVL	STTHAASETL	REGSESGVLY	900
	ALL MAGUAGE	PSSDAMMHAR	SSCREPSYAL	SUNECCORIE	TVSYSSAIPV	HDSVGVTYOG	960
	ST.PECDENTD	IPKSSLITPT	ASLIOPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
	DUCUS PROVE	TSVFGDDNKA	LONGET TYCK	RTELOIPSEN	RMVYPSESTV	MPNMYDNVNK	1080
25	IMACIOPTOU	SISSTKGMPP	GSLAHTTTKV	EDHETSOVER	NNFSVOPTHT	VSOASGDTSL	1140
20	ADAL GYREED	ASSDPASSEM	LSPSTOLLEY	RTSASESTEV	LLOPSFOASD	VDTLLKTVLP	1200
	AVDSDDTIVE	TPKVDKISST	MI-HI-TVSNSA	SSENMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
	TTOVACRYVE	PVLLKSESSH	OVVDST.VSND	RIPOTANIET	NOAHPPKGRH	VFATPVLSID	1320
	PDIAPITANTA	IHSDEILTST	KGGVTGKVPA	GIPTVASDTP	VSTDHSVPIG	NGHVAITAVS	1380
30	PHPDGSVTST	KLLPPSKATS	RESHSAKSDA	GLYGGGEDGD	TDDDGDDDDD	DRGSDGLSIH	1440
	KCMSCSSVRR	SOEKVINNDSD	THENSLADON	NPISYSLSEN	SEEDNRVTSV	SSDSQTGMDR	1500
	SDCKSDSVNG	LECKHNDGKE	ENDIOTGSAL	LPI-SPESKAW	AVLTSDEESG	SCOCTSDSLN	1560
	ENETSTDESE	ADTNEKDADG	ILAAGDSEIT	PGFPOSPTSS	VTSENSEVFH	VSEABASNSS	1620
	HESPIGLARG	LESEKKAVIP	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	PYLEDSTSPR	1680
35	VISTPPTPIF	PISDDVGAIP	IKHPPKHVAD	LHASSGPTEE	PETLKEPYQE	VQSCTVDLGI	1740
	TADSSNHPON	KHKNRYINIV	AYDHSRVKLA	OLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	OGPLKSTAED	FWRMIWEHNV	EVIVMITALV	EKGRRKCDQY	WPADGSEEYG	NFLVTQKSVQ	1860
	VLAYYTVRNF	TLRNTKIKKG	SOKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFVRKAAY	1920
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40	OYVFIHDTLV	BAILSKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIQQSDY	2040
	SAALKOCNRE	KNRTSSIIPV	ERSRVGISSL	SGEGTDYINA	SYIMGYYQSN	RFIITOHPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDGQNMAED	EFVYWPNKDE	PINCESFKVT	LMAEEHKCLS	2160
	NEEKLI IQDF	ILEATODDYV	LEVRHFQCPK	WPWPDSPISK	TPELISVIKE	EAANRDGPMI	2220
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45	SLVSTRQBEN	PSTSLDSNGA	ALPDGNIARS	LESLV			
		574 DNA se					
		id Accessio		drence			
50	Coding seq	uence: 148-	4518				

CACACATACG CACGCACGAT CTCACTTCGA TCTATACACT GGAGGATTAA AACAAACAAA CARAMARAC ATTICCTICG CICCOCTIC CICTICACTIC TRAGMAGGA AGGAGCGGC CGGCGAGGG CCGCAGACC TCTGGAAATG CGATCCTAA AGCGTTTCCT CGCTTGCATT COSCIAGOSO COCCAGACO TOTOGAMATO CUANTOCTA AGUTTTCCT COCTTOCATT AGGOTOCTO GOTTOCOCAT CAGGOTOCTO GOTTOTOCOCAT CAGGOTOCTO GOTTOTOCOCAT CAGGOTOCTO GOTTOTOCOCAT CAGGOTOCTOCATO GOTTOTOCA CAGGOTOCTOCATOCA CAGGOTOCATO ATCAMANA TIGOGAMAO ANATOCCA CATOTATAGO CACAAAACA TOTOCATCA ATATTGATA AGANTOTACA CAGGOTA AGANTATA CATOTATAGO CAGGOTOCACA CAGGOTOCA CAGGOTOCACA CA GRANANGGIA NOTTANGING TTATCCATT TROTTGRIG TIGGGECHA AGMANTTO GATTCOANG CATTATCAT CONTACTOR TO TROTTGRIG TIGGGECHA AGMANTTO CATTCOANG CONTACTOR CON CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTTGA CAGATGGCTA TCAAGACTTG
GGTGCTATTC TCAATAATTT GCTACCCAAT ATGGGTTATG TTCTTCAAAT AGTAGCCATA
TGCACTAATG GCTATTATGG AAAATCAGC GACCAACTGA TTGTCGACCAT GCCTACTGAT AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAACTG AAGAAATAAT CAAGGAGGAG GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA чининаями минисаттая манисастая аттегбалис сторгалага составля составля доставля общей в предуставля общей AACTIGICGG GGACIGCAGA ATCCTTAAAT ACAGTTICTA TAACAGAATA TGAGGAGGAG AGTITATIGA CCAGITICAA GCTIGATACI GGAGCIGAAG ATTCITCAGG CTCCAGICCC GCAACTTCTG CTATCCCATT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCCTCC GAARACCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC GAAGATCAA CTTCATCAGG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT

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•	GTATACAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTTTTTATTCCC	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	2520
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	TTTTACTTAG	ACCACACTAC	ATCCCCTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
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15	CAGCTTGCTG	CAAAAGCTTA	COURCIGACI	CATTATATOR	TORRATCORC	ACCTGRAGAT	3000
13	TACAACAGAC	TGATATGGGA	TATTGCTGCC	CHAGGECEAE	TGAMATCCAC	ABACCTCCTC	3060
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20	GTCACACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3360
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTTGTC	3420
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25	GAGGCCATAC	TTAGTAAAGA	AACTGAGGTG	CTGGACAGTC	ATATTCATGC	CTATGTTAAT	
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	 AGCCAGTCAA 	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	
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	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
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35	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTITICAAC	TTATAAGTGT	TATAAAAGAA	4200
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	CTCTTCCTAA	AATTAGGCAG	GAAAATCAGT	CTAGTTCTGT	TATCTGTTGA	TTTCCCATCA	4620
	CCTGACAGTA	ACTITICATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGTG	4680
	TOCCUTTUTO	CAAGACTTGT	AATTTACTTA	TTATGTTTGA	ACTARARTGA	TTGAATTTTA	4740
45	CACTATTTCT	AAGAATGGAA	TTGTGGTATT	TITTTCTGTA	TTGATTTTAA	CAGAAAATTT	4800
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	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TOTALATAR	ACACTETTEC	ATATCATATT	CAACATTTTA	CAACTGCAGT	ATTCACCTAA	4980
	ACTACRAATA	ATCTOTTACT	TATTTTTAAAT	ACTOCCCTAG	TGTCTCCATG	GACCARATTT	5040
50	ATATTATA	TTGTAGATTT	TTATATTTTA	CTACTGAGTC	AAGTTTTCTA	GTTCTGTGTA	5100
20	A THEFT THE CT	TTAATTAATT	AGTTCATTAG	CTGGTCTTAC	TCTACCAGTT	TTCTGACATT	5160
	ULL GITTING	ACCTANGTON	TTAACTTTGT	TTCAGCATGT	AATTTTAACT	TTTGTGGAAA	5220
	ATAGRATAC	CTTCATTTTC	ARAGARGTTI	TTATGAGAAT	AACACCTTAC	CAAACATTGT	5280
	TONNATION	TTTATCCARC	GAATTGCAAA	AATAAATATA	AATATTGCCA	AAAAAAAT	5340
55		AAAAAAAAA					
23	~~~~		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,				

Seq ID NO: 575 Protein sequence:

60	Protein Ac	cession #: 1	sos sequence	3			
••	1	11	21	31	41	51	
	1	1	1	1	1	-	60
	MRILKRFLAC	IQLLCVCRLD	WANGYYROOR	KTABBIGMAA	TGALINGKNWG	KKYPICNSPK	120
	QSPINIDEDL	TOVNVNLKKL	KFQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	
65	PKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEEAV	KGKGKLRALS	180
	ILPEVGTEEN	LOPKATIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFK	DIVSISESOL	AVPCEVLTMQ	QSGYVMLMDY	LONNPREQQY	KFSRQVFSSY	300
	TOKRETHEAV	CSSRPENVOA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	REFLITOGYOD	LGATLMNLLP	NMSYVLOIVA	ICTNOLYCKY	SDQLIVDMPT	DNPELDLPPB	420
70	LIGTERIIKE	ERRGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	DEPTROSERS	GEODVENTSL	NSTSOPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSPKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENTROCYTES	SENDETITYD	VI. I PESARNA	SEDSTSSGSE	RSLKDPSMEG	NVWFPSSTDI	66
	TACODUCAGO	ESFLOTNYTE	TRUDESEKTT	KSPSAGPVMS	OGPSVTDLEM	PHYSTPAYER	720
75	TENTOHAPTO	SSROODLVST	VNVVYSOTTO	PVYNAEASNS	SHESRIGLAR	GLESEKKAVI	786
	DIVITURALTO	ICLVVLVGIL	TVWPKCEOTA	HEYLEDSTSP	RVISTPPTPI	PPISDDVGAI	84
	DIRREDKKAY	DLHASSGFTE	EPETI-KEPYO	EVOSCTVDLG	ITADSSNHPD	NKHKNRYINI	90
	WAYDUODUVI.	AQLAEKDGKL	TOVINANYVO	GYNRPKAYIA	AOGPLKSTAE	DEWRMINEHN	96
	WALDINGTON.	VEKGRRKCDQ	VWDAINIGEEV	CHELVIORSY	OVLAYYTVRN	PTLRNTKIKK	102
80	APATANTINA	VVTQYHYTQW	DUMENDEANS!	PVI/TPVRKAA	YAKRHAVGPV	VVHCSAGVGR	108
00	MODERATE DON	LOGIQHECTV	MY POPT WHITE	SORMYLVOTE	ROYVET HOTE.	VRAILSKETE	1140
	TOT I TANDOM	NALLIPGPAG	WALL BROKUT	LECCRITOCSD	VSAALKOONR	RENRISSIIP	120
	VIDSRIBATO	LSGEGTDYIN	* CALMONALA	NEDT IMPEL	LHTTKDEWPM	TWINDAMAGEUV	126
	VERSEVGISS	DEFVYWPNKD	NOTIFICATION.	TI ME DEUVCI.	SMEDKI.TION	PILEATODDY	132
85	MIPDGQNMAB	KWPNPDSPIS	BETMCESEVA	TOTAL SANDOCTIA	TUNDENCCUM	ACTUCAL TITL	138
0.0	APEAKHEGGS	DVYQVAKNIN	KTPELISVIK	BOYON YEAR	T.OT.VOTDODD	MOTPUMPENG	144
			THICKGARADI	PATABLICAT	adyni Cruon	ME O LODDONG	
	AALPDGNIAE	SPER					

Seq ID NO: 576 DNA sequence Nucleic Acid Accession #: EOS sequence Coding sequence: 148-4494

5	Coding sequ	ience: 148-4	494				
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	CRARRARAC	ATTTCCTTCG	CTCCCCCCCCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
10	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCATT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240 300
	CTTGTTGAAG	AGATTGGCTG CATGTAATAG	GTCCTATACA	GUAGCACTGA	ATCAUUUUAA	1 TOGGGRAAG	360
	AAATATCCAA	CATGIANTAG	CARACTTARA	TTTCACCCTT	CCCATABAAC	ATCATTGGAA	420
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13							540
							600
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20	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840 900
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTIG	ACTOGRATIGE	BATGCAACAA	960
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25							1080
23							1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TITIGIACCAG	1200
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20	GGTGCTATTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320 1380
30	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TIGICGACAT	CARCIDAT	1440
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTOTICATO	CTGGTAGAGA	CARGGREGA	1500
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	TOTACCACAA	CACACTACAA	CAGTGCTACA TCGCATAGGG	1560
	ACCADOTICA	ATTENDED	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA TAAATTAGCC TCACACTGTG TCCACACTATG TGAGGAGGAG	1620
35	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
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40	GCAACTTCTG	CTATCCCATT	ATTOTOTICAG	CTTATACCAG	AATCTCCTAG	ATTTTCCTCC AAATGCTTCC GGAGGGAAAT	2040
	CARGATTCAR	CTTCATCAGG	TTCAGAAGAA	TCACTARAGG	ATCCTTCTAT	GGAGGGAAAT	2100
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	ACCTITCTCC	AGACTAATTA	CACTGAGATA	CGTGTTGATG	AATCTGAGAA	GACAACCAAG	2220
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	CATTATTCTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
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	GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	CACCCCCCAC	TGAGGGGTTG TTTTATCTGT TGCACACTTT	2520
50	GAATCCGAGA	AGAAGGCAGT	TOTCATCTAC	TOTALCOAST	GCTTCCAGAC	TGCACACTTT	2580
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	GCTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	ACAAGAATCG	TGCAGATTTA TGTTGACTTA ATACATAAAT	2820 2880
55	ATOGTTGCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	TIGCIGAAAA	GGATGGCAAA	2940
	CTGACTGATI	ATATCAATGC	CAATTATGTT	GATGGCTACA	CCACAACCAAA	AGCTTATATT	3000
	GCTGCCCAAG	GCCCACTGAA	CATAACAAGCI	CTCCTCCACA	AMORAGOAG	ATGGGAACAT AAAATGTGAT	3060
							3120
60							3180
••	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGGA	CGTGTGGTCA	CACAGTATCA	CTACACGCAG	3240
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	GCCTATGCCA	AGCGCCATGC	AGTGGGGCCT	GTTGTCGTCC	ACTGCAGTGC	TGGAGTTGGA	3360 3420
65							3480
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	CAGGTGCTGC	ACACTCATAT	TCATGCCTAT	GTTAATGCAC	TCCTCATTCC	TGGACCAGCA	3600
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	GACTATTCTC	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAGA	ATCGAACTTC	TTCTATCATC AGACTACATC CCAGCACCCT	3720
70	CCTGTGGAAA	GATCAAGGGT	TGGCATTTCA	TCCCTGAGTG	GAGAAGGCAC	AGACTACATC	3780
	AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	TCATCATTAC	CCAGCACCCT	3840 3900
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	GTTATGATTC	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	MACCONCLACIO	GCCAAATAA ACACAAATGT ACAGGATGAT TAGCCCCATT	4020
75	GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	CACTUTIO	TAGENGOTAC	ACACCATICAT	4080
13	CTATCTAATC	ASGROUNCE	CTTTCAGTGT	CCTABATGG	CAAATCCAGA	TAGCCCCATT	4140
	AGTAAAACTT	TTGAACTTAT	AAGTGTTATA	AAAGAAGAAG	CTGCCAATAG	GGATGGGCCT	4200
	ATGATTGTT	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGA	CTTTCTGTGC	TCTGACAACC	4260
	CTTATGCAC	AACTAGAAAA	AGAAAATTCC	GTGGATGTTT	ACCAGGTAGG	TCTGACAACC CAAGATGATC CTACAAAGTG	4320
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	GGTGCAGCAT	TGCCTGATGG	AAATATAGCT	GAGAGCTTAG	AGTCTTTAGT	TTAACACAGA AGGCAGGAAA	4560
	AAGGGGTGG	GGACTCACA	TCTGAGCATT	CCATCACCO	LOCIMMATI	TCATGACATA	4620
85	ATCAGTCTAC	COCALITATO	TATCATTAAC	AATGTGTGT	TTTTTGCAAC	TCATGACATA ACTTGTAATT	4680
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Seq ID NO: 577 Protein sequence: Protein Accession 8: EOS sequence

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		MRILKRPLAC	IQLLCVCRLD	WANGYYROOR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
		OSPINIDEDL	TOVNVNLKKL	KFOGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
		PKASKITPHW	GKCNMSSDGS	EHSLEGOKFP	LEMOIYCFDA	DRFSSFEEAV	KGKGKLRALS	180
- 2	20		LDFKAIIDGV					240
		TOTVOWIVEK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LONNFREQQY	KFSRQVFSSY	300
		TCKEEIHEAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKPAVLY	QQLDGEDQTK	360
		HEFLTDGYOD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLFPE	420
		LIGTEELIKE	REEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
- 2	25	RSPTRGSBFS	GKGDVPNTSL	NSTSOPVTKL	ATEKDISLTS	OTVTELPPHT	VEGTSASLND	540
		GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSPKLD	TGAEDSSGSS	PATSAIPFIS	600
			SENPETITYD					660
		TAQPDVGSGR	ESFLOTNYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTPAYFP	720
			SSRQQDLVST					780
	30		CLVVLVGILI					840
			LHASSGFTEE					900
			KLTDYIMANY					960
		NLVEKGRRKC	DOYWPADGSE	EYGNPLVTQK	SVQVLAYYTV	RNFTLRNTKI	KKGSQKGRPS	1020
			QWPDMGVPEY					1080
	35		TVNIPGPLKH					1140
			AGKTKLEKQF					1200
		SSLSGEGTDY	INASYIMGYY	QSNEFIITQH	PLLHTIEDSW	RMIWDHNAQL	VVMI PDGQNM	1260
			KDEPINCESF					1320
	40		ISKTPELISV					1380
4	40	SVDVYQVARM AESLESLV	INLMRPGVFA	DIEGAĞAPAK	VILSLVSTRQ	EEMPSTSLDS	NGAALPDGNI	1440

Seq ID NO: 578 DNA sequence Nucleic Acid Accession #: EOS sequence Coding sequence: 501-4514

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	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCATT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAT	TGGGGAAAGA	300
55		ATGTAATAGC					360
		GAATCTTAAG					420
		TCATAACACT					480
		AGTTTCAGAA					540
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		GATTATTGAT					780
		CATACTGTTG					840
		GACATCTCCT					900
65		CTCTGAAAGC					960
		CATGCTGATG					1020
		GGTGTTTTCC					1080
		AGAAAATGTT					1140
70		TCGAGTCGTT					1200
70		AGAGGACCAA					1260
		CARTARTTTG					1320
		CTTATATGGA					1380
		TGATCTTTTC					1440
		AGACATTGAA					1500
75		GAAAAAGGAA					1560
		TGAAGCCAAG					1620
	AGGGTGATGT	TCCCAATACA	TCTTTAAATT	CCACTTCCCA	ACCAGTCACT	AAATTAGCCA	1680
	CAGAAAAAGA	TATTTCCTTG	ACTTCTCAGA	CTGTGACTGA	ACTGCCACCT	CACACTGTGG	1740
00	AAGGTACTTC	AGCCTCTTTA	AATGATGGCT	CTAAAACTGT	TCTTAGATCT	CCACATATGA	1800
80	ACTTGTCGGG	GACTGCAGAA	TCCTTAAATA	CAGTTTCTAT	AACAGAATAT	GAGGAGGAGA	1860
	GTTTATTGAC	CAGTTTCAAG	CTTGATACTG	GAGCTGAAGA	TTCTTCAGGC	TCCAGTCCCG	1920
		TATCCCATTC					1980
	AAAACCCAGA	GACAATAACA	TATGATGTCC	TTATACCAGA	ATCTGCTAGA	AATGCTTCCG	2040
0.5		TTCATCAGGT					2100
85	TGTGGTTTCC	TAGCTCTACA	GACATAACAG	CACAGCCCGA	TGTTGGATCA	GGCAGAGAGA	2160
		GACTAATTAC					2220
	CCTTTTCTGC	AGGCCCAGTG	ATGTCACAGG	GTCCCTCAGT	TACAGATCTG	GAAATGCCAC	2280

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	ATTATTCTAC	CTTTGCCTAC	TTCCCAACTG	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340
	CCAGACAACA	GGATTTGGTC	TCCACGGTCA	ACCTGGTATA	CTCGCAGACA	ACCCAACCGG	2400
	TATACAATGA	GGCCAGTAAT	AGTAGCCATG	AGTCTCGTAT	TGGTCTAGCT	GAGGGGTTGG	2460
	AATCCGAGAA	GAAGGCAGTT	ATACCCCTTG	TGATCGTGTC	AGCCCTGACT	TTTATCTGTC	2520
5	TAGTGGTTCT	TGTGGGTATT	CTCATCTACT	GGAGGAAATG	CTTCCAGACT	GCACACTTTT	2580
-	ACTTAGAGGA	CAGTACATCC	CCTAGAGTTA	TATCCACACC	TCCAACACCT	ATCTTTCCAA	2640
	TTTCAGATCA	TOTOGRAGOA	ATTCCAATAA	AGCACTTTCC	AAAGCATGTT	GCAGATTTAC	2700
	ATGCAAGTAG	TGGGTTTACT	GAAGAATTTG	AGACACTGAA	AGAGTTTTAC	CAGGAAGTGC	2760
	AGAGCTGTAC	TOTTGACTTA	GGTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	2820
10	ACARGAATCG	ATACATAAAT	ATCGTTGCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880
	TTCCTCAAAA	GGATGGCAAA	CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	2940
	ACAGACCAAA	ACCTTATATT	GCTGCCCAAG	GCCCACTGAA	ATCCACAGCT	GAAGATTTCT	3000
	CCACAATCAT	ATGGGAACAT	AATGTGGAAG	TTATTGTCAT	GATAACAAAC	CTCGTGGAGA	3060
	DADDAADDAA	ABBATCTCAT	CAGTACTOGC	CTGCCGATGG	GAGTGAGGAG	TACGGGAACT	3120
15	TTCTCCTCAC	TCAGAAGAGT	CTCCAACTCC	TTGCCTATTA	TACTOTGAGG	AATTTTACTC	3180
1.5	TANGABACAC	AAAATAAAA	AAGGGCTCCC	AGARAGGAAG	ACCCAGTGGA	CGTGTGGTCA	3240
	CACACTATCA	CTACACGCAG	TOGCCTGACA	TOGGAGTACC	AGAGTACTCC	CTGCCAGTGC	3300
	TOLOGITATOR	GAGAAAGGCA	GCCTATGCCA	AGCGCCATGC	AGTGGGGCCT	GTTGTCGTCC	3360
	POWCCPOACC	TGGAGTTGGA	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	3420
20	ACATTCAACA	CGAAGGAACT	GTCAACATAT	TTGGCTTCTT	AAAACACATC	CGTTCACAAA	3480
20	CAAATTATT	GGTACAAACT	CAGGAGCAAT	ATGTCTTCAT	TCATGATACA	CTGGTTGAGG	3540
	CONTROTTAG	TAAAGAAACT	GAGGTGCTGG	ACAGTCATAT	TCATGCCTAT	GTTAATGCAC	3600
	TOTTCATTO	TGGACCAGCA	GGCAAAACAA	AGCTAGAGAA	ACAATTCCAG	CTCCTGAGCC	3660
	ACTCA AATAT	ACAGCAGAGT	CACTATTCTG	CAGCCCTARA	GCAATGCAAC	AGGGAAAAGA	3720
25	ATOGRACITO	TTCTATCATC	CTGTGGAAA	GATCAAGGGT	TGGCATTTCA	TCCCTGAGTG	3780
	GAGAAGGCAC	AGACTACATC	AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	3840
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	ACCATANTIC	CCAACTGGTG	GTTATGATTC	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	3960
	TECTTER	GCCAAATAAA	GATGAGCCTA	TARATTGTGA	GAGCTTTAAG	GTCACTCTTA	4020
30	TOCOTORANCA	ACACAAATGT	CTATCTAATG	AGGARARACT	TATAATTCAG	GACTTTATCT	4080
50	TAGAAGCTAC	TARRADRADA	TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	4140
	CARATOTAGA	TAGCCCCATT	AGTAAAACTT	TTGAACTTAT	AAGTGTTATA	AAAGAAGAAG	4200
	CTGCCAATAG	GGATGGGCCT	ATGATTGTTC	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGAA	4260
	CTTTCTCTCC	TCTGACAACC	CTTATGCACC	AACTAGAAAA	AGAAAATTCC	GTGGATGTTT	4320
35	ACCAGGGAGG	CAAGATGATC	AATCTCATCA	GGCCAGGAGT	CTTTGCTGAC	ATTGAGCAGT	4380
23	ATCACTTTCT	CTACAAAGTG	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAATCCAT	4440
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	ACTUTTACT	TTAACACAGA	AAGGGGTGGG	GGGACTCACA	TCTGAGCATT	CTTTTCCTCT	4560
	TOTALANTT	AGCCAGGAAA	ATCACTCTAG	TTCTGTTATC	TGTTGATTTC	CCATCACCTG	4620
40	ACACTAACTT	TCATGACATA	GGATTCTGCC	GCCAAATTTA	TATCATTAAC	AATGTGTGCC	4680
	THE PROPERTY OF A PARTY OF THE	ACTIVITABIT	TACTTATTAT	GTTTGAACTA	AAATGATTGA	ATTTTACAGT	4740
	ATTTCTABGA	ATGGAATTGT	CCTATTTTTT	TCTGTATTGA	TTTTAACAGA	AAATTTCAAT	4800
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	CTGTATTTGT	AGCAATTATC	AGGTTTGCTA	GAAATATAAC	TTTTAATACA	GTAGCCTGTA	4920
45	BRITABBACAC	TCTTCCATAT	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	4980
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50	AAATACCTTC	ATTTTGAAAG	AAGTTTTTAT	GAGAATAACA	CCTTACCAAA	CATTGTTCAA	5280
	ATGGTTTTTA	TCCAAGGAAT	TGCAAAAATA	AATATAAATA	TTGCCATTAA	AAAAAAAAA	5340
	AAAAAAAAA	AAAAAAAAA	AAA				

Seq ID NO: 579 Protein sequence: Protein Accession #: EOS sequence

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60	LSTLEEVOTE	BNLDFKALID	GVESVSRFGK	OAALDPFILL	NLLPNSTDKY	YIYNGSLTSP	120
•••	PCTDTVDWIV	FKDTVSISES	OLAVFCEVLT	MOOSGYVNLM	DYLONNPREQ	QYKPSRQVFS	180
	SALCKERTHE	AVCSSEPENV	OADPENYTSL	LVTWERPRVV	YDTMIEKFAV	LYQQLDGEDQ	240
	TERRELITORY	ODLGATIANL	LPNMSYVLOI	VAICTNGLYG	KYSDQLIVDM	PTDNPELDLP	300
	PELICTERII	KEEEEGKDIE	EGAIVNPGRD	SATNOIRKKE	POISTTTHYN	RIGTKYNEAK	360
65	THREPTRESE	PSCKGOVPNT	SLNSTSOPVT	KLATEKDISL	TSQTVTELPP	HTVEGTSASL	420
	NDGSKTVLRS	PHMNLSGTAE	SLATVSITEY	EEESLLTSFK	LDTGAEDSSG	SSPATSAIPF	480
	ISENISOGYI	FSSENPETIT	YDVLIPESAR	NASEDSTSSG	SEESLKDPSM	EGNVWFPSST	540
	DITAOPDUGS	GRESPLOTNY	TEIRVDESEK	TTKSFSAGPV	MSQGPSVTDL	EMPHYSTFAY	600
	PPTRUTPHAP	TPSSROODLY	STVNVVYSOT	TOPVYNEASN	SSHESRIGLA	EGLESEKKAV	660
70	IPLVIVSALT	FICLVVLVGI	LIYWRKCFOT	AHFYLEDSTS	PRVISTPPTP	IFPISDDVGA	720
	TPTKHPPKHV	ADLHASSGFT	REPRILKERY	OEVOSCTVDL	GITADSSNHP	DNKHKNRYIN	780
	IVAYDHSRVK	LAOLAEKDGK	LTDYINANYV	DGYNRPKAYI	AAQGPLKSTA	EDFWRMIWEH	840
	NVEVIVMITN	T.VEKGRRKCD	OYWPADGSEE	YGNPLVTOKS	VQVLAYYTVR	NFTLRNTKIK	900
	KGSOKGRPSG	RVVTOYHYTO	WPDMGVPEYS	LPVLTFVRKA	AYAKRHAVGP	VVVHCSAGVG	960
75	PTGTYTULDS	MICOTOHEGT	VNIFGFLKHI	RSORNYLVOT	EECYVFIRDT	LVEAILSKET	1020
	RVLDSHIHAY	VNALL IPGPA	GKTKLEKOPO	LLSQSNIQQS	DYSAALKQCN	REKNRTSSII	1080
	PVERSRVGTS	SLSGEGTDYI	NASYIMGYYO	SNEFILTOHP	LLHTIKDFWR	MIWDHNAQLV	1140
	VMI PDGONMA	EDEFVYWPNK	DEPINCESFK	VTLMAEERKC	LSNEEKLIIQ	DFILEATODD	1200
	YVLEVEHEOC	PKWPNPDSPI	SKTFELISVI	KEEAANRDGP	MIVHDERGGV	TAGTFCALTT	1260
80	LMHOLEKENS	VDVYQVARMI	NLMRPGVFAD	IEQYQFLYKV	ILSLVSTRQE	ENPSTSLDSN	1320
- •	GAALPDONIA						

Seq ID NO: 580 DNA sequence Nucleic Acid Accession #: EOS sequence Coding sequence: 148-4632

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	CAAAAAAAAC CGGCGAGGGG	ATTTCCTTCG	CICCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
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5	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA TTOGGGAAAA ATCATTGGAA ATCATTGGAA TGACTACOGT TCACTGGGGA ATTTCCACTT	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAA	TTGGGGAAAG	300
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	CAAGTAAATG	TGAATCITAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
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	TCTCCTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	ACCTOTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
20	ACTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
	TOCCANAGAC	CTCGAGTCGT	TTATCATACC	ATCATTCACA	AGTTTGCAGT	TTTGTACCAG	1200
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25	10CACIAA10	OCT INTALOG	CCCTCAATTA	ATTOCARCE	AACAAATAAT	CAACGAGGAG	1440
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	GAAGAGGGAA	COLLABORE	ACCOMMODICATE	TOTACCACAA	CACACTACAA	TOGOTATAGGG	1560
	AACCAAATCA	GGAAAAAGGA	CACCOCAGATT	TOTALCOACOA	CACACTACAA	ATTOTOTOGA	1620
	ACGAAATACA	ATGAAGCCAA	GACTAACCOA	TOCCOMON	PACCACTOR	TATATEMOOR	1680
30	AAGGGTGATG	TTCCCCAATAC	CROTTERANT	ICCACT ICCC	AACCAGICAC	TCACACTOTO	1740
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	GAAGGTACTT	CAGCCTCTTT	MOCTONIGGE	ACACHETCEA	TARCAGARA	TGAGGAGGAG	1860
	AACTTGTCGG	GGACTGCAGA	AICCIIAAAI	CCACCOCCA	PATCHECK CO	CTCCAGTCCC	1920
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35	GCAACTTCTG	CTATCCCATT	GCTTGATACT CATCTCTGAG ATATGATGTC	AMCATATCCC	AAGGGIAIAI	ANATOCTTCC	2040
33	GAAAACCCAG	AGACAATAAC	ATATGATGIC	CITATACCAG	MATCIGCIAG	CCACCCCAAAG	2100
	GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TCACTADAGG	ATCCTTCTAT	ACCCACACAC	2160
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	AIGIIGGAIC	CACAACCAAC	2220
	AGCTTTCTCC	AGACTAATTA	CACIGAGATA	COTOTTONIO	THE CLOSURE	ARATGETTEC GGAGGGARAT AGGCAGAGAG GACAACCAA GGAAATGCA TACCCCATCC AACCCAACCG TGAGGGGTTG TTTTATCTTT TGCACACTTT TATCTTTCCA TGCAGATTTA	2280
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Seq ID NO: 581 Protein sequence: Protein Accession #: EOS sequence

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							480 540
20	RSPTRGSEPS	GKGDVPNTSL MNLSGTAESL	NOTSUPVIKE	RSLLTSFKLD	TGARDSSGSS	PATSAIPPIS	600
20	PHILOGRAPHE	CAMBELLIAN	VI.T PESARNA	SEDSTESSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESPLOTNYTE	TRVDESEKTT	KSPSAGPVMS	OGPSVTDLEM	PHYSTPAYPP	720
	TEVTPHAPTP	SSROODLVST	VNVVYSOTTO	PVYNGETPLO	PSYSSEVEPL	VTPLLLENQI	780 840
25	LNTTPAASSS	DSALHATPVF SDKVPLHASL	PSVDVSPESI	LSSYDGAPLL	PPSSASPSSE OTTUANCETT.	PROSPECUT.V	900
23	I LPQVISATE	PSSDAMMHAR	SSGDEDSYAL	SDNEGSOHIP	TVSYSSAIPV	HDSVGVTYOG	960
	SUPSCIPSHIP	IPKSSLITPT	ASLLOPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
	PVSVABFTYT	TSVFGDDNKA	LSKSEIIYGN	ETELQIPSEN	BMVYPSESTV	MPNMYDNVNK	1080 1140
30	LNASLQETSV	SISSTKGMFP ASSDPASSEM	GSLAHTTTKV	PONEISOVPE	NNPSVQPTRT	VSQASGDTSL	1200
30	AUDCODITIVE	TOKUNKISST	MI.HI.TVSNSA	RSENMLHSTS	VPVFDVSPTS	HMHSASLOGL	1260
	TISVASEKVE	PVIJKSESSH	OVVPSLYSND	ELFOTANLEI	NOAHPPKGRH	VPATPVLSID	1320
	RDINTLINKL	THEORILIST	KSSVTGKVFA	GIPTVASDTF	VSTDHSVPIG	NGHVAITAVS	1380
35	PHRDGSVTST	KLLFPSKATS QEKVMNDSDT	ELSHSAKSDA	GLVGGGEDGD	TODDGDDDDDD	RDSDGLSIKK	1440 1500
33	DOVODOMES.	CRKAWNDEDL	NDTOTGSALL	PLSPESKAWA	VLTSDEESGS	GOGTSDSLNE	1560
	NETSTOPSFA	SQKHNDGKEE DTNEKDADGI	LAAGDSEITP	GFPQSPTSSV	TSENSEVERV	SEAEASNSSH	1620
							1680
40	ISTPPTPIPP	ISDDVGAIPI HKNRYINIVA	KHPPKHVADL	HASSGFTEEF	ETLKEFYQEV	QSCTVDLGIT	1740
40							1860
	LAYYTVRNFT	LENTKIKKGS	OKGRPSGRVV	TOYHYTOWPD	MGVPEYSLPV	LTPVRKAAYA	1920
	REHAUCEUUU	HCSAGVGRTG	TYIVLDSMLO	OIOHEGTVNI	PGFLKHIRSQ	RNYLVQTEEQ	1980
45	YVFIHDTLVE	AILSKETEVL	DSHIHAYVNA	LLIPGPAGKT	KLEKQPQLLS	QSNIQQSDYS	2040
45	AALKQCNREK	NRTSSIIPVE DHNAQLVVMI	RSRVGISSLS	GEGTOYINAS	THUST TOSHE	MARCHECISM	2160
	PRETITIONNE	LEATODDVIII.	EADRECCERM	DNDDSDTSKT	PELISVIKEE	AANRDGPMIV	2220
	HDEHGGVTAG	TPCALTTLMH	QLEKENSVDV	YOVAKMINLM	RPGVFADIEQ	YOPLYKVILS	2280
50	LVSTRQEENP	STELDSNGAA	LPDGNIAESL	ESLV			
30	Seq ID NO:	584 DNA 8	non con on				
	Nucleic Ac	id Accessio	n#: NM_00	6688.1			
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55	1	11	21	31	41	51 .	
55	ī	Ī	1	i	1	Ī	
	CCGGGCAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCCTGGAGC	60
	AGGGGCGCAG	GAATTCTGAT	GTGAAACTAA	CAGTCTGTGA	CCCCACTCCT	GGGTATAGAA	120 180
60	AGAAGATGAA	GGATATOGAC GAGAACCAGC	ATAGGAAAAG	CCCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
00	GGAGAACTYY	ACCUTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
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	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	TCTTCTCTGG	420
65	ACCCAGTGGA	CAATGCTGGG	GCGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
05				TAGAGAGACT	GTGGCDAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGACGCTGCT CATCGTGTGC	TCCCTGCGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720 780
70	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CTTGCACTGA	840
70	CTTGGGGCATT	GAATTACCGA	ACCCGTGTCC	GCTTGCGGGG	GGCCATCCTA	ACCATGGCAT	900
	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGCTCCAA	CGATGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
75	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
13	GCTTCCTGGG	TTTCAGGAGA	ANATOCTCI	CCGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
	ATGRACITTCT	TACTTACATT	ABATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
	AGAGTGTTCA	AAAAATCCGC	GAGGAGGAGC	GTCGGATATT	GGAAAAAGCC	GGGTACTTCC	1320
80	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTG	CACCACCACA	COCCAGCGTG	GTGACCTTCT	1380 1440
οU	CIGITCATAT	GACCCTGGGC CATGACTTTT	GCTTTGAAAC	TAACACOGTT	TTCAGTAAAG	TCCCTCTCAG	1500
							1560
	TAAAGAACAA	NCCNGCCNGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
85	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCCAAA	ATGAAAAAAG ACTGAGCATC	1680
83	ACAAGAGGGC						1800
	COGAAGAGGA	AGAAGGCAAG	CACATCCACC	TGGGCCACCT	GCGCTTACAC	AGGACACTGC	1860

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	AAACCAGTGG	TTCACAGAAG	AAGTCACAAG	ACAAGGGTCC	TAAAACAGGA	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG		2640 2700
15	TOTTCAGTGCC	TATOGCOCTT	TATGGTGTCT TTCATGCTGA	ACATECAGGC	CACCGCCTTC	AGCACCTGGT	2760
13	CCTTCACTTA	CTCCATCAAG	CARGGARGOG	GGAACACCAC	TYTTGACTCGA		
	CCTCCCTCAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCATG	CTGATCCTGA	AAGCCATTCG	AGGAGTTGTC	TTTGTCAAGG CTTCGAAGCC	2940
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20	TGGATGAAGT	TGACGTGCGG	CTGCCGTTCC	AGGCCGAGAT	GTTCATCCAG	AACGTTATCC	3120
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25	TGAAGCGTCT	GGACAATATC	CCCTACAATA	ANGGGCAGGA	GTTTCTGCAC	TCCAGCATAC AGATACCAGG	3360
23							
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						CGATTCACCT	
30							
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35	CCCTCTTCCG	TCTGGTGGAG	CTCCCAACCA	AACTOTOTAT	CATTCCTCAA	GAGCCGGTGC	3960
55	TOTAL CARGO	CACTGTCAGA	TOBBATTTOO	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
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40							
	GTACCATGCT	GACCATTGCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG TCCAACGACA AAGGGCTGAC	4260 4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCCTTCTG	TCCAACGACA	4380
	GTTCCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCGCTGTC	CTGGGGCGGG	4440
45	CCCCTCATCG	CGTCCTCCTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TCGCACAGCA	4560
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTTCTTA	ATTGCACTCT	AAAAGGTTCA TGTAGCTATA GTTTATTTTA TTTGTACAGT	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	ANTOTANCO	GTTTATTTTA	4800
50	TATTAAAATA	AGCACTGTGC	TAATAACAGT	GCATATTCCT	TTCTATCATT	TTTGTACAGT	4860
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	CTCTAGCTGG	TGGTTTCACG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
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	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
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	TCCCACTGCC	RECOCTORE	COALCIGCIO	CTTTTTGAGG	TGGCACTTTT	TCCAAGACCT TCATTTGCCT	5400
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	CTCACCGCAG	TCGTCGCACA	GTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
	CAGCTCTTGC	TAATCAGTGT	CTCACACTGG	CGTAGAAGTT	TTTGTACTGT	GTTTTCCTTT CAACTTTAAG AAAGAGACCT TTTGTGCTGT	5580
	ACCTCAGGTT	GCTGGTTGCT	GTGTGGTTTG	GIGIGITICCC	ACTTONATO	TOTAL	5700
65	ATGTCGTGAC	CAACTAGACA	TTCTGTCGCC	TTAGCATGTT	TGCTGAACAC	TOTAGCGTTGC TCAGCGTTGC CTTGTGGAAG	5760
			TAAAATTATT	TTGGATTTTG	TARABARARA	AAAAAAAAA	5820
	алалалала	AAAAAAA					
	C ID NO.	EGE Dyoto	in sequence				
70			nn sequence NP 005679.1				
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	1	11	21	31	41	51	

70	Protein Acc	cession #: 1	NP_005679.1				
	1	11	21	31	41	51	
		TTDCDCCC	RERTSTEGTH	DODDONESD P	TERRETORIAL.	PTAADAUCT.S	60
75	LOASMISOLR	ILDEENPKGK	YHHGLSALKP	IRTTSKHOHP	VDNAGLESCM	TFSWLSSLAR	120
	VAHKKGELSM	EDVWSLSKHE	SSDVNCRRLE	RLWOEELNEV	GPDAASLRRV	VWIFCRTRLI	180
	LSIVCLMITO	LAGFSGPAFM	VKHLLEYTQA	TESNLQYSLL	LVLGLLLTEI	VRSWSLALTW	240
	ALMYRTGURL	RGAILTMAPK	KILKLKNIKE	KSLGELINIC	SNDGQRMFEA	AAVGSLLAGG	300
	PVVAILGMIY	NVIILGPTGF	LGSAVFILFY	PAMMFASRLT	AYFRRKCVAA	TDERVQKMNE	360
80	VLTYIKFIKM	YAWVKAPSQS	VQKIREEERR	ILEKAGYFQG	ITVGVAPIVV	VIASVVTPSV	420
	HMTLGFDLTA	AQAPTVVTVF	NSMTFALKVT	PPSVKSLSEA	SVAVDRPKSL	FLMEEVHMIK	480
	nkpasphiki	EMKNATLAWD	SSHSSIQNSP	KLTPKMKKOK	RASRGKKEKV	RQLQRTEHQA	540 600
	VLAEQKGHLL	LDSDERPSPE	EEEGKHIHLG	HLRLQRTLHS	IDPRIORCE	VGICGSVGSG	660
85	KTSLISAILG	OMATPEGGIY	ISGTPAYVAQ	QAWILNATLR	DNILFGREID	DICALDAUDO	720
63	CCLRPDLAIL	PSSDLTEIGE	RGANLEGGOR THOLOYLVDC	OKISPAKADI	SUKSTITUUU	MULHODYATI	780
	FNNLLLGETP	PVEINSKKET	SGSQKKSQDK	GPKTGSVKKE	KAVKPEEGQL	VOLEBRGOGS	840

5	KPPDTTPTGR LVILFSVLHI LDDNQAPFFL GLFQFTVRLA RYRENLPLVL IGLADLRSKL SEVMENGDNF	QAAGGPLAFL MQYYASIYAL ILNRFSKOMD VSRVLIRELK FTCAMRWLAV SETEARFTSV KKVSFTIKPK SIIPQEPVLP SVGERQLLCI VLGSDRIMVL	EVDVRLPPQA RLDNITQSPP RLDLISIALI ERINHYIKTL EKIGIVGRTG SGTVRSNLDP ARALLRHCKI	EMFIQNVILV LSHITSSIQG TTTGLMIVLM SLEAPARIKN SGKSSLGMAL FNQYTEDQIW LILDEATAAM	FFCVGMIAGV LATIHAYNKG HGQIPPAYAG KAPSPDWPQE FRLVELSGGC DALERTHMKE DTETDLLIQE	PPWFLVAVGP QEFLHRYQEL LAISYAVQLT GEVTFENAEM IKIDGVRISD CIAQLPLKLE TIREAFADCT	900 960 1020 1080 1140 1200 1260 1320
	Seq ID NO: Nucleic Aci Coding sequ	586 DNA se id Accession sence: 89	#: NM_001	327.1			
15	1 AGCAGGGGC	11 GCTGTGTGTA GGCAGAGGCT	21 CCGAGAATAC	31 GAGAATACCT GCAGGCCGAA	41 CGTGGGCCCT GGCCGGGGCA	51 GACCTTCTCT CAGGGGGTTC	60 120
20	GACGGGCGAT TGGCGGCCCA AAGGGCCTCG GCTGAATGGA	GCTGATGGCC GGAGAGGCGG GGGCCGGGAG TGCTGCAGAT	CAGGAGGCCC GTGCCACGGG GAGGCGCCCC GCGGGGCCAG	TGGCATTCCT CGGCAGAGGT GCGGGGTCCG GGGGCCGGAG	GATGGCCCAG CCCCGGGGCG CATGGCGGCG AGCCGCCTGC	GGGGCAATGC CAGGGGCAGC CGGCTTCAGG TTGAGTTCTA	180 240 300 360 420
25	GGATGCCCCA CATACTGACT	CCTTTCGCGA CCGCTTCCCG ATCCGACTGA CAGCTTTCCC CCCTCAGGGC CTAGGGAATG	TGCCAGGGGT CTGCTGCAGA TGTTGATGTG	GCTTCTGAAG CCACCGCCAA GATCACGCAG	GAGTTCACTG CTGCAGCTCT TGCTTTCTGC	CCATCAGCTC CCGTGTTTTT	480 540 600 660 720
30	Seq ID NO:	587 Protes	GGCTTACATG	TTTGTTTCTG	TAGAAAATAA	AACTGAGCTA	,20
	Protein Ace	cession #: 1	₹P_001318.1				
35	1	11	21	31	41	51 1	
40	MOAEGRGTGG PRGPHGGAAS VLLKEFTVSG	STGDADGPGG GLNGCCRCGA NILTIRLTAA	PGIPDGPGGN RGPESRLLEF DHRQLQLSIS	AGGPGEAGAT YLAMPFATPM SCLQQLSLLM	GGRGPRGAGA EABLARRSLA WITQCPLPVP	ARASGPGGGA ODAPPLPVFG LAQPPSGQRR	60 120
40	Seq ID NO: Nucleic Ac Coding seq	588 DNA se id Accession Lence: 52	1 #: Eos se	equence			
45	1 CCTCGTGGGC	11 CCTGACCTTC	21 TCTCTGAGAG	31 CCGGGCAGAG	41 GCTCCGGAGC	51 CATGCAGGCC	60
50	CCTGATGGCC GGTCCCCGGG CCGCATGGCG GACAGCCGCC	GCACAGGGG CAGGGGGCAA GCGCAGGGG GTGCCGCTTC TGCTTCAGTT	TGCTGGCGGC AGCAAGGGCC TGCGCAGGAT CCGACTGACT	CCAGGAGAGG TCGGGGCCGA GGAAGGTGCC GCTGCAGACC	GAGGAGGCGC CCTGCGGGGC ACCGCCAACT	GGGCGGCAGA CCCGCGGGGT CAGGAGGCCG GCAGCTCTCC	120 180 240 300 360
55	GTGTTTTTGG	GTCTCCAGCA CTCAGGCTCC CTCCTCCCCT TTGTCGCTGG	CTCAGGGCAG AGGGAATGGT	AGGOGCTAAG CCCAGCACGA	CCCAGCCTGG	CGCCCCTTCC	420 480 540 600
60	Seq ID NO: Protein Ac	589 Protes cession #: 1	in sequence Eos sequence	e 31	41	51	
65	MQAEGQGTGG	STGDADGPGG	PGIPDGPGGN	AGGPGEAGAT	GGRGPRGAGA	ARASGPROGA	60 120
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70	PLPVFLAQAP Seq ID NO: Nucleic Ac Coding seq	SGORR 590 DNA soid Accession uence: 90	RRPDSRLLQF equence n #: NM_0055 3671	RLTAADHRQL 662.1 31	41 	51 	120
70 75	PLPVFLAQAP Seq ID NO: Nucleic Ac Coding seq 1 ACAGCGGAGC AGACAGAGC ACTCTCGCT ATGGGAAGTC	SGORR 590 DNA seid Accession uence: 90 11 GCAGAGTGAG TGAGGGGCCC CAGGCAGTGT	equence n #: NM_0055 3671 21 AACCACCAAC GCACCGCC GCACCCGGG ATCTTGATC	RLTAADHRQL 311 CGAGGCGCCG TGCCTGCGCT CCACCTCCAG	41 GGCAGCGACC CTGGCTGGGC GAGGGAAGT CAGACAAACT	51 - CCTGCAGCGG TGCTGCTCT TGTGATTGCA GGTAATGGAT	60 120 180 240
	PLPVPLAQAP Seq ID NO: Nucleic Ac Coding seq 1	SGORR 590 DNA 8- id Accession uence: 90 11 - - - - - - - - - - - - -	RRPDSRLLQF equence n #: NM_0055 8671 21 AACCACAAC GCACCGCGA ACCATTGATC GACAACACTG AAGGACCGCT AAGGACCGTA CCAGGGTAC	BLTAADHRQL 31 GAGGGGCGCG TGCCTGCGG TGCCTGCAG GGGAACTTCA ATGGCATTCA GTTTGCCTG GGTGCAGCTG	41 GCAGCGACC CTGGCTGGGC GAGCGAAGTC CTGCCAGAAG CAATTGTAAC TAAACCAGGT TAAACCAGGT GGATGCGGG	51 CCTGCAGCGG TGCTGCCTCT TGTGATTGCA GGTAATGGAT TGCAGAATG TCCAAAGGTT TGTGACGGAG TGCACCCAAG	60 120 180

		TGCCAAATTT	Ommooos s.m.o.	TARGETTE A	OTRECCCO A	AGCCTGTCCT	900
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5	man amount	TGAGTATCGA	ACCURACTOC	CCARTCTCAC	AGCCCTCCGC	ATCCGACCTA	1140
,	IGAGITACIT	IGAGIAICGA	AGGITACIGC	- CALL MODICAG	CODGRAGGE	accorderer:	1200
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		GCTCTGTGCT	ar magamit on	mmacaaa acc	CTRECCTORS	CATGGCCCAG	1620
	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	11000000000	CITIOGIGAA	managan Land	1680
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	ACCACTOCAA	AGCAGGCTAC	TTCGGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAGTGTC	1800
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	GAGCTTGCAA	CIGIAACCCC	MIGGGCICAG	MUCCIGINGG	AIGICOANG!	ani oddicci	
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	GCAGGATGCA	GCAGGCTGAG	CAUGCCCTTC	MOGNERATION	anananiacc	CAGALITCAG	
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25	MOTACCAGAM	AGCTTCCTTG		* C*************************	CECTACTOCAC	TACCTOCCCC	2340
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	Ch CTTCCTTCCC	CAAGGCCCTG	CATTGAAGGAG	TOGGAAGOGG	AAGCGGTAGC	CCGGACGGTG	2520
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	CAMMONOGAI	TACACAAAAG		10100000	ACAACCA CAC	CAGCTCTTAC	2820
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	AGAATGGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCCGTGCC	AATCTTGCTA	2880
35	AAAGCAGAGC	ACAAGAAGCA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTTGAGAGCA	2940
	maranes s s s s	CCTCAGAGAG	TTTTCACCTCC	ACCITICATO	CAGRARAGCA	GAAGCTGAAG	3000
	ICCITATAGA	CCICAGAGAG	TI TORCCIO	AGO LOGICATION	ACAMCCCACAC	CACAACACCC	3060
	AAGCCATGAA	GAGACTCTCC	TACATORICC	MOMMOGITIC	MONTOCCHOI	GACAAGACCC	
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
	CCGGGGGAGGC	CCTGGAAATC	TCCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACTTGG	3180
40	AACCCAATCT	GACAGCAGAT	CCACCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
40	MOCCMATO	GGAAGTGGAA		*********	COMOCHOTTO	CACACGAATA	3300
	GTGAGATGAG	GGAAGTGGAA	GGAGAGCIGG	MANGGANGON	GCIGGMGIII	GACACGAAIA	3360
	TGGATGCAGT	ACAGATGGTG	ATTACAGAAG	CCCAGAAGGI	TGATACCAGA	GCCAAGAACG	
	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCCTGCAT	CTGATGGACC	3420
	BCCCMCTCBC	TGTAGATGAA	a Accidentate	TOTTACTYCA	GCAGAAGCTT	TCCCGAGCCA	3480
45	MOCCICICAG	CAACAGCCAA	ONGGGGGGGGG	man-manas da	COMOCHACAC	NOCCOUNT COTTO	3540
43	AGACCCAGAT	CAACAGCCAA	Crecesce	TGATGICAGA	GCIGGRAGAG	AGGGCACGIC	3600
	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	
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	ACCA ACACTO	AAGCTGCCAT	ABATATTTCT	CAACTGAGGT	TCTTCCCATA	CAGATCTCAG	3720
	AGCANCAGI C	- ANGCIGCONI	TO A CONCECTO	CCATCCCCCAC	ATTTCAACAT	GTTTAATGGG	3780
50	GGCTCGGGAG	CCALGICALG	IGAGIGGGIG	GGMIGGGGAC	- A1110000CA1		3840
30	TATGCTCAGG	TCAACTGACC	TGACCCCATT	CCTGATCCCA	TGGCCAGGTG	GITGICTIAL	
	TGCACCATAC	TCCTTGCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATCATCABGG	ATCTGGACCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACI	GCACAGGCAG	3960
	**************************************	CATAATAGTC	COURS DESCRICE A C	TOTAL STORES	TOCACAACTO	CTGTTCGGAT	4020
	ATGTTTGCCT	CHIMAIAGIC	GIMMIGGMG	ICCIGONALI	TOGIC TO	maadaraad	4080
	ATAGTCAACI	TATTCTTTGA	GTAATGTGAC	TAAAGGAAAA	MACIFICACI	TTGCCCAGGC	
55	ATGAAATTCI	TCCTAATGTC	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAAT	4140
	ACTATTCCCT	CATATTOTO	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTCCT	CCTACTTACA	4200
	ACIMITACCI		COLOGO MINISTER	B B C CTC C B B C	ANGTGAGCAG	TGTTGGAGTG	4260
	ACCCAGGGT	TGAACATGTT	CICCATILIC	MUCTOUNN	ANGIGNOCHO	2011000010	4320
	AGGACCTGTA	AGGCAGGCCC	ATTCAGAGCT	ATGGTGCTTG	CIGGIGCCIG	CCACCTTCAA	
	GTTCTGGACG	TGGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCAACT	TAGAGATTGC	4380
60	A TOTAL PARTY	ANCONTITUO	TACCACCAA	CCADATGTTC	GGAAAGTATT	TACTTTTTCG	4440
00	WILLIAM	ANGCALLICO		000000000000000000000000000000000000000	1 00000 0 0 0 000	CTCTAGATTT	4500
	GITTCAAAGI	GNINGAAAAG	1010001100	OCK LIGHTAN	ADDIAMOTI	DATE TO THE PARTY OF THE PARTY	4560
	ATTAGTCCTA	ATTCAATCCT	ACTITICGAR	CACCAAAAA	GATGCGCATC	AATGTATTT	
							4620
	CACACTTCAC	CTGGGTCACA	TOCATOCTO	CATTCATCCI	TCCATCCATC	TTTCCATCCA	4680
65	CHUMUI I'CAU	CAUGACACA		mamman const	COMP CHINADOWN	CCNGGGGGGGG	4740
U.S	TTACCTCCAT	CUATCUTTCC	AACATATATI	INTIGAGIAC	CIACIGIGIG	CCAGGGGCTG	
	GTGGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTC	ATTGTCTAGT	GAGGAAGACA	4800
	AGCATTTT	TABBATABA	TTARACTTAC	AAACTTTGT	TGTCACAAG1	GGTGTTTATT	4860
	CC2 2 man 2 CC	CONTROL CONTROL	PACCACAMAN	CTCAACAGAS	CATATGTTG	AAGACCCTCC	4920
	GCMTAACCC	CILGGIIIGC	Ancelellie	Lacatomore	commonact	C. POTOCONTOC	4980
~~	CATGGGGGC	CTTGAGTTTI	GGCAAGGCTG	ACAGAGCTCI	GGGTTGTGCF	CATTTCTTTG	
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	TAACACCAGT	GGGAATTGCT	GGAGGAACCA	GAGGCACTTC	CACCTTGGCT	GGGAAGACTA	5100
	WORK OF CO.	TTCCTTC	ATTTYTTE	ATTTTCCTG	AAGTGTTTT	AADAAATAAA	5160
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75 Seq ID NO: 591 Protein sequence Protein Accession #: NP_005553.1

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80	MPALWLGCCL	CFSLLLPAAR	ATSRREVCDC	NGKSRQCIFD	RELHROTONG	PRCLNCNDNT	60
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	PEGCTOCPCY	GHSASCRSSA	EYSVHKITST	FHODVDGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSACREDRAY	PUAPAKELON	COVEYGOSLS	PDYRVDRGGR	HPSAHDVILE	GAGLRITAPL	300
85	MRI CYTT. DCG	T.TETYTFRLN	EHPSNNWSPO	LSYPEYRRLL	RNLTALRIRA	TYGEYSTGYI	360
	DNUTLISARP	VSGAPAPWVE	OCICPVGYKG	OFCODCASGY	KRDSARLGPP	GTCIPCNCQG	420
	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDPRSCK	PCPCHNGFSC	SVMPETEBVV	480

	WU 02/						F0
	CNNCPPGVTG	ARCELCADGY	FGDPFGEHGP	VRPCQPCQCN	NNVDPSASGN	CDRLTGRCLK	540 600
	CIENTAGIYC	DQCKAGYFGD	PLAPNPADKC	RACINCIPAGE	BPVGCRSDGT	CVCKPGFGGP	660
	NCEHGAPSCP	ACYNQVKIQM	DOLMOOPOWW	EALISKAQGG	DGAAADLEDE	OVONDUMENT	720
5	QDILRDAQIS	EGASRSLGLQ AESEASLGNT	LAKVRSQENS	TOSKLODDIKM	ATTI BECOME	CL CHMEOLTH	780
,	RLITOMQLSL	SLVRKALKEG	NIPASDRIVG	PROFESERVE	WINDSOUAN AUGUS	MODAYONETE	840
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	ADRSYOHSLR	ONGKEGEEKS	VSDQSFQVEE	KARIKUKADS	PRIDATKUMD	TI KAT DEPOT	960
	NWKEEAQQLL	EAMKRLSYIS	DQLLSKANLA	CONFRACTOR	ANDAODAKNO	ACEALETSSE	1020
10	QVDNRKABAB	EANVTADGAL	QKVSDASDKT	ACOUNTAINO	POWEL DELLAR	MUNICIPALITY	1080
10	TEGETGSTWT	AGVTIQUELN	MI DOLLIU MD	ONT CUNEDAL	W.T.FONT.CDA	KTOINSOLDD	1140
	AUKVDTRAKN	QQRGHLHLLE	TOTOGERALIN	WIT PATERNIT.	PROCENTIAL.	FOO	
	PENSELBERAR	QQRGHUNDID	TOTOGLUMDY	MUDINITIONE	TTOCTH TOTAL	244	
	Seq ID NO:	592 DNA 86	ecuence				
15	Nucleic Aci	d Accession	#: AP1010	51.1			
		ence: 221.					
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	1	1	ì)	1	1	
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50	CACAACTTTA	TOCCCATTCC	TITIONGCIA	DOTTOTICALA	MATGEMATER	TCATGCGTTT	1860
50	ACCTITIGI	TAATAAGGTG	MOCTOTOTAL	CTCTCSSCSS	AGTGCTAGAC	TTTCTCGAGT	1920
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	ATTOTTOTAL	ADDITION OF THE PERSON	CATGTTTGTG	CTCTGTTCCA	TTTTTAACAAC	TGCTCTTACT	2400
60	TTTCCAGTCT	GTACAGAATG	CTATTTCACT	TGAGCAAGAT	GATGTATGGA	AAGGGTGTTG	2460
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65	GTGGTTTTGT	AATTTGAAAA	GTGCTATACT	AAGGGAAAGA	ATTGAGGAAT	TAACIGCATA	2760
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,,,	TTATATOTI	AATTTGTATA	AAGCATTACT	CTTTTTCAAT	AAATTGTTTT	TTAATTTAAA	3420
	AAAAAAAAA	AAAAAAAAA	AAA				
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	j	1	1	1		1	
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85	OTOCKUPDOT.	TAILSSTIAT	PALMVVGTLL.	CVIAIFVATV	GMXCMKCLED	DEVOKMRMAV	120
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	LLCCSCPRKT	TSYPTPRPYP	KPAPSSGKDY	v			

180

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660 720

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1080 1140 1200

1260 1320

1560

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1960

1920

3240

3300

3420

3480

3540

WO 02/086443 Seq ID NO: 594 DNA sequence Nucleic Acid Accession #: NM_006180.1 Coding sequence: 352..2820 CCCCCATTCS CATCTAACAA GGAATCTGCG CCCCAGAGAG TCCCGGACGC CGCCGGTCGG 10 COCCUTATA AGCOGITOSC TATGCOGOGA CCACTGTGAA CCCTGCOGCC TGCOGGAACA CTCTTCGCTC COGACCAGCT CAGCCTCTGA TAAGCTGGAC TCGGCACGCC CGCAACAAGC ACCGAGGAGT TAAGAGAGCC GCAAGCGCAG GGAAGGCCTC CCCGCACGGG TGGGGGAAAG ACCOMMOND THE MANAGEMENT GRANT CONTROL OF THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING TO THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING TO THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING THE MANAGEMENT ACCORDING TO THE MANAGEMENT ACCORDING THE MANAGEMENT ACCOR GGCTTCTGGA GGGCGCTTT CGCCTGTCC ACGTCCTGCA AATGCAGTGC CTCTCGGATC
TGGTTCAGGA ACCTTCTCC TGGCATCGTG GCATTTCCGA GATTGGAGCC TAACAGTGTA 15 GATCCTGAGA ACATCACCGA AATTTTCATC GCAAACCAGA AAAGGTTAGA AATCATCAAC GRAGATGATO TIGAAGCITA TOTGGGACTO AGAANTCIGA CARTITUGA ETICATOA AAATTITUG CICATAAAGC ATTICIGAAA AACAGCAACC TGCAGCACAT CAATTITACC 20 ARATTITIGG CICATARAGC ATTICIGARA ARCAGCARC INCAGCACAI GALITIACC GGARACARAC TGACGAGITT GICTAGGARA CATTICCOTC ACCITGACIT GICTARACIG ATCCIGGIGG GCARICCAIT INCATGCICC IGIGACAITA IGIGGATCAR GACTCICCAR GAGGCTAAAT CCAGTCCAGA CACTCAGGAT TTGTACTGCC TGAATGAAAG CAGCAAGAAT ATTCCCCTGG CAAACCTGCA GATACCGAT TETGGTTTGC CATCTGCAAA TCTGGCGGCA 25 CONSTITUCTA ATATOTATTO GOATOTOGT ARCTOGTTT CCALACATAT GAATGAAACA AGCCACACA AGGCTCCTT AAGGATAACT ARCATTACTA CCGATGACAG TOGGAGAAA TCTCTTTGT TGGCGGAAAA TCTCTTTGT TGGCGAAAA TCTCTTTGT TGGCGAAAA TCTCTTTGA GAAGATCAG ATATOTTCAA CATTITOCAC CAACTATCAC ATTICTCOAA TCTCCAACCT CAGACCACCA CTGGTGCATT
CCATTCACTG TGAAAGGCAA CCCCAAACCA GGGCTTCAGT GGTTCTATAA
TTGAATGAT CCAATTACAT TCTAATAAA ATACATGTTA CCAATCACAC GGGGTACCAC 30 TRIGATIANT COMMITTAN ATTACKTORY OF THE STREET OF THE STREE ATTGACGATG GTGCAAACCC AAATTATCCT GATGTAATTT ATGAAGATTA TGGAACTGCA GOGANTORO TOGGGGACC CACGAAGGA AGTANTAGA TOCCTICACA AGACOTACAG GATATAGACCO GTCGGGAACA TCTCTCGGGT TATGCTGTGG TGGTGATTG CTCTGTGGTG GANTITIGCC TITTGGTAAT GCTGTTCTG CTTAGGTG CAGACACTC CAAGTTTGGC 35 GGATTTTGCC TITTGGTAAT GCTGTTTCTG CITAAGTGG CAGGCCCCAGCATTGG ATGANAGGCC CAGCCTCCGT TATCAGCAAT GATGATGACT CTGCCAGCCC ACTCCATCAC ATCTCCAATG GGAGTAACAC TCCATCTTCT TCGGAAGGTG GCCCAGATGC TGTCATTATT ARTICOLART GENERALCE TECRITORIS TEGRANDOS GEOCHARTOS CONTRATA GENERALCE CONTRATA CONTRATA CONTRATA TECRITORIS CONTRATA TECRITORIS CONTRATA CONTRATA CONTRATA TECRITORIS CONTRATA CONTRA 40 45

2040 2100 2220 GACCTCAACA AGTTCCTCAG GGCACACGGC CCTGATGCCG TGCTGATGGC TGAGGGCAAC 2280 2340 2460 2520 2640 TOGGRADATITI TORCUTATOS CARACTOCAS CONTROLOGO CONTROLOGO GAGGGTOTAT GAGGTGTATC TOGGGTGCTG GCAGGGAGAG CCCCACATAA GGAAGAACAT CAAGGGCATC 2700 CATACCCTCC TTCAGAACTT GGCCAAGGCA TCTCCGGTCT ACCTGGACAT TCTAGGCTAG 2820 GGCCCTTTTC CCCAGACCGA TCCTTCCCAA CGTACTCCTC AGACGGGCTG AGAGGATGAA 2880 CATCITITÀ C'OCCCCCC AGCCCACA GCRCCTCC TTCACTCRA CAGTATTAAC
ATCAAAGACT CCGAGAAGCT CTCGAGGGAA GCAGTGTTAT CATCITCTCAT CATGACACA
300
GTATTGACT CTTTTTGGCA TATCTCTTT CATCITTCC ATCTCCCTTQ GTGGTCCTT
306 TITCTITITI TANATITICI TITTCTICIT TITTTTCGTC TICCCTGCTT CACGATTCTT 3120

ACCOUNTER TEGRATICANT CEGGGETTONG CATTACTANT AACTOTGCAT AGACAAAGGC

CTTAACAAC GTAATTTGTT ATATCAGCAG ACACTCCAGT TTGCCCACCA CAACTAACAA TGCCTTGTTG TATTCCTGCC TTTGATGTGG ATGAAAAAA GGGAAAACAA ATATTTCACT

TRANCITRE TATICCINCU THINKING ANDAROUS CORRARCH ATTICATIA
THANCITRE CACTICINC TRANSPORT CARGACTIC TATGGATIC CITCATTA
THATTATTA TRACTICT TATINTITT GGANGCITA AGCCUNTATA TAAAAAAAAA

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11 41 MSWIEHRICP AMARINGECK LVVGFNRAAF ACPTSCKCSA SRIMCSDPSP GIVAPPRLEP NSVDENITE IPIANGREE IINEDDWAY VGLENITIVD SCLEFVARKA PLANSNICHI NFTRRIKITSI SEKREPHILDI SELILUKNEP TECCILIMIK TILARASSEP TOLICIANS SKNIPLANIQ IPNCGLPSAN LAAPRILTVEE GKSITLSCSV AGDPVPNAYM DVGRIMSKUM 1 90 240 BRITEDWING IFFICULPSAN INVESTIGES OF STATES LIAKNEYGKO EKOISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARIS KFGMKGPASV ISNDDDSASP LHHISNGSNT PSSSBGGPDA VIIGNTKIPV IENPQYFGIT NSQLKPDTFV QHIKRHNIVL 480 KREIGEGAFG KVFLAECYNL CPEQDKILVA VKTLKDASDN ARKOFHREAE LLTNIQHEHI 400 VKPYGVCVEG DPLIMVPEYM KHGDLNKPLR AHGPDAVLMA EGNPPTELTQ SQMLHIAQQI 660 AAGMVYLASQ HEVHRDLATR NCLVGENLLV KIGDEGMSRD VYSTDYYRVG GHTMLPIRWM

WO 02/086443 PCT/US
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EVYEMALGOG REPRURSHNI KOHNTLIQHI. AKASPYLDI LG

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	ATTCTGGATT	CCGAAACAAA	GCTCATAAAG	CATTTCTGAA	AAACAGCAAC	CTGCAGCACA	900
25	TCAATTTTAC	CCGAAACAAA	CTGACGAGTT	TGTCTAGGAA	CTCTCACATT	ATGTGGATCA	960
23	ACACTOTOCA	ACACCCTARA	TOTAGTOTAG	ACACTCAGGA	TTTGTACTGC	CTGAATGAAA	
	GCAGCAAGAA	TATTCCCCTG	GCAAACCTGC	AGATACCCAA	TIGIGGITTG	CCATCTGCAA	1080
	ATCTCCCCCC	ACCTAACCTC	ACTGTGGAGG	AAGGAAAGTC	TATCACATTA	TCCTGTAGTG	1140
	TOGCAGGTGA	TCCCCTTCCT	AATATGTATT	GGGATGTTGG	TAACCTGGTT	TCCAAACATA	1200
30	TGAATGAAAC	AAGCCACACA	CAGGGCTCCT	TAAGGATAAC	TAACATTTCA	TCCGATGACA	1260
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	ACCTCACTGT	GCATTTTGCA	CCAACTATCA	CATTTCTCGA	ATCTCCAACC	TCAGACCACC	1380
	ACTGGTGCAT	TCCATTCACT	GTGAAAGGCA	ACCCCAAACC	AGCGCTTCAG	ACCUATOR	1440 1500
35	ACGGGGCAAT	ATTGAATGAG CGGCTGCCTC	CACCAGGATA	ATCCCACTCA	CATGAACAAT	GGGGACTACA	1560
55	CTCTTATTACC	CAAGAATGAG	TATOGGARGO	ATGAGAAACA	GATTTCTGCT	CACTTCATGG	1620
	CCTGCCCTGG	ARTYGACGAT	GGTGCAAACC	CAAATTATCC	TGATGTAATT	TATGAAGATT	1680
	ATGGAACTGC	AGCGAATGAC	ATCGGGGACA	CCACGAACAG	AAGTAATGAA	ATCCCTTCCA	1740
	CAGACGTCAC	TGATAAAACC	GGTCGGGAAC	ATCTCTCGGT	CTATGCTGTG	GTGGTGATTG	1800
40	CGTCTGTGGT	GGGATTTTGC	CTTTTGGTAA	TGCTGTTTCT	GCTTAAGTTG	GCAAGACACT	1860
	CCAAGTTTGG	CATGAAAGAT	TTCTCATGGT	TTGGATTTGG	GAAAGTAAAA	TCAAGACAAG	1920 1980
	GTGTTGGCCC	AGCCTCCGTT	ATCAGCAATG	ATGATGACTC	CCCAGATCCT	CTCCATCACA GTCATTATTG	2040
	CARTGO	CARCOCTORO	ATTGARANTC	CCCAGTACTT	TGGCATCACC	AACAGTCAGC	2100
45	TCAACCCAA	CACATTTGTT	CAGCACATCA	ACCGACATAA	CATTGTTCTG	AAAAGGGAGC	2160
45	TAGGCGAAGG	AGCCTTTGGA	AAAGTGTTCC	TAGCTGAATG	CTATAACCTC	TGTCCTGAGC	2220
	AGGACAAGAT	CTTGGTGGCA	GTGAAGACCC	TGAAGGATGC	CAGTGACAAT	GCACGCAAGG	2280
	ACTTOCACOG	TORGESCOGAG	CTCCTGACCA	ACCTCCAGCA	TGAGCACATC	GTCAAGTTCT	2340
	ATGGCGTCTG	CGTGGAGGGC	GACCCCCTCA	TCATGGTCTT	TGAGTACATG	AAGCATGGGG	2400
50	ACCTCAACAA	GTTCCTCAGG	GCACACGGCC	CTGATGCCGT	GCTGATGGCT	GAGGGCAACC	2460 2520
	CGCCCACGGA	ACTGACGCAG	TOGCAGATGO	ACCCCCATATAGC	CONGCAGATO	AACTGCCTGG	2580
	TOGGETCTACCT	CTTCCTCCTC	AAAATCGGG	ACCOCCRITI	GTCCCGGGAC	GTGTACAGCA	2640
	CTGACTACTA	CAGGGTCGGT	GGCCACACAA	TGCTGCCCAT	TCGCTGGATG	CCTCCAGAGA	2700
55	GCATCATGTA	CAGGAAATTC	ACGACGGAAA	GCGACGTCTG	GAGCCTGGGG	GTCGTGTTGT	2760
	CCCACATTT	CACCTATGGC	AAACAGCCCT	GGTACCAGCT	GTCAAACAAT	GAGGTGATAG	2820
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							3240
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	TIGTTTCTCA	AGCGCTATCC	ACAGAACCTT	TUTCAACTTC	MUTTGAAAAG	AGGTGGATTC	4020
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Saq ID NO: 597 Protein sequence Protein Accession #: AAL67965.1

	1	11	21	31	41	51	
85	NSVDPEN ITE NFTRNKLTSL	IFIANQKRLE SRKHFRHLDL	SELILVGNPF	VGLRNLTIVD TCSCDIMWIK	SGLKFVAHKA TLQEAKSSPD	GIVAFPRLEP FLKNSNLQHI TQDLYCLNES DVGNLVSKHM	60 120 180 240

5	KPDTFVQHIK FHREAELLTN PTELTQSQML DYYRVGGHTM CITQGRVLQR	RITNISSDDS PKPALOMFYN EKQISAHFMG LSVYAVVVIA DDSASPLHHI RHNIVLKREL LQHEHIVKFY HIAQQIAAGM LPIRNMPPES PRTCEQEVYE	GAILMESKYI WPGIDDGANP SVVGPCLLVM SNGSNTPSSS GEGAPGKVFL GVCVEGDPLI VYLASQHFVH IMYRKFTTES LMLGCWQREP	CTKIHVTNHT NYPDVIYEDY LPLLKLARHS EGGPDAVIIG AECYNLCPEQ MVFEYMKHGD RDLATRNCLV DVWSLGVVLW	EYHGCLQLDN GTAANDIGDT KPGMKDPSWF MTKIPVIENP DKILVAVKTL LNKFLRAHGP GENLLVKIGD EIFTYGKQPW	PTHMMGDYT TMRSNEIPST GPGKVKSRQG QYFGITNSQL KDASDNARKD DAVLMAEGNP FGMSRDVYST YQLSNNEVIE	300 360 420 450 540 600 660 720 780
15	Seq ID NO: Nucleic Aci Coding sequ	ence: 74 . 8	i#: AB0529 114				
20	CTCTGGGTCC	GGTGATTCAT TTAATGGCAG TCCGGCTGGT	CAGCCGCCGC	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	60 120 180 240
25	GGTGGTGGAC GGAACCCCTC TGGATCTTGG	ATCCCTAAGT ACTTTTCTTC AAACTAAATG ATACTTACAG ACCCTGCAGG CAGTTCAGTT	AGCAACTGCG CCAGGATGTC TCGATGGGCA	TGACATTCAG TTGTGAGCAG GATCTTCCTC	AAAGCTGAAG CTCTTTGACT	GACACAGCAG CAGAGAAGAG	300 360 420 480 540
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	Seq ID NO: Protein Acc	599 Prote: cession #: 1	in sequence BAB61048.1				
45	1 	11 -	21 GWSPAGRADP	31 -	41 PKFRPGPRWC	51 AVOGOVDEKT	60
45 50	FLHYDCGNKT	11 - - - 	GWSRAGRADP LNVTTAWKAQ PSPDGOIPLL	HSLCYDITVI NPVLREVVDI PDSEKRMWTT	PKFRPGPRWC LTEQLRDIQL VEPGARKMKE	AVQGQVDEKT ENYTPKEPLT KWENDKVVAM	60 120 180 240
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50 55	FLHYDOGNET LQARMSCEDK SFHYSMGDC PILPGI Seq ID NO: Nucleic Ac: Coding sequ GGCTCTCACC CCCAGTATCT GCCCCAGGA AGTGGGTACA ACTACTACAC ATTACTCTT TACACCTGTCC TCTACGAAGT	LCLPLLLLLS VTPVSPLGKK AEGHSSGSWG IGWLEDFLMG 600 DNA sid Accession Lence: 57 11 CTCCTCTCCT GAGTACCCTG GAGGATAGG GCOTGCCCTT CGACGTAGGAT CCTCCGTGGAGG CTTCCATGAA TCCTGGGAGG GCCATGGAGG GCCAGGCCAT	GWSRAGRADP LNVTTAWKAQ FSPDGQIFLL MDSTLEFSAG Equence a #: NM_00: 482 21 1 GCAGCTCCAG CTGCTCCTGC CATTCCCGG CACTTCCCGA CAGCTACTAA GTGGGCCGCA CAGCTACTAA GTGGGCCGCA ACAGAAGAT TTGCCACCACC	HSLCYDITVI NPVLREVVDI PDSERRHHTT APLANSSTT 1898-1 11 CTTTGTGCTC GTGGCACCTCT GTGGCACCTAT CAGCGAGTAT CAGCGAGTA CCATATGTAG CCTTGGTGAAGA	PREFREDRIC LTEQUED IQUE VHEGARIONE QURATATTLI VHEGARIONE QURATATTLI VHEGARIONE AGCOTTANCOLAGACOTTANCOLAGACOTTCANGTOCCAG ACAGTICTIC ATCAGGTTTTCCCAGGTTTTCCCAGGCCCCC	AVQQQVDERT ENTPREPUT KWEENDKVVAM LCCLLIILPC 51 GAGACCATGG CTGACCTGGA CTCAATGATG ACCAAAGATG CCTAAATGATG ACCAAAGATGT TCTTTTGAGA CAAGAATGT TGTAGTGGTC	120 180 240 60 120 180 240 300 360 420 480 540
50 55 60	FLHYDOMKT LQARMSCEQK SFHYPSMGDC FHLPGI Seq ID NO: Nucleic Ac: Coding seq GGCTCTCACC CCCAGTATCT GCCCCAGGTACT GCCCCAGGTACT ACTACTACAG ACTACTACAG ACTACTACAG ACTACTACAG ACTACTACAG ACTACTACAG ACTACTACAG ACTACTACAG ACTACTACAG	LCLPILLLIS VTPV9PLGK AEGHSSGWA AEGHSSGWA IGWLEDFLMG 600 DNA 81 dd Accession uence: 57 11 CTCCTCTCCT GAGTACCCTG GGAGACATAGG CCTTCCATGAGA CTTCCATGAGA GCCAGGCCAT ACTGGGGC GAGGGCTGAA ACTGGGGC GAGGGCTGAATAATA	GWSRAGRADP LNVTTAWKAG FSPDGOIFLL MDSTLEPSAG EQUENCE n 8: NM_00: 482 21 [GCAGCTCCAG CTGCTCCTGC ATAATCCCAG CACTTGCCA CAGTTACTAA GTGGGCCACAA AACAGAAGGT	HSLCYDITVI NPVLESVUDI PDSEKRMHIT APLAMSSGTT 1898-1 11 CTTTGTGCTC TGGCCACCCT GTGGCATCA GAGCAGGAGTA GAGCAGGCA CCATATGTAC TGCAGAGGAA CACCACCCCAC	PREFREDRIKO LTEGLRD TOL VEPGARKIKE QURATATTLI 41	S1	120 180 240 60 120 180 240 300 360 420 480
50 55 60 65	PLHYDOMKT LOARMSCEOK SPEYFSMODC PILDGI Seq ID NO: Nucleic Acc Coding seq COCCAAGAA ACTACTACAC ACTACTACA ACTACTACAC ACTACTACAC ACTACTACAC ACTACTACAC ACTACTACAC ACTACTACAC ACTACTACAC ACTACTACAC ACTACTACAC ACTACTACAC ACTACT	LICLPILLILIS VTPUSPIGKK ARGHSSOSNO IGMLEDFIMO 600 INA BI dd Accession ence: 57 11 TOCTICTICCT GAGTACCCTT GOMGNATGACCTT GOMGNATGACCTT GOMGNATGACCTT GOMGNATGACCTT GOMGNATGACCTT GOMGNATGACCTT GOMGNATGACCTT GOMGNATGACCT ACCESTIGACCT GAGGACCTATA ATOGCC GAAGGCTATATA ATOGCCC	GENERAGRADP LANTIANEAQ FSPRODO FILM PSPRODO FILM PSPRODO FILM STLEPSAG GUANCE 1	IBSLCTDITVI NPVLBEVUDI PUDERENHITI APLAMSGOTT 11 11 11 CTTTGTGCTC GTGGCATCT GTGGCATCT TCACCAGGTA GACCAGGA CCATATGTA TCACAGGAGA GGGAGCTC GTGGCACCA GGGAGCACT TCACAGGAGA TCACAGGAGA TCACAGGAGA TCACAGGAGA TCACAGGAGA TCACAGGA	PREFREDRIKO LTEGLRD TOL VEPGARKIKE QURATATTLI 41	AVGQVDEKT ENYTPKEPLT KNEEDKVYM LCCLLITEKC SI GAGACCATGG CTGACCATGG CTGACCATGG CCCAACTGG CCCAACTGG CCCAACTGG CCCACTGG CCCACTGG CCCACTGG CCCACTGG CAGGGGGGGG CCCACTGG CCCACTGG CCCACTGG CAGGGGGGGGGG	120 180 240 60 120 180 240 360 420 540 660
50 55 60 65 70 75	PLAINDOONNT LOANMASCEAN STEIPSMADC STEIPSMADC STEIPSMADC SEQ IN No. COGING SEQ COCCANAGE COCCCANAGE COCCCANAGE COCCCANAGE ACTACCTACA COCCCANAGE ACTACCTACA COCCCANAGE ACTACCTACA COCCCANAGE ACTACCTACA COCCCANAGE ACTACCTACA ACTACCTACA ACTACCTACA ACTACCTAC	LCLPHLLLLS VPWSPLGKK ARASSOSSAN 166LEPPING 1660LEPPING 160LEPPING 160LEPPING 160LEPPING 160LEPPING 160LEPPING 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GREAGRADE AND ALL CONTROL OF THE AND ALL CONT	I I I I I I I I I I I I I I I I I I I	### PREPROPRIED TO THE PROPRIED AVGQVDEKT ENYTPKEPLT KNEEDKVYM LCCULITURC 51 GAGACCATGG CTGACCATGG CTGACCATGG CTGACCATGG CTGACTGGA CTGACTGGA CCCAAGAATCG CCCAAGAATCG TCTTCGAGA CAAGAATCG TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA	120 180 240 60 120 180 240 360 420 540 660	
50 55 60 65 70	FLHTWOONNT LOAMMSCEAD FILED FI	LCLPILLILIS VTPUSPICIEN VTPUSPICIEN VTPUSPICIEN SOD DIA s. 1d Accession GAGNACCTR GAGN	INTERNATION INTERNATION	I I I I I I I I I I I I I I I I I I I	### PREPROPRIED TO THE PROPRIED AVGQVDEKT ENYTPKEPLT KNEEDKVYM LCCULITURC 51 GAGACCATGG CTGACCATGG CTGACCATGG CTGACCATGG CTGACTGGA CTGACTGGA CCCAAGAATCG CCCAAGAATCG TCTTCGAGA CAAGAATCG TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA	60 120 120 120 120 120 300 420 360 420 540 660 720	
50 55 60 65 70 75	FLHTWOONNT LOAMMSCEAD FILED FI	LCLPHALLLIS VPDVSPLGKK VPDVSPLGKK VPDVSPLGKK VPDVSPLGKK VPDVSPLGKK VPDVSPLGKK 600 DMA sid d Accession 57 11 11 11 11 11 11 11 11 11 11 11 11	INTERNATION INTERNATION	I I I I I I I I I I I I I I I I I I I	### PREPROPRIED TO THE PROPRIED AVGQVDEKT ENYTPKEPLT KNEEDKVYM LCCULITURC 51 GAGACCATGG CTGACCATGG CTGACCATGG CTGACCATGG CTGACTGGA CTGACTGGA CCCAAGAATCG CCCAAGAATCG TCTTCGAGA CAAGAATCG TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA TCTTCGAGA	60 120 120 120 120 120 300 420 360 420 540 660 720	

	WO 02/		TGTTTGCTCA				60
			GCTGCAAAGC				120
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35							
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45 50	GGACCCCAA TCGCTCCCCG CGCGTGTCTA CTCCATATCC CAAGCTAGGG CGGGGCAGGG CACCGGACGG CACCGGACGG CCCGGCCGG	ATCTGCACGT CCCTCACTCA CAAACTCAAC GAGGGGCCCC GGGACTGGAT GCGCTCCCAG CTGCGGCGGC CCGGGGGGCTC GAGCCCCACA	ACCAGCAGTC CTTTCTCCCG TCCCGGTTTC TCCCAGCATC CCGACCCCG GGCAGCAGC CGCCAGCAGC CGCCAGCAGC	AGCCGCCCCA CCCTCGGCCC CGTGCCTCTC TACCCCCTC GAGCAGCCAG GGATCTGGTG CTGCTGAGGG AGGTCCCTCG CAGACTGGCT	CGCAGGGACC GGCTCCCAG CACCGCTCGA CCAACCTCGG GTGAGCCCCG ACGCTGGGGC ATGGAGTTGG GGCCCCAGCC GCCAAGGCCA	GGCTTACCCC CTCTCACTT GTTCTCTACT GGGACCTAGC AAAGGTGGGG TGGAATTTGA GCCCGGCCCC CTCGCTGCCA CACTTTTGGC	120 180 240 300 360 420 480 540 600
	GGACCCCAA TCGCTCCCCG GGCTGTCTA CTCCATATCC CAAGCTAGGG CGGGCAGGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGGCCTG TABABGGGG	ATCTGCACGT CCCTCACTCA CAAACTCAAC GAGGGCCCC GGGACTGGAT GCGCTCCCAG CTGCGGGGGCTC GAGCCCCAG ACCCCAGGGGCTC	ACCAGCAGTC CTTTCTCCCG TCCCGGTTTC TCCCAGCATC CCCACCCCG GGGCAGGAGG CGCCAGCAGG CGCCAGCAGG CGCCAGGAGGT CCCCAGGGTG CCCAGGGTG CCCAGGAGGTG CCCAGGGTG CCCAGGGTG CCCAGGGTG	AGCCGCCCA CCCTCGGCCC CGTGCCTCTC TACCCCCCTC GAGCAGCCAG GGATCTGGTG CTGCTGAGGG AGGTCCCTCG GGGATCCGCT GGGCATGCGCT	CGCAGGGACC GGCCTCCGA CACCGCTCGA CCAACCTCGG GTGAGCCCCG ACGCTGGGGC ATGGAGTTGG GGCCCAGCC GCCAAGGCCC ATGTTGAGCC	GGCTTACCCC CTCTCTACTT GTTCTCTACT GGGACCTAGC AAAGGTGGGG TGGAATTTGA GCCCGGCCCC CTCGCTGCCA CACTTTTGGC TCCGGGGAGA	120 180 240 300 360 420 480 540 600 660
	GGACCCCAA TCGCTCCCCG CGCGTGTCTA CTCCATATCC CAAGCTAGGG CGCGGACGG CACCGGACGG CACCAGCACGG CCCGGGCCTG TAAAAGAGGC CCCGGGCCTG TAAAAGAGGC CCCAGCACT	ATCTGCACGT CCCTCACCTCA CAAACTCAAC GAGGGCCCC GGGACTGGAT GCGCCTCCCAG CTGGGGGGCTC GAGGCCCCACA ACTGCCACGT GGTCCCCGGA	ACCAGCAGTC CTITCTCCCG TCCCGGTTTC TCCCAGCATC CCGACCGG GGGCAGGAGG CGCCAGCAGC CCCGAGGAGG CCCGAGGAGG CCCAGCAGC CCCAAGCAGC CCCAAGCAGC CCCAAGCAGC CCCAAGCAGC CCCAAGCAGC CCCAAGCAGC CCCAAGCAGC CCCAAGGAGG CCCAAGCAGCAGC CCCAAGCAGC CCCAAGCAGC CCCAAGCAGC CCCAAGCAGC CCCAAGCAGCAGC CCCAAGCAGCAGC CCCAAGCAGCAGCAGC CCCAAGCAGCAGCAGCAGCAGCAGCAGCACACCACACCAC	AGCCGCCCA CCCTCGGCCC CGTGCCTCTC TACCCCCTC GAGCAGCCAG GGATCTGGTG CTGCTGAGGG AGGTCCCTCG CAGACTGGCT GGGCATGGCG GAAGAACAAG	CGCAGGGACC GGCCTCCCAG GACCCCGGC CCAACCTCGG GTGAGCCCCG ACGCTGGGGC ATGGAGTTGG GGCCCAGGCC GCCAAGGCCA TGTTTGAGCT GTGCAGGACC	GGCTTACCCC CTCTCTACTT GTTCTCTACT GGGACCTAGC AAAGGTGGGG TGGAATTTGG GCCGGGCCCC CTCGCTGCCA CACTTTTGGC TCGGGGAGA CCGTGCTGCCC	120 180 240 300 360 420 480 540 600 660 720
50	GGACCCCAA TCGCTCCCCG CGCGTGTCTA CTCCATATCC CAAGCTAGGG CGGGCAGGG CACCGGACGG CAGACAAGGC CCCGGGCCTG TAAAAGAGGC GCCAGCACT TCAACAGGAG	ATCTGCACGT CCCTCACCTCA CAAACTCAAC GAGGGGCCCC GGGACTGGAT GCGCTCCCAG CTGCGGGGGCTC GAGCCCCACA ACTGCCAGGA GGTCCCCGGA GGTGGGGGAA	ACCAGCAGTC CTTTCTCCCG TCCCGGTTTC TCCCAGCATC CCGACGGGTG CCCCACCCG GGGCAGGAGG CGCCAGCAGC CGCCAGCAGC AGGGGTG AAGGTGCT AAGGTGCT AAGGTGCTAACA	AGCCGCCCA CCCTCGGCCC CGTGCCTCTC TACCCCCTC GAGCAGCCAG GGATCTGGTG CTGCTGAGG AGGTCCCTCG CAGACTGGCT GGGCATGCGC GAGACAGACAAG ATGCCTGATG	CGCAGGGACC GGCCTCCCAG CACCGCTCGA CCAACCTCGG GTGAGCCCCG ACGCTGGGGC ATGGAGTTGG GGCCCCAGCC GCCAAGGCCA TGTTTGAGCT GTGCAGGACC GGCGCCAGCC	GGCTTACCCC CTCTCTACTT GTTCTCTACT GGGACCTAGC AAAGGTGGGG TGGAATTTGA GCCCGGCCCC CTCGCTGCCA CACTTTTGGC TCGGGGAGAA CCGTGCTGCC GTGTTGATAG	120 180 240 300 360 420 480 540 600 660 720 780
	GGACCCCAA TCSCTCCCCS GGCGTGTCTA CTCCATATCC CAAGCTAGGG CGGGGCAGGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGACGAC TAAAAGAGGC GCCAGCACT TCAACAGGAACT AGCTGCACT	ATCTGCACGT CCCTCACTCA CAAGGGGCCCC GGGACTGGAT GGGCTCCCAG CCGGGGGCTC GAGCCCCACA ACTGCCAGGT GGTCCCCGGA GGTGGGGGGA TGGACTTGGA AGTGCCAGT GGTCCCCGAA ACTGCAGGT GGTCCCCGAA ACTGCAGGT AGTGCCCCACA ACTGCAGGT AGTGCCCCACA ACTGCACCT ACTGCACCT ACTCCCACA ACTGCACCT ACTCCCACA ACTGCACCT ACTCCCACA ACTGCACCT ACTCCCACA ACTGCACCT ACTCCCACA ACTCCACA ACTCCCACA ACTCCACA ACTCCCACA ACTCCACA ACTCCCACA ACTCCCACA ACTCCACA ACCAGCAGTC CTITCTCCCG TCCCGGTTTC TCCCAGCATC CCCACCCCG GGGCAGGAG CGCCAGCAGG CGCCAGCAGG TACAGTCCT AAGGTGCTA CAGCTCAACA GGCCTCTCAC CTGGCCGCC	AGCGGCCCA CCCTGGGCC CGTGCCTCTC TACCGCCTC GAGCAGCCAG GGATCTGGTG CTGCTGAGGG AGGTCCCTCG CAGACTGGCT GGGCATGGGC GAAGAACAAG ATGGCTGATG CGCTGTCCCA TGGCTCTGCT	CSCAGGGACC GGCCTCCCAG GACCTCGAG CAACCTCGG GTGAGCCCCG ATGGAGTTGG GGCCCAGGC GCCAAGGCCA TGTTTGAGCT GTGCAGGACC GGCGCTCCTG GGCGCTCCTG GAGCAGGCG GAGCAGGCGT	GGCTTACCCC CTCTCTACT GTTCTCTACT GGGACCTAGC AAAGGTGGG TGGAATTTGA GCCGGCCCC CTCGCTGCCA CACTTTTGGC TCGGGGAGA CCGTGCTGCC GTGTTGATAG CCTAGGCGGC GCAGAGGGCCT	120 180 240 300 360 420 480 540 600 660 720 780 840 900	
50	GGACOCCAA TCGCTCCCCC GGCGTGTCTA CTCCATATCC CAAGCTAGGG CGGGCAGGG CAGCACAGGC CAGCACAGGC CCCGGCCTG TAAAAGGC GCCAGCACT TCAACAGGA AGATGGAACT AGCCTGCCCT CCCTGGGCTC	ATCTGCACGT CCTCACTCA CAAACTCAAC GAGGGCCCC GGGACTGGAT CTGCGGCCCCACA ACTGCCACGT GGGCCCCCCGGA ACTGCCACGT GGTCCCCGGA ACTGCCACGT GGTGCCCCGCGA ACTGCCACGT GGTGCCCCCGCGA CGGGCCCCCGCGCCCGCCGCCCGCCCGCC	ACCAGCAGTC CTTTTCCCG TCCCGGTTTC TCCCAGCATC CCCACGCGG CCCACCCG GGCAGCAGC CCCACAGCAGC CCCACAGCAGC GCCAGCAGC AGGCCAGCAC AGGCCAGCAC AGGCCAGCAC AGGCCAGCC AGGCCAGCC AGGCCAGCC AGGCCAGCC AGGCCAGCC AGGCCAGCC AGGCCAGCC AGGCCAGCC AGGCCAGCC AGGCCAGCC AGGCCAGCC AGCCAGCC	AGCCGCCCA CCTTGGCCC CGTGCCTCT TACCCCCTC GAGCAGCAG GGATCTGGTG CTGCTGAGGG AGGTCCCTCG CAGACTGGCT GGGCATCGCT GGGCATCGCT GGGCATCCCC GAAAACAAG ATGGCTGATG GGCTGTCCCA TGGCTCTCCCT CCCCCGAAGG	CICAGGGACC GGCCTCCAG CACGCTGGA CCAACCTGGG GTGAGCCCGG ATGGAGTTGG GGCCCAGCC GCCAGGCC GCCAGGCC GTGAGACC GTGCAGCC GTGCAGCC GTGCAGACC CTGCCCTGGG GAGCAGCGC CCCCCGCCT CCCCCCGCCT	GGCTTACCCC CTCTCTACT GTTCTCTACT GGGACCTAGC AAAGGTGGGG TGGAATTTGA GCCGGCCC CTCGCTGCCA CACTTTTGGC TCCGGGGAA CCTGCTGCCA CCTGCTGCCC GCTGCTGCC GCAGGGCCC GCAGGGCCC GTCTGGCCG GTCTGGCCGT GTCCTGGCCT GTCCTGGCCT	120 180 240 300 360 420 540 600 720 780 840 900 960
50	GGACCCCAA TCGCTCCCCG GCGGTGTTA CTCCATATCC CAAGCTAGGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGACGG CAGACAAGGC CCCGGCCTG TAAAAGAGGC CCCAGCACT CCAACAGGAACT CAACAGGAACT CAACAGGAACT CCCCTGGCCTC CCCTGGGCTC CCCCCGCCGGCCCGA	ATCHICACOT CCCTCACTCA CARACTCAAC GAGGGCCCC GGGACTGGAT GCGCTCCAG CTGGGGGCCC GAGGCCCCACA ACTGCACACA ACTGCACACA GGTCCCCGGA GGTGCCCGGA GGTGGGGGAA GTGGCCCACC GGGGCCCCGC CGCCCCGCC CCCCCCCCCC	ACCAGCAGTE CTTTTCCCCG TCCCGGTTTC TCCCAGCATC TCCCAGCATC CCGACGCGG CCGACCCG GGCAGAGGG GTACAGCGG GTACAGCGG GTACAGCGC GGCAGCGCC CTGCCCCC CTGCCCGCCC CTGGCCGCCC CGGGCGACCCC CGGGGAGAGACGCA CGGGGAGACGCA CGGGGAGACGCA CGGGGAGACGCA	AGCGCCCA CCCTTGGCCC CGTGCCTCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCCCC	GICAGGALC GIGCTTCCAG CACGCTTGA CCAACTCGG GTGAGCCCG ACGCTGGGC ACGCTGGGCC ACGCTGGGCC ACGCTGGGCC ACGCTGGGCC GCCAAGCCCA GCCCAGCC GCCAAGCCCA GCCCTCCTG GAGCAGCCC CCCCCCCCC CTGCCCGGCT GTGCAGTGGA	GGCTTACCCC CTCTCTACTT GTTCTCTACT GGGACCTAGC TGGAATTTGA GCCGGCCCC CTCGCTGCCA CACTTTTGGC TCGCGGCAC CCTTGCTGCA CCTTGCTGCA CCTTGCTGCATA CCTAGGGGCC GCAAGGCCT GTCCTGGCGT GTCCTGGCGT AGACCCGGC	120 180 240 300 360 420 540 600 720 780 840 900 960 1020
50 55	GACCOCCAA TCGCTCCCCAA TCGCTCCCCCA TCGCCTCTCATATCC CAAGCTAGGG CAGGCAGGG CACGGGCAGGG TAAAAAGGG CCCCAGCAC TCAACAGGT TCAACAGGT TCAACAGGT AGCTTGCCT CCCTGGGCT CCCTGGGCT CCCTGGGCT CCCCCGCGGG GGCGCCCCC	ATCHORACUT CCCTCACTOR CARACTCRAC GAGGGCCCC GGGACTGGAT GGCCTCCAG GTGCCCAG GTGCCCAG GTGCCCAG GTGCCCAG GTGCCCAG GTGCCCAG GTGCCCCCG GTGCCCCCC GGGCCCCC GGGCCCCC GGGCCCCC GGGCCCCC GGGCCCCGC CCACCTGCCG GCACCCTCCCG GCACCCTTCCT	ACCAGCAGTE CTTTCTCCCG TCCCGGTTTC TCCCAGCATC CCGACCCG GGCCAGGAGG GGCCAGGAGG GGCCAGGAGG GTACAGTCCT AAGGTGCTAACA GGCCTCTCCA GGCCTCCCC GGGGAGCGC GGGGAGCGC GGGGAGCGC GGGCCGGGG	AGCCOCCCA CCTTCCTTACCCCCTC GGTGCTTCT TACCCCCTC GAGCAGCCAG GGATCTGGTG CTGCTAGGG AGGTCCCTCG CAGACTGGCT GAGCAATGGCT GAGCAATGGCT GAGCATGGCC GAAAAACAAG ATGGCTTACCCA TGGCTTCCCA TGGCCTCCCC CCCCGGAAGG CGCCCCCCCC CCCCCGCACGC CCCCCCCC	GICAGGALC GICCTCCA GICCTCCA CACGCTGA CCAACCTCGA GIGAGCCCC ACGCTGGGGC GICCAAGCCC GICCAAGCCC GICCAAGCCC GICCAGGCC GICCAGGCC GICCAGGCC CIGCCCGCCC CIGCCCGCC CIGCCCGCCT GICCAGGCC TICCAGGCC TICCAGGCC TICCAGGCC TICCAGGCC TICCAG	GGCTTACCCC CTCTCTACT GTTCTCACT GTTCTCACT GGGACCTAGC AAAGGTGGG TGGAATTTGA GCCCGGCCC CTCGCTGCCA ACTTTTGGC CTCGGGGAGA CCTTGCTGCCG GTGTTGCTGCC GCAGAGGCCT GTCTGGCGT GCAGAGGCCT GTCTGGCGT TCTGCTGCT TCTGCTGTTT AGACCCGGC TCTTGCCTT	120 180 240 300 420 480 540 600 660 720 780 840 900 960 1020
50	GGACCOCCAA TCGCTCCCCA TCGCTTCTA TCCCATATCC CAAGCTAGGG CGCGGCAGGA CACGGACGG CCCAGCACT TCAAAAAGGG GCCCAGCACT CCCTCGGCCT CCCTCGGCCT CCCCCGCGGG GGCCGCCC CCCGCGGGGCT CCCCCGCGGG	ATCHORACUT CCCTCACTOR CARACTCRAC GAGGGCCCC GGGACTGGAC GGGCCCCCAG GGCCCCAG GGGCCCCAG GGGCCCCAG GGGCCCCAG GGGCCCCAG GGGCCCCAG GGGCCCCAG GGTCCCGGGGAC GGGCCCCGC CGGGGGCCCC CGCCCGCGGGGAC CGCCCCGCC CCACCTCCCG CCCCCCGCGCGC CCCCCCCCCC	ACCAGCAGTE CTTTCTCCCG TCCCGGTTTC CCCAGCATC CCGACCCG GGCCAGCAG GGCCAGCAGC CCCAGCAGC GGCCAGCAGC CCCAGCAGC CCCAGCC CCCAGCAGC CCCAGCC CGGCCAGC CGGCCCGGC CGGCCCGGC CGGCCGGGC CGGCCTGGGC CGGCCCGGCC CGGCCTGGGC CGGCCTGGGC CGGCCTGGGC CGGCCTGGGC CGGCCTGGGC CGGCCTGGGC CGGCCTGGGC CGGCCCGGCC CGGCCCGCC CGGCCCGCC CGGCCCGCC CGGCCCGCC CGCCCGCC CGCCCGCC CGGCCCGCC CGCCCCC CGCCCCCC	AGCCOCCA COTTOCOCA GRACAGO GRA	GICAGGALC GOCCTOGA CACGGTGGA CACGTGGAG GTGAGCCCA ACGCTGGAG GCCAAGC GCCAAGC GCCAAGC GTGTTGAGC GTCCAGAC GCCACG GCCCACG GCCACC CGCCCCG GTCCAGC GTCCAGC GTCCAGC CCCCCGCC CCCCCCCC CCCCCCCC CCCCCCCC	GGCTTACCCC CTCTCTACT GTTCTCACT GGGACCTAG AAAGGTGGG TGGAATTTGA GCCGGGCCC CTGGTGCCA CACTTTTGGC CACTTTGGC GCTGTGCTGC GCAGGGCC GTGTGCTGC GCAGGGCC GTCTTGGCGC GTCTTGGCGC GTCTTGGCGC GTCTTGGCGC GTCTTGCCGCT GCCGGGGCC CTGCCTGC	120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1140 1200
50 55	GGACCOCCAA TCGGTCCCCAA TCGCTCCCCAA TCGCTCCAATCCC CAAGCTAGGG CGGGGCAGGG CAGGACAAGGC CCCAGGCACT TAAAAAGAGGC CCCAGGCACT TCAACAGGAA AGCCTGCCCT CCCTGGGCTC CCCTGGGCTC CCCCGCGGGGGGGG	ATCHORACH CONTROLOGY CONTROLOGY CARACTERAC GAGGGCCCC GGGGCTCCAG GGGCCCCCAG GAGCCCCACA ACTGCAGGGCAC GTGGGGGGAC GTGGGGGAA GTGGGGGAA GTGGCAGAA GTGGCCACA GTGGCCACA GTGGCCCGA GTGGCCCCG GCACCTCCC GCACCTTCCC GCACCTGCG CCGCCTGCG	ACCAGCAGTE CTTTCTCCAGCATT CCCAGCATTC CCCACCCCG GGCCAGCAGG GGCAGCAGG GGCAGAGAG GCCAACCAG AGGGTA AGGTGCTA AAGGTGCTA AGGTCAACA CTGGCCGCC CGGGGAACAC CTGGCCGCC CGGGGAACAC CGGCCTCCC CGGGGAACAC CGGCCCGCGC CGGGGAACAC CGGCCCGGGG	AGCCIOCCA COCTIGOCO COTTGCCTCT TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCTC TACCCCCCCC	GUCAGGGAC GOCCTCOA CACCACTGGA CCAACCTGGA CTGAGCCCA ACGCTGGGGC GCCAAGGCCA TGTTTGAGCT TGTGAGGCCC GGCCCTCGG GTGAGCCCCCCCCCT TGTCAGGAC CCCCCCCCT TGCCAGGAC CCCCCCCCCT CCCCCCCCT TGCCAGTGGA TGCAGCCCCA CCCCCCCCCC	GGCTTACCCC CTCTCTACT GTTCTCTACT GGGACCTACC GGGACTACC GGGACTGCA AAGGTIGGG TGGAATTTGA CACTTTGGC TCGGGGAGA CCGTGCTGCCA CCTGCTGCCA GTTTGATAG CCTAGGCGC GCAGAGGCCT GTCCTGGCGT GTCCTGCGT TCCTGGCGT CCAGGGGGGG CCAGGGGGGCCCCCCCCCC	120 180 240 300 360 420 660 720 840 900 900 1020 1080 1140 1200
50 55	GGACCOCCAA TCGGTCGCCAA TCGGTCGCCAA TCGGTCGCCAA TCGCTAGGCAC CAAGCTAGGC CACGGCACGCAC TCAAAGAGGC CCCAGGCACT TCAAAAGAGGC TCCACCGCGCAA AGCCTGCCCCCCCGCCGA GGCCCCCCCGCCGG GGCCCCCCCCC	ATCHORACIT CONTRACTOR CANACTORAC CARGOGOCOCO GGARTICAT CCGCTCCCAG GGACTCCAA CTGCCACA CTGCCACA CTGCCACA CTGCCCACA CTGCCCACA CTGCCCACA CTGCCCACA CTGCCCACA CTGCCCACA CTGCCCACA CTGCCCACA CTGCCCCCC CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CCACCTGCCG CTGGTGCGC CAGCCTGCCC CACCTGCCG CCACCTGCCG CCACCTGCCC CCACCTGCCC CCACCTGCCC CCACCTGCCC CCACCTGCCC CCACCTCCC CCACCTCCC CCACCTCCC CCACCTCCC CCACCTCCC CCACCTCC CCACCTCC CCACCTCC CCACCTCC CCACCTCC CCACCTCC CCACCTCC CCACCTCC CCACCTCC CCACCT CCACCT	ACCAGCAGTA CONTITUTE CONTI	AGCCGCCCCA GTIGCTCTC GTIGCTCTC GAGCAGCCAC GAGCAGCCAC GAGCAGCCAC GAGCAGCCAC GAGCAGCCAC GGCCATGCCC GGCCATGCCC GGCCATGCCC GGCCATGCCC GGCCATGCCC GCCCGCCAA GGCCCGCCC GCCCGGCCAC GCCCGGCCAC GCCCGGGCCA GCCCGGGGCC GCCCGGGGGC	GICAGGACAC GOCCTCGGAC CACCTGGGAC GTGAGCCCA ACGCTGGGGC ACGCTGGGGC ACGCTGGGGC ACGCTGGGGC ACGCTGGGGC ACGCCAACC ACGCTGGGGC ACGCCAACC ACCCAACC ACC ACCCAACCAACC ACCCAACCAACC ACCCAACCAACCAACC ACCCAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	GGCTTACCCC CTCTCTACTT GTTCTCACTT GTTCTCTACTT GGGACCTAGC AAAGGTGGGG GGGACCTCC CCGGGCCCC CCGGGCCCC CCGGGCCCC CCGGGCCCC CCGGGCCCC CCGGGGCCCC CCTGGGGGCCC GCTTTGGC GCAGGGGGCCCCC GCGGGCCCCC CCGGGGCCCCC CCCCGGGGCCCCC CCCCGGGGC	120 180 240 300 360 420 480 600 660 720 840 900 900 1080 1140 1200 1260 1320
50 55 60	GGACCOCCAA TCGGTCCCCAA TCGGTCCCCC GGGGGTGTTTA TCGCTTCCC CAAGCTAGGG GGGGCAGGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGACGG CACCGGCCT CACCGGGCCT CACCGGCCCT CACCGGCCCT CACCGGCCCT CACCGGCCCT CACCGGCCCT CACCGCGCCCT CACCGCGCCCT CACCGCCCCC CACCGCCCC CACCGCCCC CACCCCCCC CACCGCCCC CACCCCC CACCGCCCC CACCCCC CACCGCCCC CACCCCC CACCGCCCC CACCGCCCC CACCCC ACCCC CACCC ATCHORACIT COTPONETO CARACTERAC CARACTERAC GAGGGCCCC GGGGCTCCAG GGGCCCCCAG GAGCCCCACA ACTGCAGGGCAC GAGCCCCACA ACTGCAGGAC GTGGGGGGAC GTGGGGGGAA GTGGCGGGAA GTGGCCACA GTGGCCACA CTGGCAGGT CGCCCGGA GTGGCCACC CGCCCCGC CCACCTTCCC GCACCTTCCC GCACCTTCCC GCACCTTCCC GCACCTGCCC CCGCCTGCCC CCCCTCCCC CCGCCCTGCCC CCGCCTGCCC CCGCCTGCCC CCCCCTCCCC CCCCCCCC	ACCAGCAGTOR CTTTCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	AGCCIOCCA COTTGCOCA COCA COCA COCA COCA COCA COCA COCA	GUCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	GGCTTACCCC CCCCGGGCCC CCCCCCCCCCCCCCCCCC	120 180 240 300 360 420 420 600 660 720 780 840 900 960 1020 1140 1200 1260 1320 1380	
50 55	GGACCOCCAA TCGGTCCCCAA TCGGTCCCCC CAGGCTGTCTA TCCATATGC CAGGCTAGGG CAGCCAGCAGC CAGCCAGCAGC CAGCCAGCAGC CAGCCAGC	ATCIVACADI COCTUCATO ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA ANALOTICA GARGE GEORG GEO	ACCAGCAGTOR CTTTTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	AGCCGCCCCA CCCCGCGCCCCCCCCCCCCCCCCCCCCC	GUCAGGGACCE GUCAGGGACCE GUCAGGGACCE GUCAGGGACCE GUCAGGCACCE GUCAGCACCE CE GUCAGCACCACCE GUCAGCACCACCACCACCACCACCACCACCACCACCACCACC	GGCTTACCCC CTCCTATACCCC GGGACCTAGC ANAGGTGGGG CTGGACTTGC CTGGACTTGCA CCTGGCGCCC CTGCTGCA CCTTTTGGC CTGGGGACC GCTGCATAGC GCTGCATAGC GCTGCATAGC GCTGCATAGC GCTGCATAGC GCTGCATAGC GCTGCATAGC GCTGCCTC GCCCCG GCCCCC GCCCCGGGCT CCCCCCGGGGT CCTGCGCT CCCCCCGGGGT CCCCCCGGGGGCACC GCCCCCCCCCC	120 180 240 300 360 480 540 600 720 780 840 960 1020 1140 1200 1320 1380 1410 1500
50 55 60	GGACCOCCAA TCGGTCGCCAA TCGCTTCGCCAA TCGCTTCGCAA TCCCTTATCC CAAGCTAGGG CAGCCAGCACT TAAAAAGAGC CCCAGCACT TCAACAGGA AGATGGAACT CCCCAGCACT CCCTTGGGCCC CCCTTGGCCC CCTTGGCCC CCCTTGCC CCCTTCC CCCTTGCC CCCTTGCC CCCTTGCC CCCTTCC CCCTTGCC CCCTTGCC CCCTTCC CCCTTGCC CCCTTGCC CCCTTCC CCCTTCC CCCTTGCC CCCTTCC CCC	ATCIVICACUT COCTICATOR CARACTCRAC CARACTCRAC CAGGGGCCCC GGGACTGGGAT CGGCTCCCAG CTGCUGCCGC CGGGGCTC GAGCCCCACA ACTOCCACA CTGCUGCGGCC CGGGGGCTC CAGGCCCCACA CTGCCCCACA CTGCCCCCACA CTGCCCCCACA CTGCCCCCACA CTGCCCCCCACA CTGCCCCCCCACA CTGCCCCCCCCCC	ACCAGCAGTE CTTTCTCCCG TCCCGGTTTC TCCCAGCATC CCGACAGCATC CCGACAGGATC CCGACAGGATG CCCCAGCAGGATG CCCCAGCAGGATG CCCCAGGAGAGAGG CCCAGGAGAGAGG CCCAGGAGAGAGG CCCAGGAGAGAGA	AGCCACCCA COCTOGOCO COTOGOCO COTOGOCO COTOGOCO COTOGOCO COCTOGOCO CTOGOCO COCTOGO	GUCAGGGACC GOCAGCGAC GOCACCCCA GOCACCCCA GOCACCCCA GOCACCCCA GOCACCCCA GOCACCCCA GOCACCCCA GOCACCCCA GOCACCCCA GOCACCCCA GOCACCCCA GOCACCCC GOCACCCC GOCACCCC GOCACCCC GOCACCC GOCACCC GOCACCC GOCACCCC GOCACCC OCACCC OCACCC GO	GGCTTACCCC CTCCTTACTC GTTCTTACTT GTTCTTACTT GTTCTTACTT GGGACTAGC ANAGGTGGGG CTCGGGCCCC CTCGGGGCCCC CTCGGGGCCCC CTCGGGGAAAAAC CCTAGGGAAAAAC CCTAGGGAAAAAAC CCTAGGGAAAAAAC CCTAGGGAAAAAAC CCTAGGGAAAAAAC CCTAGGGAAAAAC CCTAGGAAAAAC CCTAGGAAAAAC CCTAGGAAAAAC CCGGGCTCTC CCCCGGGGCTCCT CCCTGGCTT	120 180 240 300 360 480 540 660 720 720 720 1080 1140 1200 1260 1380 1440 1560
50 55 60	GGACCOCCAA TCGATCCCAA TCGATCCCAA TCCATATCC CAAGCTAGGG CACGGAGGA CACGGAGGAGGA CACGGAGGAGA CACGGAGGACT CAACAGGAA AGACTAGGG CCCCGGCGGG AGACAAAGGACT CCAACAGGAACT CCACCGGCGGG GGCCCCGCGGGGGC CCCCGCGGGGGCCCCCT CCCCCGCGGGGCCCCCT CCCCCGCGGGGCCCCCT CCCCCGCGGGGGCCCCCCCC	ATCHICACOT COTCACTO ATCHICACOT COTCACTO ATCHICACOT	ACCAGACATE CTTTCCCCG TCCCGGTTTC TCCCAGCATC CCGACACGCTTC CCGACACGCTG GGCAGAGGATC CCGACAGGATC CCGACAGGATC CCGACAGGATC CCGCAGGATC CCGCAGGATC CCGCAGGATC CCGCAGGATC CCGCAGGATC CCGCAGGATC CCGCCC GGGGACCCC GGGGACCCC CGGCCGCC CGGCCCCC CGCCCCC CGGCCCCC CGCCCC GCCC CGCCC CGCCC CGCC GCC CGCC CGCC CGCC CGCC CGCC CGCC CGCC CGCC CGCC CGCC CGCC CGC CGC CGCC CGC CGCC CGC CGCC CGC CGC CGC CGC CGC CGCC CGC CGC CGC CGC CGC CGC CGC CGC CGC CG	AGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGCTAACCCC CTCCTAACTT GTTCTTACTT GTTCTTACTT GGGACCTAGC ANAGGTGGGG CCC CTCGGCGCCC CTCGGCCCC CTCGGCCCC GTGTTGATAG GCCGGCCCC GTGTTGATAG GCTGGCGCC GCAGGCCC GCAGGCCC GCAGGCCC CTCGCCCC GCGCGCC GCGCCC CTCGCCCC GCGCGCC GCGCCCC GCGCGCCC GCGCGCCC GCGCGCCC GCGCGCCCC GCGCGCCCC GCGCGCCCC GCGCGCCCC GCGCCCCC GCGCCCCC GCGCCCCC GCGCCCCC GCGCCCCC GCGCCCCC GCGCCCCC GCGCCCCC GCGCCCCC GCCCCCC	120 180 240 300 360 480 540 660 720 780 900 900 1080 1140 1200 1260 1320 1380 1440 1500 1500
50 55 60 65	GRACCOCCAA TOGOTCOCCAO GGGTGTCTA TCGCTTCCCCG GGGTGCAGG CACCGGACGG	ATCHICAGOT COTTACTO CANAGTORAC ANACTORAC AGRIGGICOCO GGATTORAT GGATGCACA GGATGCACA GGATCCACA CACACTGCAGA CACACTGCAGA CACCTGCAGA CACCTGCAGA CCCTCACAG CCCTCCACAG CCCTCCACAG CCCTCCACAC CCCTCC	ACCAGCAGTC CTTTGTCCCG TCCCGGTTTC TCCCAGCATC CCCACCCCC CGCACCCCC GGGCAGGGGGGGGCC GGGCAGGGGGGGG	AGCCICCCCA COTTGGCCCTA COTTGGCCCTA AGCAGCCTA GAGCAGCCA GAGCTGAGCCA AGGCCCA GAGCTGAGCCA AGGCCCA GAGCTGAGCCA AGGCCCA GAGCTGGCCA AGGCCCA GGCCCAGCCA CCCCCACA GGCCCCAGCC GCCCGGGCAGC GCCCGGGCAG GCCCGGGCA GCCCGGGCAC GCCCGGGCAC GCCCGGCCAC GCCCGGCCAC GCCCCGCCAC GCCCGGCCAC GCCCGGCCAC GCCCGGCCAC GCCCGGCCAC GCCCCGCCAC GCCCCCCCC	GEGAGGARCE GGCTCCABC GGCTCCABC GGCTCCABC GGCTCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCABC GGCCCABCC GGCCCCABC GGCCCABC GGCCCCABC GGCCCABC GGCC	GGCTTACAGG GGGCTGAGG GGGCGCGG GGGCCGGG GGGCCGGG CCGGGCGC CCGGGCCGC CCGGGCCGC CCTGGGCCGC CCTGGGCCGC GCGGCGCC CCTGGGCCGC GCGGGCC CCTGGGCCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC CCTGGGCCGC GCGGGCGC CCGGGGGGG GCGGGC	120 180 240 300 480 540 660 720 840 900 1020 1120 1260 1320 1320 1340 1560 1560
50 55 60	GRACCOCCAA TOGOTCOCCAO GGGTGTCTA TCGCTTCCCCG GGGTGCAGG CACCGGACGG	ATCHICAGOT COTTACTO CANAGTORAC ANACTORAC AGRIGGICOCO GGATTORAT GGATGCACA GGATGCACA GGATCCACA CACACTGCAGA CACACTGCAGA CACCTGCAGA CACCTGCAGA CCCTCACAG CCCTCCACAG CCCTCCACAG CCCTCCACAC CCCTCC	ACCAGCAGTC CTTTGTCCCG TCCCGGTTTC TCCCAGCATC CCCACCCCC CGCACCCCC GGGCAGGGGGGGGCC GGGCAGGGGGGGG	AGCCICCCCA COTTGGCCCTA COTTGGCCCTA AGCAGCCTA GAGCAGCCA GAGCTGAGCCA AGGCCCA GAGCTGAGCCA AGGCCCA GAGCTGAGCCA AGGCCCA GAGCTGGCCA AGGCCCA GGCCCAGCCA CCCCCACA GGCCCCAGCC GCCCGGGCAGC GCCCGGGCAGCC GCCCGGGCAGC GCCCGGGCAC GCCCGGGCAC GCCCGGCCAC GCCCGGCCAC GCCCCGCCAC GCCCCCCACA GCCCCCCCC	GEGAGGARCE GGCTCCABC GGCTCCABC GGCTCCABC GGCTCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCABC GGCCCABCC GGCCCCABC GGCCCABC GGCCCCABC GGCCCABC GGCC	GGCTTACAGG GGGCTGAGG GGGCGCGG GGGCCGGG GGGCCGGG CCGGGCGC CCGGGCCGC CCGGGCCGC CCTGGGCCGC CCTGGGCCGC GCGGCGCC CCTGGGCCGC GCGGGCC CCTGGGCCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC CCTGGGCCGC GCGGGCGC CCGGGGGGG GCGGGC	120 180 240 300 360 480 540 660 720 780 900 900 1080 1140 1200 1260 1320 1380 1440 1500 1500
50 55 60 65	GRACCTCCAA TOGOTCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ATCHICAGOT CONTINUENT AND TO THE ATCHICAGOT AND TO THE ATCHICAGO AND TO THE ATCHICAGO AND THE ATCHICAG	ACCAGAGATE TECCHAGATA TECCHAGAT TECCHAGATA TECCHAGATA TECCHAGATA TECCHAGATA TECCHAGATA TECCHAGAT	AGCCICCCCA COTTAGCCCTA COTTAGCCCCTC GAGCAGCCA GAGCTGGGGC CAGCCTGGCC CAGCCCAGCC	GEGAGGARCE GGCTCCABC GGCTCCABC GGCTCCABC GGCTCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCABC GGCCCABCC GGCCCCABC GGCCCABC GGCCCCABC GGCCCABC GGCC	GGCTTACAGG GGGCTGAGG GGGCGCGG GGGCCGGG GGGCCGGG CCGGGCGC CCGGGCCGC CCGGGCCGC CCTGGGCCGC CCTGGGCCGC GCGGCGCC CCTGGGCCGC GCGGGCC CCTGGGCCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC CCTGGGCCGC GCGGGCGC CCGGGGGGG GCGGGC	120 180 240 300 360 420 480 540 720 780 900 960 1080 1140 1200 1320 1320 1440 1500 1620 1620
50 55 60 65	GRACCTCCAA TOGOTCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCAC TOGOTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ATCHICAGOT COTTACTOR CANASTICANO GROSSICOTO	ACCAGCAGTO CTTTCTCCCG CTTTCTCCCG CTTCCCGGTTTC CCGAGCCTC CCGACCCCG GGGCAGCAGC GGGCAGCAGC GGGCAGCAGC GGCACCAGC GGCACCAGC GGCACCACCC GGCACCAGC GGCACCAGC GGCACCAGC GGCACCAGC GGCCACCCCG GGCCACCAGC GGCCACCAGC GGCCACCAGC GGCCACCAGC GGCCCACCC GGCCCCCC GGCCCCCC GGCCCCCCC GGCCCCCC	AGCCICCCCA COTTAGCCCTA COTTAGCCCCTC GAGCAGCCA GAGCTGGGGC CAGCCTGGCC CAGCCCAGCC	GEGAGGARCE GGCTCCABC GGCTCCABC GGCTCCABC GGCTCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCABC GGCCCABCC GGCCCCABC GGCCCABC GGCCCCABC GGCCCABC GGCC	GGCTTACAGG GGGCTGAGG GGGCGCGG GGGCCGGG GGGCCGGG CCGGGCGC CCGGGCCGC CCGGGCCGC CCTGGGCCGC CCTGGGCCGC GCGGCGCC CCTGGGCCGC GCGGGCC CCTGGGCCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC CCTGGGCCGC GCGGGCGC CCGGGGGGG GCGGGC	120 180 300 360 480 540 660 660 670 780 960 1020 1140 1260 1380 1560 1560 1560 1680 1740
50 55 60 65	GRACOCCCAN TOGOTICCCOS GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ATCHICAGOT CONTINUENT AND TO THE ATTORNO AND TO THE ATTORNO AND TO THE ATTORNO AND TO THE ATTORNO AND TO THE ATTORNO AND TO THE ATTORNO AND TO THE ATTORNO AND TO THE ATTORNO AND TO THE ATTORNO AND THE ATTOR	ACCAGAGTE TTTCTCCCC TTTCTCCCCC TCCCGGTTTC TCCCGGTTTC TCCCGGTTTC TCCCAGCATC TCCCGGTTTC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCACCCC TCCCACCCCC TCCCACCCC TCCCACCCC TCCCACCCC TCCCACCCC TCCCACCCC TCCCCCC TCCCCCCC TCCCCCC TCCCCCC TCCCCCC	AGCCICCCCA COTTAGCCCTA COTTAGCCCCTC GAGCAGCCA GAGCTGGGGC CAGCCTGGCC CAGCCCAGCC	GEGAGGARCE GGCTCCABC GGCTCCABC GGCTCCABC GGCTCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCABC GGCCCABC GGCCCCABC GGCCCCABC GGCCCCCCCCCC	GGCTTACAGG GGGCTGAGG GGGCGCGG GGGCCGGG GGGCCGGG CCGGGCGC CCGGGCCGC CCGGGCCGC CCTGGGCCGC CCTGGGCCGC GCGGCGCC CCTGGGCCGC GCGGGCC CCTGGGCCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC CCTGGGCCGC GCGGGCGC CCGGGGGGG GCGGGC	120 180 300 360 480 540 660 660 670 780 960 1020 1140 1260 1380 1560 1560 1560 1680 1740
50 55 60 65 70	GRACOCCCAN TOGOTICCCOS GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ATCHICAGOT CONTINUENT	ACCAGAGTE TTTCTCCCC TTTCTCCCCC TCCCGGTTTC TCCCGGTTTC TCCCGGTTTC TCCCAGCATC TCCCGGTTTC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCAGCATC TCCCACCCC TCCCACCCCC TCCCACCCC TCCCACCCC TCCCACCCC TCCCACCCC TCCCACCCC TCCCCCC TCCCCCCC TCCCCCC TCCCCCC TCCCCCC	AGCCICCCCA COTTAGCCCTA COTTAGCCCCTC GAGCAGCCA GAGCTGGGGC CAGCCTGGCC CAGCCCAGCC	GEGAGGARCE GGCTCCABC GGCTCCABC GGCTCCABC GGCTCCABC GGCAGCCABC GGCAGCCABC GGCAGCCABC GGCAGCABC GGCCCABC GGCCCCABC GGCCCCABC GGCCCCCCCCCC	GGCTTACAGG GGGCTGAGG GGGCGCGG GGGCCGGG GGGCCGGG CCGGGCGC CCGGGCCGC CCGGGCCGC CCTGGGCCGC CCTGGGCCGC GCGGCGCC CCTGGGCCGC GCGGGCC CCTGGGCCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC GCGGGCGC CCTGGGCCGC GCGGGCGC CCGGGGGGG GCGGGC	120 180 300 360 480 540 660 660 670 780 960 1020 1140 1260 1380 1560 1560 1560 1680 1740
50 55 60 65 70	GRACCICCIAN TOGOTICCOO GROSSINTEN TOGOTICCOO TOGOTICCOO TOGOTICCOO TOGOTICCOO TOGOTICCOO TOGOTICCOO TOGOTICCOO	ATCHICAGOT CENTRACTIC CANACTERIC CANACTERIC CANACTERIC CONTINETO C	ACCAGOAGTE TECTTTETCAGO TOCCAGTTTC TOCCAGTTTC TOCCAGTTTC TOCCAGTTTC TOCCAGTTTC TOCCAGTTTC TOCCAGTTTC TOCCAGTTTC TOCCAGTTC TOCC	AGCCICCOCA COCTOGGICCOCA COTTAGE COCTOGGICCOCA COCTOGGICCOCA COCTOGGICCOCA COCTOGGICCOCA COCTOGGICCOCA COCTOGGICCOCA COCTOGGICCOCA COCTOGGICCOCA COCCOCOCA COCOCA COCCOCA COCCOCA COCCOCA COCCOCA COCCOCA COCCOCA COCCOCA COCO	GECAGGGANCE GACCACCAGA GACCACCAGA ACCACTAGA AC	GGCTTACCCC CTCCTACTC GTTCCTCACTC GTTCTCACTC GCACCCCCTC GTCCTCCTCC GCACCCCCTC GTCCTCCTCC GCACCCCCTC GGACAACTCA GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACACCTC TCTCCTCCTCCTC GTCCTCCTCCTC GTCCTCCTCCTC GTCCTCCTCCTC GGACAACCTC GGACAACTCA GGACACTCA GGACCCTCAT TOTCCTCCTCCTC GTCCTCCTCCTC GGACAACTCA GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACCTCT TOTCCTCCTCACTC GGACACTCA GGACACTCA GGACACTCA GGACACTCA GGACCTCAT TOTCCTCCTCACTC GTCCTCCTC GTCCTC CCT GTCCTC GTCC GTCC GTCCT GTCCT GTCCT GTCCT GTCCTC GTCC GTCC GTCC GTCC GTCC GTCC GTCC GTCC GTCC GTCC GTCC GTCC GTC GT	120 180 240 360 420 420 420 660 660 6720 780 1020 1020 11200 10200
50 55 60 65 70	GRACCICCIAN TOSTICCCO GROSSIA TOSTICCCO GROSSIA TOSTICCCO GROSSIA TOSTICCCO GROSSIA TOSTICCCO GROSSIA TOSTICCCO GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICCC GROSSIA TOSTICC GROSSIA TOSTICCC ROSSIA TOSTICC TOSTICCC TOSTICC OSTIC TOSTI	ATCHICAGOT CANACTICAGO CANACTICAGO CANACTICAGO CONTROLO C	ACCAGAGATE TECTTETECOGO TOCCOGATTA TOCCOCAT TOCCOGATTA TOCCOCAT TOCCOGATTA TOCCOCAT TOCCOCA	AGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GECAGGGANCE GOCTOCOAG GOCT	GOCTINACCIC CICKTATACTI CICKTATACT CIC	120 180 240 300 420 420 420 420 660 660 6720 780 900 900 910 1020 11200 11320
50 55 60 65 70	GRACCICCCAN TOSTICCCO TOSTICCC TOSTICCCO TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICC TOSTICCC OSTICCC OSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC	ATCHICACOT CONTINUENT GRANTICA	ACCAGOAGTO TOCCAGTT TOCCAGOTT TOCCAG	AGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GUCAGGGGACC GUCAGGGGACC GUCAGGGACC GUCAGGGACC GUCAGGGACC GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGCA GUCAGCCA GUCAGCCA GUCAGCCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCCA GUCAGCCA GUCACCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCACCCA GUCACCA GUCACCCA UCACCCA GUCACCA GGCTTACCCC CTCCATACCC CTCCATACCC CTCCATACCC GGGACTTACC AAAGGT000 CTCGAGCGC CTCCATACC CTCGAGCGCC CTCCATACC CTCGAGCCC CTCCATACC CTCCATACCC TCCATACCC CTCCATACCC CTCCATACCC CTCCATACCC CTCCATACCC CTCCATACC CTCCATACCC TCCATACCC 120 180 240 360 420 420 420 660 660 720 780 1020 1020 11200 1380 11200 1380 1400 1500 1620 1620 1620 1620 1620 1630 1630 1630 1630 1630 1630 1630 163		
50 55 60 65 70	GRACCICCCAN TOSTICCCO TOSTICCC TOSTICCCO TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICC TOSTICCC OSTICCC OSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC TOSTICCC	ATCHICACOT CONTINUENT GRANTICA	ACCAGAGATE TECTTETECOGO TOCCOGATTA TOCCOCAT TOCCOGATTA TOCCOCAT TOCCOGATTA TOCCOCAT TOCCOCA	AGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GUCAGGGGACC GUCAGGGGACC GUCAGGGACC GUCAGGGACC GUCAGGGACC GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGGCA GUCAGGCA GUCAGCCA GUCAGCCA GUCAGCCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCCA GUCAGCCA GUCACCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCAGCCA GUCACCCA GUCACCA GUCACCCA UCACCCA GUCACCA GGCTTACCCC CTCCATACCC CTCCATACCC CTCCATACCC GGGACTTACC AAAGGT000 CTCGAGCGC CTCCATACC CTCGAGCGCC CTCCATACC CTCGAGCCC CTCCATACC CTCCATACCC TCCATACCC CTCCATACCC CTCCATACCC CTCCATACCC CTCCATACCC CTCCATACC CTCCATACCC TCCATACCC 120 180 240 300 300 360 420 660 780 860 1020 1080 1140 1260 1320 1560 1560 1660 1860 1860		

Seq ID NO: 606 DNA sequence Nucleic Acid Accession #: NM_057160.1

	Coding sequ	ence: 17	14				
	1	11	21	31	41	51	
5	CACCTGGGTG	TGATCTCAGC CCCTCTTTCT TGGCCGCTCT	CCCTGAGGCT GGCTCTGCTG	CCACTTGGTC	CAGAGGCCTC	CCTGGGCTCC	60 120 180 240
10	CAGCCTTCTC	GCCCTGCCCC GGGGACGCAC GGCCCGCGCC GGCTGGGG CGCAGCTGGT TCCGCTTCTG	CCCCCCCCCCC	GCACCCCCAT	CTGCTCTTCC	CCGCCGGGGGC	360 420 480
15	AGCCAGCCCT ACCTGGAGAA GCTCCAGGGC	GCCTACTGGG GCTGCCGACC CCGTGGACCG TTTGCAGACT	CGCCGGGGCC CACGCGCTAC CCTCTCCGCC GGACCCTTAC	GAAGCGGTCT ACCGCCTGCG CGGTGGCTCT	CCCCGGGCTC CCTTCATGGA GCTGCCTGG TCCTGCCTGG	CCGGCCCGTC CGTCAACAGC CTGAGGGCTC GACCCTCCCG	540 600 660 720 780 840
20	AGAGCCCTCA TTCGGACCCA CTGATGAACA TTGAAGGACA	CTAGCCAGCG TGATGGATAT CCCTGCGGAT CTTCTCACAG CTACAGTGGC CATATTGCAG	CCCAGCCTAA ACTCTGGCAC TGAGGCATCA TTGCTTGGTT	AAGACACCAG	AGACCTCAGC	TATGGAGCCC	900 960 1020 1080 1140
25	Seq ID NO:	GAGCTGGCCC 607 Protes cession #: 1	in sequence				
30	APRSPAPREG RAARAGGPGS	11 PLLEVLPPQA PPPVLASPAG RARAAGARGC LRPPPGSRPV	HLPGGRTARW RLRSQLVPVR	CSGRARRPPP ALGLGHRSDE	QPSRPAPPPP LVRFRFCSGS	APPSALPRGG CRRARSPHDL	60 120 180
35	Seq ID NO: Nucleic Ac: Coding sequ	608 DNA se id Accession sence: 29	1 # : NM_057	7090.1			
40	GTCCCACTGC	11 CTCCTGGTGT CCCTGGCCTA	GGCGGCAGGC	TCCACTTGGT	CTCTCCGCGC	AGCCTGCCCT	60 120
45	CGCGCCCCGC	CTGGCCGCTC AGCCCTGCCC GGGGGACGCA CGGCCCGCGC CGGGCTGGGG	CCCGCGAAGG CGGCCCGCTG	CCCCCCGCCT GTGCAGTGGA	GTCCTGGCGT AGAGCCCGGC	CCCCCCCCCCC	180 240 300 360 420
50	CAGCCTGGCC CAGCCAGCCC CACCTGGAGA	CGGGCTGGGG TCGCAGCTGG TTCCGCTTCT AGCCTACTGG TGCTGCCGAC ACCGTGGACC	GCGCCGGGGC CCACGCGCTA GCCTCTCCGC	CCTGCGACCG CGAAGCGGTC CACCGCCTGC	TCCTTCATGG GGCTGCCTGG	ACGTCAACAG GCTGAGGGCT	480 540 600 660 720 780
55	GCAGAGTCCC CTACCGGTGG	CTTTGCAGAC ACTAGCCAGC GTGATGGATA ACCCTGCGGA ACTTCTCACA ACTACAGTGG	GGCCTCAGCC TCATCCCCGA	AGGGACGAAG ACAGGTGAAG	GCCTCAAAGC GGACAACTGA GAGACCTCAG	TGAGAGGCCC CTAGCAGCCC CTATGGAGCC	780 840 900 960 1020 1080
60	TTTGAAGGAC CTCACTCATG	ACATATTGCA GGAGCTGGCC	CC	TGAAAGTGCC	TGTGCTGGAA	CTGGCCTGTA	1140
65	Seq ID NO: Protein Acc	ession #: 1	In sequence PP_476431.1	31	41	51 1	
70	GPPPVLASPA SRARAAGARG	LSHCPWPRRQ GHLPGGRTAR CRLRSQLVPV VSQPCCRPTR	WCSGRARRPP RALGLGHRSD	PQPSRPAPPP ELVRFRFCSG	PAPPSALPRG SCRRARSPHD	GRAARAGGPG	60 120 180
75		610 DNA se id Accession sence: 11	#: Eos se				
80	GCCTACCATG	11 AGCATTATCT GCTGCCCTAG TTGTGGCGGT ACATCACTGA TTGAGAAGAA	CGAGTGTACC	TGCTCCAGGG	ACCCCATGAG	GGAGTGCACC	60 120 180 240
85	TTCCAGGGCC	TTGAGAAGAA GCTATCTCAG TGGACAGCCT ACTTCTCCCA TCCCTGACGG	TGAGTCTCTC	CTTCTGTCCA	GTAACCAGCT	GTTGCAGATC	360 420 480 540

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	GGCAAGAATA GTCCTCCGGC	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCCTCCGGC	TGTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACTTT	TGATGGGCTT	660 720
		AGGAACTGGC ACCACAACCT					780
5	CCLCCCACACA	TCTTCATGCA	GCTCCCCCAC	CTCAACCCTC	TEACTCTCTT	TOCCOMOCIO	840
•	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
	TATGACAACC	ACATOTOTO	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCCTGATTC	TTAGCCGCAA GGGAGCTGTC	TCAGATCAGC	TTCATCTCCC	CGGGTGCCTT	CAACGGGCTA	1020
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10	TTCCGCATGT	TGGCCAACCT	GCAGAACATC	TCCCTGCAGA	MOCACCTCCA	CAGACAGCTC	1140 1200
	CTCGAGAACT	TCTTCGCCAA TGCCCCTCGG	CATCTTCGAT	CACCTGGGGA	AACTGTGTGA	GCTGCGGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCCTGCTC	1320
	AACCAGCCTA	GGTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCCAGC	CAATGTCCGA	1380
15	GGCCAGTCCC	TCATTATCAT	CANTGTCANC	GTTGCTGTTC	CAAGCGTCCA	TGTCCCTGAG	1440
	GTGCCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCGTCTCTT	CTACCACTGA	CACCCETTEC	CCTGTGGAAG	ACTACACTGA	COOCCTOCCC	1620
	ATTOCOGCCA	TTGTAATTGG	CATTGTCGCC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTCGGC	1680
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	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCCTAC	CTCTTCCTGA	CTTGCCTGAT	CCCCATCCCA	AGAAGCACCTCC	1980
25	GGATTTCCCGA	CTTCCTACAA TTCATACCCC	TOOGCTTCCT	TOGAGAGGGC	TCTTCCTCCA	AATCCTCCCC	2040
	ACCTGTCCTC	CAAGAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCCT	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	CCCCCTCTCG	2160
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30	ACCCAGCATG	TCCCCTCAAA CCTCAAAGAA	TGAAAGTTCT	CCCCTTGATT	CTTTCTGCTCCT	ACCCCCCCAAT	2280
50	CACCOTCCTT	TTGGGGATGC	TATCABAGAG	AGAAGGAAAA	TOATGOOGG	CAGTTCCTGG	2400
	AGACAGAAGA	GCCGTCATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAAGAAACA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTTAGAG	AAGGATATTT	CCARACTGCA	AACTTTGCTT	2520
35	TGAAAAGTTT	AGCCCTTTAA	GGAATGAAAT	CATGTAGAAT	TTTGGACTTC	TAAAAACATT	2580
33	AAAATCAGCT	TATTAATACG GTTTGTTTTA	GGATAGAGAA	AGAAATCTGG	TGCCTGGGGG	TCCCTGTGTT	2640 2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCCAGA	2820
	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCCATGA	GCCAGGACGG	2880
40	TCCCCCCACA	GTCAGCCTGT	GCAAAGGCCC	CCTCGCCACG	GGTGGAGGAG	AATATGTGGG	2940
	TOTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCCTG	3000 3060
	AGAGACCCTG	AGACCTGGGG CCACACCCTC	TTCCCTGCCA	GCCAGGTCA	TOTOGCTCAT	CGGAGGCCCC	3120
	TOUGOTTOGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTTAATT	TTCATTCTTC	3180
45	ACTTAGGGGA	AGTGAAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAACG	AAGTGTAACG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TGAACTTCAG	AATCTCACTT TCCCTGGAGC	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACACTGG	3360 3420
	TOTAGGGGGC	TTCTCCTCCT	CCACTCACAG	TCACACGAAT	ACCIGCCTTC	TCTGGCTTTC	3480
50	CTGCTATACA	CATATTCACA	TGGCGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
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	TCTTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGCTTTGG	TOTOGRAPATO	TACCACCAAT	3720 3780
55	COCCATOGG	TCTTATTAGC	TOCOGGGGGG	ACARGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCACG	TGCTGACCAG	TTTTCCCTTC	CAGTTCCTGC	ACAAAAAGTG	TCCAGAGGGC	3900
	TOTTTGCAAA	CACTAGTGCA	CTTTGTAGCT	TTTCACCCTC	TGTCCCAGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGAGTC	AAGAGATGTC	ATCCCCCCAG	GGTCTCCAAG	GCATTTCCAC	4020 4080
60	ACTATTGGTG	GCACCTGGAG	ATCACCOCCT	CATOGRAGO	MAGGCCAACA	GGTGCCAACA	4140
00	GGGGCATCCC	GCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGCCCAC	AGACCTGTCG	4200
	COTGCTCCTC	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCCTTA	4320
65	GGTATTCCTG	GCAGTAGCCA GTCCTCAGAT	TGACATTGGA	GCACCTTCCT	CTCCAGCCAG	AGGCTGACCT	4380
05	GAGGGCCACT	ACCTCTTGCC	TOPISOCHETE	TOTTATORGA	CHARTERIAGE	GGAGCCATTG	4500
	CCCTCCTTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGA	GTCTCCTTTC	CAACAGGATG	ATGCATTTGC	TCAATTCTCA	4620
=0	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCAGTTTT	4680
70	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGGAGTTA	4740
	GTGTTGGAGA	AGAAACAACA CTCTTCAAGC	AAAGCCAATT	AGAACCACTA	TTTTTTAAAAA	CCACCCCTCC	4860
	COVECGEGGG	CONCURRAC	CCACTTGTGA	TOGGGGTACAG	AGGCACTTGC	TCTTCTGCAT	4920
	GGTGTTCAAT	AGGCTGGGAG	TITTATTTAT	CTCTTCAAAC	TTTGTACAAG	AGCTCATGGC	4980
75	TTGTCTTGGG	CTTTCGTCAT	TAAACCAAAG	GAAATGGAAG	CCATTCCCCCT	GTTGCTCTCC	5040
	TTAGTCTTGG	TCATCAGAAC	CTCACTTGGT	ACCATATAGA	TCAAAAGCTT	TGTAACCACA	5100 5160
	GGAAAAAATA	AACTCTTCCA GTATATTGTT	TCCCTTAAAG	AATAGAATAG	CATACAAGAG	TCATGGGAAT	5220
	B & CHESTER C & TO	CCACACABET	TOTACABOTE	TTCAGATGCT	CATCTACACC	TATTCCCAAA	5280
80	GAACTTCCAA	ACTCAGGAAG	TTTGCAGAGA	GCAGACAGCT	AGAGATAACT	CGGGACCCAG	5340
	ACCOMPOSED AND ADDRESS OF THE PARTY OF THE P	CACATOTTAG	ATTEMPTOTA	COMPTAGOO	ATRABOCACT	CARAGATTCA	5400
	GCCCCCAGAT	CCCACAGTCA	GAACTGAATC	TGCGTTGTTG	GGAAGCCAGC	AGTGGCCTTG CCGGGGAAAA	5460 5520
	UGAAGGAAGC	CCCAGGTTTC	GITCAGAGAG	ANGGAGAGAG	CAAGCCACTT	ALCCCCCCCCC	5520
85	CTTCATGCTG	CCTTCAAAGC	TAGATCATGT	TTGCCTTCCT	TAGAGAATTA	CTGCAAATCA	5640
-	GCCCCAGTGC	TTGGCGATGC	ATTTACAGAT	TTCTAGGCCC	TCAGGGTTTT	CTGCAAATCA GTAGAGTGTG	5700
	AGCCCTGGTG	GGCAGGGTTG	GGGGGTCTGT	CTTCTGCTGG	ATGCTGCTTG	TAATCCATTT	5760

GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

	GGTGTACAGA	ATCAACAATA	AATAATATAC	ATGTAT			
	Seq ID NO:	611 Protei	n sequence				
5	Protein Acc	cession #: E	AB84587.1				
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	MPLKHYLLLL	VGCQAWGAGL	AYHGCPSECT	CSRASQUECT	GARIVAVPTP	LPWNAMSLQI	60
10	ENTHITELNE BOGLDGLESI.	SPFLNISALI LLSSNQLLQI	OPAHESOCSN	LKRLOLHGNH	LEYI PDGAPD	HLVGLTKLNL	120 180
	GKNSLTHISP	RVFQHLGNLQ	VLRLYENRLT	DIPMGTFDGL	VNLQELALQQ	NQIGLLSPGL	240
	FHINHNLORL	YLSNNHISQL	PPSIFMQLPQ	LNRLTLFGNS	LKELSLGI FG	PMPNLRELWL	300
	YDNHISSLPD	NVFSNLRQLQ SLQNNRLRQL	VLILSRNQIS	PISPGAFNGL	TELRELSLHT	NALQDLDGNV	360 420
15	VDNPWRCDSD	II.PLRNWI.I.L	NOPRIGIDITY	PVCPSPANVR	GOSLIINVN	VAVPSVHVPE	480
	VPSYPETPWY	PDTPSYPDTT	SVSSTTELTS	PVEDYTDLTT	IQVTDDRSVW	GMTQAQSGLA	540
	IAAIVIGIVA	LACSLAACVG	CCCCKKRSQA	VLMQMKAPNE	c		
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	Coding sequ	uence: 14	17				
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23		TGCTCAATTC AGAGTTCAGT					120
	TCTGGAGTGG	GAGCTGGGAG	TCAGTGTTGG	AGAAGAAACA	ACAAAAGCCA	ATTAGAACCA	180
	CTATTTTTAA	AAAGTGCTTA	CTGTGCACAG	ATACTCTTCA	AGCACTGGAC	GTGGATTCTC	240 300
30	CAGAGGCACT	TCAGCACCCC	CATGGGGGGGG	AATAGGCTGG	GAGTTTTATT	TATCTCTTCA	360
	AACTTTGTAC	TGCTCTTCTG AAGAGCTCAT	GGCTTGTCTT	GGGCTTTCGT	CATTAAACCA	AAGGAAATGG	420
	AAGCCATTCC	CCTGTTGCTC	TCCTTAG				
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40	MHILLNSQGW	NEPAGPPESW ILPKHWTWIL	SGVQSSVFLS	VYSSLTVPRP	SGVGAGSQCW	RRNNKSQLEP	60 120
40	NPVOELMACL	GLSSLNQRKW	RPFPCCEP	VPPLPTCDGV	OKHERSCHAR	MKLGVLFISS	120
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45	Coding sequ	uence: 77	1372				
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	Coding sequents	uence: 77	21 CCCTCCTGCC	31 GCAGGCCACC	GAGGCCGCCG	CCGTCTAGCG	60
45 50	Coding sequents Greecegeag	11 CGCCGTCGCG	21 CCCTCCTGCC GAGCCCTGCT	31 GCAGGCCACC GGCGCGCCTG	GAGGCCGCCG CTTCTCTGCG	CCGTCTAGCG TCCTGGTCGT	120
	Coding sequents I GTCCCCGCAG CCCCGACCTC GAGCGACTCC	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA	
	Coding sequence of the control of th	11 	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCAA CTCCAACATT	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG	120 180 240 300
50	Coding sequence of the control of th	11 	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGGC	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG CGGCCCTGCC	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCTGGAA	120 180 240 300 360
	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT CGAGGAAAGG GTCCTTCAGC CATAATTACT	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGGACTGA AAACGTACCA GCAGGAACCC	31 GCAGGCCACC GGCGCGCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGGC TGCCCACAGA AGACAACCGG	GAGGCCGCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCTTGGAA TTCAGCTGGG GGTGCTATGT	120 180 240 300 360 420 480
50	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT CGAGGAAAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACSTACCA GCAGGAACCC TTGTCCAAGA	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGGC TGCCCACAGA AGACAACCGG GTGCATGGTG	GAGGCCGCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCTTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAAA	120 180 240 300 360 420 480 540
50 55	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT CGAGGAAAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC TCTCCTCCAG ATTATTGGGG	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAGTACTT GTGAAATAGA CCAGCACTGA AAAGGTACCA GCAGGAACCA TTGTCCAAGA AAGAATTAAA	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGGC TGCCCACAGA AGACCAACGG GTGCATGGTG ATTTCAGTGT ATTTCAGTGTG	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT CATGACTGCG GGCCAAAAGA AACCAGCCCT	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA ACTGCCCAAA TTCAGCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTCTGCGGC	120 180 240 300 360 420 480
50	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT CGAGGAAAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC TCTCCTCCAG ATTATTGGGG	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAGTACTT GTGAAATAGA CCAGCACTGA AAAGGTACCA GCAGGAACCA TTGTCCAAGA AAGAATTAAA	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGGC TGCCCACAGA AGACCAACGG GTGCATGGTG ATTTCAGTGT ATTTCAGTGTG	GAGGCCGCCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT CATGACTGCG GGCCAAAAGA AACCAGCCCT	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA ACTGCCCAAA TTCAGCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTCTGCGGC	120 180 240 300 360 420 480 540 600 660 720
50 55	coding sequence of the control of th	11 GGCGTCGGG GCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT CGAGGAAAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC ATTATTGGGG AGGCACCGGG GTGATCAGGG GTGATCAGGG GTGATCAGGG	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA ACAGTACTT GTGAAATAGA AAGAATTCA GCAGGCACTGA AAAGAATTAAA AAGAATTCAC GGGGCTCTGT GCACACACTG GCGCCTCGT CCCCCACACTG	31 GCAGGCCACC GGCGGCCTG TCAAGATTCAA CTCCAACATT TAAGTCAACA AGCAACCG GGCACTGGG GTGCATGGG ATTCAGTGT CACCATCAGG CACCTACGAG CACCTACGAG	GAGGCCGCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG CGCCCTGCC TCTGATGCTC AGGCGACCCT CATGACTGCG GGCCAAAAGA AACCAGCCCT TCTGGAGGCC TCTTGGAGGCA TACCCAAAGA	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TCCCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA ACTGCGGC GCTTTCCGGC GCTTCATCAG AGGAGGACTA	120 180 240 300 360 420 480 540 600 660 720 780
50 55	coding sequence of the control of th	11 GGCGTCGGG GCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT CGAGGAAAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC TCTCCCAG ATTATTGGGG AGGCACCGGG GTGATCAGCG CTGGGTCGCCT	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA ACACGTACCT GTGCAACTACA AAGAATTACA AAGAATTACA GAGGGTACA GAGGATTCAC GGGGCTCTGT CACACACTG CACACACTT CACACACT	31 GCAGGCCACC GGCGGCCTG TCAAGATT TAAGTCAAAA CACCATGGGC TGCCACAGA AGACAACGG GTGCATGGT CACCATCAGTG TATTCAGTGT CACCATCAGTG CACCATCAGTG CACCATCAGTG CTTCAATCAGTG CTTCAATCAGTG	AGGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	CCGTCTAGOS TCCTGGTOGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAG TCTTGGGGC GGTTTGCGGC GCTCATCAG AGGAGGACTA TGAAGTTTGA ACCACAACGA	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60	coding sequence of the control of th	11 CGCCGTCGG GCACCATGA ANAGGCAGCA TOTOTOTCA GGGGAAGG GTCATCAG GTCATCAG CTAAATACT CTAAAGGCACGA ATTATTGGG GTGATCAGG GTGATCAGG GTGATCAGG GTGATCAGG GTGATCAGG GTGATCAGG GTGATCAGGG GTGATCAGGG GTGATCAGGG TGATCAGGG TGATCAGGG TGATCAGGG TGATCAGGG TGATCATGC TCTAACTTAC TGAAAGATAC	21 CCCTCCTGCC GAGCCCTGCT ATGACTTCA ACAGTACTA GTGAAATAGA CAGCACTGA AAACGTACCA GCAGGAACCC GCAGGAACCC GCAGGAACCC GCAGGAACCC GCAGCACCTG GCACCCTGT CCACACACTG CAAGGCTTAA ACAAGGACTTA ACAAGGACTTA ACAAGGACTA ACAAGGACTA ACAAGGACTA	31 GCAGGCCACC GGCGGCCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGG GTGCATGGTG ATTTCAGTGT ACTTCAGTGT CACCTACGAG CACCTACGAG CTCCATGAT CTCCAACACG CAGGGCTGAC CAGGGCTGAC	AGGCCGCCC GAGGCCACA GAGGCCACA ACCTGCTATG ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT CATGACTGCA GGCAAAAGA AACCAGCCT TGTGGAGGCA TACCCAAAGA ACCAGCCT AGGGGGAA ACGCTGCTC GGCGAGCAC GGCCAGCAC GGCAGCCAC GGCCAGCCA	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA AGGGGATTGG TGCCTTGGAA TTCAGCTGGAA TTCAGCTGGA TTCAGCTGGGG GGTGCTATGGAGCC GCTTGGGG GCTCATCAG AGGAGGACTAT TGAAGTTTTGA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	coding sequilibrium control co	111	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT ACAAGTACTT GTGAAATAGA CCAGCACTGA AAAGGTACCA GCAGGAACCC GAGAATTAAA GAGAGTTAAA CAAGGCTTTAA ACAAGGCTTCA ACAAGGCTTCA GTCCCACGAGA ACAAGGACTA CACACTG CACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACTG CACACACTG CACACACTG CACACACTG CAC	31 GCAGGCCACC GCAGGCCACAT TCAAGTTCCA CTCCAACATT TAAGTCAAAA CACCATGGG GTGCATGGTO ATTTCAGTGT CACCATCGAG CACCTACGTG CACCTACGTG CACCTACGTG CACCATCAGTG CACCATCAGTG CACCATCAGTG CACCATCAGTG CACCATCAGTG CACCATCAGTG CACCATCAGTG CAGCGCTGAC CAGCACTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCCCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCGCTGAC CAGCCTGAC CAGCG	GAGGCCGCG CTTCTCTGCG CTTCTCTGCG CACTGGTATG CACTGGTATG CGCCCTGCC TCTGATGCTC AGGGACCCT CATGACTGCG CATGACTGCG CATGACTGCG TGTGGAGGCA TACCCAAAGA CAAGGGAGGA CAAGGGAGGA TACCCAAGGCCT TCTGGAGGCA TACCCAAGAC TCTGGAGGCA TACCCAAGAC TTTGGCAGCCAT TTTGGCAGCCAT	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG GGTGCTATGG CATGGAAC TCAGCGGG GGTCTATGG CACTGGAA CTCTGAGAC TCTGAGGC CCCTATCAG AGGAGGACTA TGAAGTTTGA ACCACAACGA CCGGACTAT	120 180 240 300 360 420 480 540 600 720 780 840 900 900
50 55 60	coding sequilibrium control co	111	21 COCTOCTGC GAGCCCTGGT GAGCCCTGGT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAAGGTACCA GCAGGAACCG GAGGAATCA GAGAATTACA GAGGATTCA CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG CACACACTG ACAAGGACTA ATTCCAAGGA CQATCTTACCGA ACATCTACCGA ACCAGGAGTTA ACCAGGAGTTA ACCAGGAGTA ACCAGGAGTTA ACCAGGAGTTA	31 GCAGGCCACC GCAGGCCACAT TCAAATTCCA CTCCAACATT TAAGTCAAAA CACCATGGGG GTGCATGGTG GTGCATGGTG ATTTCAGTGT CACCATCGAG CACCATCGAG CACCATCGAG CACCATCGAG CACCATCGAG CACCATCGAG CACCATCGAG CAGCGCTGAC GGGCGGTGT GGATCCCCAG CATTCTCTAT TCAGCAGGCCC	GAGGCCGCG CTTCTCTGCG CTTCTCTGCG CTCGACTGTG ACCTGCTATG CGGCCCTGCC CTTGATGCTC ATGACTCC ATGACTCC ATGACTCC ATGACTCC ATGACTGCA AACCAGCCCT CTTGTGAGCCC TTGTGAGCCCT CTGTGAGCCCT TTGTGAGCCCT TTGTGAGCCCT TTTGTGAGCACA CAGGGAGCAT TTTTGCACACA CGGAGCAT CTTTTGGCACA CGGAGCAT CAGGAGCAT CAGTATACCG ACTACTACCG ACTACTACCC ACTACTACC ACTACTACCC CTACTACCC ACTACTACCC ACTACTACCC ACTACTACCC ACTACTACCC ACTACTAC	CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG GGTGCTATGGTGGG GGTGCTATGGTGGG GGTTGCATGGGC GGTTTGCGGG GCTTACGGG GCTCATCAG AGGAGGACTA TGAAGTTTGA ACCACAACGA CCGGACTAT TGAAGTTTGAAGT TGAAAATGAC GCTTGAAGT TGAAAATGAC	120 180 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	Coding sequipolar control cont	111	211 CCCTCCTGCC GAGCCCTGCT GAGCCCTGCT GTGAACTTCA ACAGGTACT GTGAAATAGA CCAGCCACT GTGCAAGAA AAACGTACCA GGAGGACC TGTTCCAAGA AAACGTACCA GGGGCTTGCT CAAGGCTTAA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACAAGGACTA ACCAGGA CGGGGGCTTAA ACAAGGACTA ACCAGGA CGGGGGCTGCTGGCGGACCC CTGCCTGGACCC CTGCCTGACCC CTGCCTGACCC CTGCCTGACCC CTGCCTGACCC CTGCCTGACCC CTGCTGACCC CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	31 GCAGGCCACC GGCAGGGCACACATT TAAGTCAAAAAAAAAA	GAGGCCGCG CTTCTTCGG CTCTCTTCGG CTCGCTATG CACTGCTATG CGCCCTGCC CTCTGCTATG CGCCCTGCC CATGATCTCC CATGATCTCC CATGATCTCC CATGACTCC CATCACTCCG CGCCAAAAAA AACCAACAC CAAGGGGAC TACCCAAAGA CGGGGGAGCAT TTTGGCACAA CGGGAGCAT TTTGGCACAA CGGAGCAT CTCGCACAA CGGAGCAT CAGGCAGCAC CACTACTAC CAGGCAGCAC CACTACTAC CACAACAC CACAACAC CACAACAC CAAGGCAGC CACTACTAC CACACAC CACACAC CACACAC CACACAC CACACAC CACAC CACACAC CACA	CCGTCTAGGG TCCTGGTGGT ACTGCCCAAA AGGGGAATGG TCCCGGAA TTCAGCTGGG GGTGCTATGT CAGTGGG GGTTCTATGT CAGATGGAA AGGGGACTA TGAGATGGAA ACCACACGA CCCGGACTAT CCTGGAGG TTCAGAGGTTGAAGT TGAAATTGA CCTGTAGAGC CCTGTAGAGT TGAAATTGAG CCTGTAGAGT CCTGTAGAGT CCTGTAGAGT CCCGGAGGAGA CCCCGGAGGAGA CCCCGGAGGAGA CCCCGGAGGAGA CCCCGGAGGAGA CCCCGGAGGAGA CCCGGAGGAGA CCCGGAGGAGA CCCGGAGGAGA CCCGGAGGAGA CCCGGGAGGAGA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140
50 55 60 65	Coding sequilibrium of the control o	III GECOTCOGO GECACCATGA AAAGGCAGCA GEGAGAACA GEGACACGGG GTGATCAGC CTCATCCTCAA GTGATCAGC CTGATCAGC CTGATCAGC GTGATCAGC GGAAAAGATAC GGAAAAGATAC GGAAAAGATAC GGAAAAGATAC GGAAAAGATAC GGAAAAGATAC GGAAAAGATAC GGAAAAGATAC GGAAATACAC GGAAAAGATAC GGAAATACAC GGAACACGGGC GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT GGAATACAC CCCAGCT CGACT CGACT CGACT CGACT CGACT CCCAC CC	1372 21 21 21 21 21 22 21 21 22 21 22 23 24 24 25 26 26 26 26 26 26 26 26 26 26 26 26 26	31 GCAGGCCACC GCACGACA ANTICAN CACCATGGAC CACCACGAC GCACCACCA ANTICACC GCACCACCA CACCACCACC GCACCACCACCA CACCACCACC GCACCACCACCACCACCACCACCACCACCACCACCACCAC	GAGGCCGCG CTTCTTCGG CTCTCTTCGG CTCGCTATG CACTGCTATG CGCCCTGCC CTCTATCTCC CATCATCTCC CATCATCTCC CATCACTCC CATCACTCC CATCACTCC CATCACTCC CATCACTCC CATCACTCC CATCACTCC CATCACTCC CATCACTCC CATCACC CCGTCTAGGG TCCTGGTGGT ACTGCCCAAA AGGGGAATGG TCCCGGAA TTCAGCTGGG GGTTCTATGT CAGTGGG GGTTCTATGT CAGATGGAA AGGGACTACA AGGAGGACTACA AGGAGGACTACA AGGAGGACTACA CCCGGACTAT CCTGGAGG ACCACACGA CCTGGAGG TGAAATGAAA	120 180 300 360 420 480 540 660 720 780 840 900 960 1020 1080	
50 55 60	Coding sequility of the control of t	LINE CONTROL OF THE C	21	31 GARGGCCACC GGCGGCCTG TCAGATTCCA CTCCAACATT TAAGTCAAAA AGGAACCGG GTGCATGATA CACCTAGGGT CACCTAGGT CACCT	GAGGACCGCG CTTCTCTGCG CTTCTCTGCG CTTCTCTGCG CTTCTCTGCG CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CATGACTGCG GGCCAAAAGA CACTGCTAC CATGACTGCG GGCCAAAAGA CAACGGCAAAGA CAACGGCAAAGA CAACGGCAAAGA CAACGCCAC CGCCAACGCAC CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CACTGCTCC CTGCCCCTCT CACACGACGCC CTGCCCCTCT CTCACACC CTGCCCCTCT CTCACACCACAC	CCGTCTAGGG TCCTGGTGGT TCCTGGTGGT TCCTGGTGGT TCCTGGTGGT TCCTGGTGGT TCCCCAAA ACTGCCTGGAA TCCACTGGGG GGTGCTATCGT TCAGCTGGG GGTTGCACTGGAGCC TCTGAGGAC TCTGAGGACT TGAAGTTTGA TCCACTGAGACT TGAAGTTTGA TCCACTGAGACT TGAAGTTTGA TCCACTGAGACT TGAAAGTTTGAG TCCACTGAGACT TGAAAGTTTGAG TCCACTGAAGT TGAAAATGAC TGAAAATGAC TGAAAATGAC TCCACACTT TCACACCTT CACACCT TCACACC TCACACCT TCACACC TCACACCT TCACACCT TCACACCT TCACACCT TCACACCT TCACACCT TCACACCT TCACACCT TCACACCT TCACACCT TCACACCT TCACACCT TCACACC TCACACCT TC	120 180 240 300 420 480 540 660 720 840 900 1020 1020 1140 11260 11380
50 55 60 65	Coding sequilibrium of the control o	LINE CONTROL TO CONTRO	21 21 21 21 21 21 21 21 21 21 22 21 21 2	31 GARGICCACC GICIGICACTT TOLAGITTICA CTCOAACATT ACACTTAGAC ACACTTAGAC ACACTTAGAC ACACTTAGAC ACACTTAGAC CACATCAGA CTCAAACAC ACACTTAGAC CTCAAACAC AGGACTAC AGCAC AGGACTAC AGG	GAGGCCGCG CTTCTCTGCG CTTCTCTGCG CTTGAACTOTG CACTAGTGCA AGCGGCTATA CGGCCTGCC AGGCGACCCT TGTGATGCTC AGGCGACCCT TGTGATGCTC TGTGATGCTC AGGCGACCAT TACCCAAAGA CAGGCTACCC CACTACTACG CGCACCAA CGCACCAC CACTACTACG CACTACTACC CACTACTACG CACTACTACG CACTACTACG CACTACTACG CACTACTACG CACTACT CACTACTACG CACTACT CACT	COSTCTAGO TCCTGGTOGT TCCTGGTOGT ACTOTCTAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAGAA TCCAGCTGGG GGTGCTATGG GGTCTATGGG GCTCTATCAG AGGGGAACT TGAAGTTTGAGCC CCCGAACGA CCCCGAACGA CCCCTGAACGA CCCAGGGAAGA GAATTGTGAA GAACGACT CTCCAACGT CTCAACACT AGAGGTCCCC TAGAGGTCCCC TAGAGGTCCACC	120 180 240 300 420 480 540 660 720 780 840 960 960 1020 1080 11260 11320 11320 11320
50 55 60 65 70	coding segment of the comment of the	LINEAR TO THE CONTROL OF THE CONTROL	21	31 GARGACCACC GOCHOLOCATO GO	GAGGCOGCO CTTCTCTCO CTTCTCTCO CTTCCTCTCO CTTCCTCTCO CTTCCTCTCO CTTCCTCTCO CACCTGTTCC ACCTGTTCC ACCTGTTCC ACCTGTTCC ACCTGTTCC ACCTGCTTCC ACCTGCTTCC ACCTGCTTCC ACCTGCTTCC ACCTGCTCC ACCTGCTCC ACCTGCTCC ACCTGCTCC ACCTGCTCC ACCTGCTCC ACCTCTCC ACCTCCTC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCTCC ACCTCT ACCTCTC ACCTCT ACCTCTC ACCTCT ACCTC	COGRETAGO TOCTUGATOGT TOCTUGATOGT ACTOTOTANA ACTICCONA ACCANCON ACCANC	120 180 240 300 420 480 540 660 720 840 900 1020 1020 1140 11260 11380
50 55 60 65	coding sequipolic control cont	LINE CONCENTRATION CONTROLLED TO CONCENTRATION CONTROLLED TO CONCENTRATION CONTROLLED TO CONCENTRATION CONTROLLED TO CONTROLLED	21	31 CARGOCACC GOCGLOCATO GOCGLOCAT	GAGGCOGCG ACTITICT GAGGCGC GAGGCGC GAGGCGC GAGGCGCG GAGGCGC GAGGCC GAGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGCC GAGGCC GAGCC GAGGCC GAGGCC GAGCC GACC GAGCC G	COTTCTAGO TOCTOGRAP ACTOSCOAA ACTOSC	120 180 300 360 420 480 540 660 660 720 780 840 960 1020 1140 11260 11380 1140 11500 11500 11500
50 55 60 65 70	coding sequipolic control cont	LINE CONCENTRATION CONTROLLED TO CONCENTRATION CONTROLLED TO CONCENTRATION CONTROLLED TO CONCENTRATION CONTROLLED TO CONTROLLED	21	31 CARGOCACC GOCGLOCATO GOCGLOCAT	GAGGCOGCG ACTITICT GAGGCGC GAGGCGC GAGGCGC GAGGCGCG GAGGCGC GAGGCC GAGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGGCC GAGCC GAGGCC GAGCC GAGGCC GAGGCC GAGCC GACC GAGCC G	COTTCTAGO TOCTOGRAP ACTOSCOAA ACTOSC	120 180 240 300 420 480 540 600 600 600 720 780 960 960 1020 1020 1030 1240 1380 1340 1560
50 55 60 65 70	coding sequipolic control cont	LIBRORY 77 I CICCOTTGGG GCCACCATGA ANAGCAGGG GCCACCATGA ANAGCAGGG GTGGTTCAGG GTGTTCAGG	1372 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	31 GONGGOCACC GOGGGGCT91 TANABAGGGCCACC GOGGGGCCT91 TANABAGGGCCACC GOGGGGCT91 TANABAGGGCACC GOGGCACGACACACC GOGGCACGACACACC GOGGCACGACACACC GOGGCACGACACACC GOGGCCATGGACACC GOGGCACCACC GOGCACCACC GOGGCCACC GOGCACCACC G	GAGGCOGGG CTTCTTTGGG CTTCTTTGGG CTTGGACTTGG CACTGGTGGA CACTGGTGA ACTGGTGA CACTGGTGA CACTGGTGA CACTGGTGA CACTGGTGA CACTGGTGA CACTGGTGA CACTGGTGA CACTGGTGA CACTGGTGA CACTGGTGA CACTGGTGA CA	CONTENSION OF THE CONTENSION O	120 180 240 300 300 300 420 480 540 660 720 780 900 1020 1140 1260 1120 1260 1320 1320 1340 1560 1680 1740
50 55 60 65 70 75	CODING SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEGON CONTROLL SEG	LEBROE! 77 1 1 1 COCCOTTGGG GCCACCATGA ANAGCCAGG GCCACCATGA ANAGCCAGG GCCACCATGA GCCACCATGA GCCACCATGA GCCACCATGA GCCACCATGA GCCACCAGGAAAAG GCCACCAGGAAAAG GCCACCAGGAAAAG GCCACCAGGAAAAG GCCACCAGGAAAAG GCCACCAGGAAAAG GCCACCAGGAAAAG GCCACCAGGAAAAG GCCACCACGAGAAAG GCCACCACGAGAAAG GCCACCACGAGAAAAGAGAAAGCAACAAGCAAAGCAACACACACAGGAAAAGCAGAAAAGCAGAAAAGCAGAAAAGCAGAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGAAAAGAAAAAA	21 21 20 COCTOCTIGOC GARCOCTIGOT A ROBARTACTI GIRANATAGA CONGOCACTER A ACAGATACTI GIRANATAGA CONGOCACTER A ARACOTACOG GONGORACOC CARGOCTARA ARACOTACOG CONGOCACTER ARACOTACOG CONGOCACTER ARACOGGARACOC CONGOCACTER ARACOTACOG CONGOCACTER ARACOGGARACOC CONGOCACTER CONGOCACT	11 CONGRECACE GRIGGISCHIS TRANSTICANA TRANSTICANA CACCATOGGE TROCCACAGA AGACIAC AGACAC CATAGAGA CATAGAC CATAG	GAGGCOGCG GAGGCOCCG GAGGCCCC GAGGCCCCC GAGCCCCC GAGCCCCC GAGCCCCC GAGCCCCC GAGCCCCC GAGCCCCC GAGCCCCC GAGCCCCC GAGCCCCC GAGCCCCCC GAGCCCCCC GAGCCCCCC GAGCCCCCC GAGCCCCCCC GAGCCCCCCCC	COSTICTAGO TOCTOSTORI ACTOSTORI ACTO	120 180 240 360 360 360 420 480 660 720 660 780 840 960 1020 1080 1260 1380 1440 1560 1560 1560 1680 1800 1860
50 55 60 65 70	CODING SEGON CONTROL SEGON CON	uence: 77 Coccorrection	1372 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	31 GOAGGICANC GUIGGGCTH TCAAGTTCAA TTCAAGTTCAA TTGCACAA TTGCACAA TTGCCAAA TTGCCAAA TTGCCAAA TTGCCAAA TGCCAAA TGCCAAA TGCCAAA TGCCAAA TGCAAA TGCCAAA TGCAAA TGCCAAA TGCAAA TGCAAA TGCAAA TGCCAAA TGCAAA TGCAAA TGCAAA TGCAAA TGCAAA TGCAAAA TGCAAAA TGCAAAA TGCAAAA TGCAAAA TGCAAAAA TGCAAAAA TGCAAAAA TGCAAAAAA TGCAAAAAA TAAAAAAAA TGCAAAAAAA TGCAAAAAAAA TGCAAAAAAAA TGCAAAAAAAA TGCAAAAAAAAA TGCAAAAAAAA TGCAAAAAAAA TGCAAAAAAAA TGCAAAAAAAAA TGCAAAAAAAAAA	GAGGICOCCG GAGGICOCCCC GAGGICOCCC	COGNETAGO TOCHIGATORI ACTOSCIANA	120 180 240 360 360 360 360 540 660 720 960 960 960 1020 1140 1120 11320 1140 1150 1680 1740 1740 1740 1860 1740 1860
50 55 60 65 70	COSING SEGO COSTING LEGICE 1 77 I COCCUTCIGO GCCACCATGA ANAGCCAGO TOGOGO GCCACCATGA ANAGCCAGO COCCUTCAGO GCCACCATGA COCCUTCAGO GCCACCATGA COCCUTCAGO GCCACCAGO CCAGO GCCACCACCACCACCACCACCACCACCACCACCACCACCA	1372 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	31 GOAGGCCACC GUGGGCCTO TCAAGTTCA CTCAAGTTCA CTCAAGTTCA CTCAAGTTCA CTCAAGTTCA CTCAAGTTCA CTCAAGTTCA CTCAAGTTCA CTCAAGTTCA CTCAAGTTCA CTCAAGTCA G	GAGGCACCACA GAGGCACCAC GAGGCACCAC GAGGCACCAC GAGGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GAGCACCAC GACCACCAC GACCAC GACCACCAC GACCAC GACCACCAC GACCAC GACCACCAC GACCAC GACCACCAC GACCAC GACCACCAC GACCAC GACCACCAC CONTENSION OF CO	120 180 240 360 360 360 420 480 660 720 660 780 840 960 1020 1080 1260 1380 1440 1560 1560 1560 1680 1800 1860		
50 55 60 65 70 75	CODING SEGNICATION OF THE PROPERTY OF THE PROP	LILIE I COCCOTTO CO COCCOTTO CO COCCOTTO CO COCCOTTO CO COCCOTTO CO COCCOTT	21 21 21 21 21 21 21 21 21 21 21 21 21 2	31 GRAGGICCACC GICHOGICCTON TO CALONTOCAC GICHOGICCTON TO CALONTOCAC GICHOGICCTON TO CALONTOCAC GICHOGICCAC GICH	GAGGCOCCG GAGCOCCG GAGGCOCCG GAGGCOCCG GAGCCOCCG GAGCC G	COSTICTAGOS TOCTOCTOS OS TOCTOCTOS OS TOCTOCTOCTOS TOCTOCTOCTOS TOCTOCTOCTOS TOCTOCTOCTOCTOCTOCTOC TOCTOCTOCTOCTOCTOC TOCTOCTOCTOCTOCTOCTOCTOC TOCTOCTOCTOCTOCTOCTOCTOC TOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCT	120 180 240 360 360 360 420 480 660 720 720 1020 1020 1140 1260 1320 1320 1320 1340 1560 1660 1790 1860 1990 1990 1990 1980
50 55 60 65 70 75 80	COLING SEGON COLORIDADO CONTROL COLORIDADO C	LIBRORY 77 CICCOTOGGG GCCACCATGA ANAGGCAGGG TOGGGGTATGGGGGTATGGGGGTATGGGGATATGGGGTATGGGGTATGGGGTATGGGGTATGGGGATGGGGTATGGGGATGGGGAAAGGGAAGGAAGGGAAGAG	21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	31 GARGGCCACC GUCGGCCTGCACGACACACACACACACACACACACACACACA	GAGGAGGCAN AGGARANAGA AGCAGGAGA AGCAGGAGA AGCAGGAAAAGA AGCAGGAGAAAAGA AGCAGGAGAAAAGA AGCAGGAGAAAAGA AGCAGGAGAAAAGA AGCAGGAGAAAAGA AGCAGGAGAAAAGA AGCAGGAGAAAAGA AGCAGGAGAAAAGA AGCAGGAGAAAAGA AGCAGGAGAAAAAAAA	COSTICTAGOO TECTIGATOOT TECTIGATOOT TECTIGATOOT TECTIGATOOT TECTIGATOOT TECTIGATOOT TECTICATOOT TECTIC	120 180 240 360 360 360 420 480 660 660 720 780 900 1020 1020 1140 1120 1140 1150 1150 1150 1162 1164 1
50 55 60 65 70 75	COOLING SEGO COOLI	LISTER TO THE CONTROL OF THE CONTROL	21 21 21 21 21 21 21 21 21 21 21 21 21 2	31 GRAGGICCACC GRICGGICCACC GRICGGICCACC GRICGGICCACC GRICAGGICCACC GR	GAGGICOCCI GAGGICOCCI	COSTICTAGOO TECTIGATOOT TECTIGATOOT TECTIGATOOT TECTIGATOOT TECTIGATOOT TECTIGATOOT TECTICATOOT TECTIC	120 180 240 360 360 360 420 480 660 720 720 1020 1020 1140 1260 1320 1320 1320 1340 1560 1660 1790 1860 1990 1990 1990 1980
50 55 60 65 70 75 80	COOLING SEGO COOLI	LISTON TO THE CONTROL OF THE CONTROL	21 21 21 21 21 21 21 21 21 21 21 21 21 2	31 GRAGGICCACC GRICGGICCACC GRICGGICCACC GRICGGICCACC GRICAGGICCACC GR	GAGGICOCCI GAGGICOCCI	COSTICTAGOS TOCHOSTOS TOCH	120 180 240 360 360 360 360 360 660 720 660 720 1020 1140 1200 1240 1320 1320 1320 1320 1340 1560 1680 1680 1780 1880 1980

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	MRALLARLLL	CVLVVSDSKG	SNELHOVPSN	CDCLNGGTCV	SNKYFSNIHW	CNCPKKFGGQ	60
	HCBIDKSKTC	YEGNGHFYRG	KASTDTMGRP	CLPWNSATVL	QQTYHAHRSD	ALQLGLGKHN	120
	YCRNPONRRR	PWCYVQVGLK	PLVOECMVHD	CADGKKPSSP	PEELKFQCGQ	KTLRPRFKII	180
10	GGEFTTIENO	PWFAAIYRRH	RGGSVTYVCG	GSLISPCWVI	SATHCFIDYP	KKEDYIVYLG	240
	RSRLNSNTOG	EMKFEVENLI	LHKDYSADTL	AHHNDIALLK	IRSKEGRCAQ	PERTIQUICL	300
	PSMYNDPOFG	TSCEITGFGK	ENSTDYLYPE	OLKMTVVKLI	SHRECQOPHY	YGSEVTTKML	360
	CAADPOWKTD	SCOGDSGGPL	VCSLOGRMTL	TGIVSWGRGC	ALKOKPGVYT	RVSHFLPWIR	420
1.0	SHTKEENGLA						
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20	1	11	21 	31	41 	51 	
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	CTCTCCCCCC	GCCCCACCTC	CTCCGCCTCG	CCCTCCTCCT	GAGCAGCGGG	CCCAGACTGC	120
	GCTCCGGCCG	CGGCCCTCGC	CCCGCGGAGC	CCTCCTACCC	CGGCCCGACG	CTCGGCCCGC	180
25	GACCTGCCCC	GAGCCCTCTC	CATGGAGGCA	GCCCGCCCCT	CCGGCTCCTG	GAACGGAGCC	240
	CTCTGCCGGC	TGCTCCTGCT	GACCCTCGCG	ATCTTAATAT	TTGCCAGTGA	TGCCTGCAAA	300
	AATGTGACAT	TACATGTTCC	CTCCAAACTA	GATGCCGAGA	AACTTGTTGG	TAGAGTTAAC	360
	CTGAAAGAGT	GCTTTACAGC	TGCAAATCTA	ATTCATTCAA	GTGATCCTGA	CITCCAAATT	420
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30	TTTACCATAT	TACTTTCCAA	CACTGAGAAC	CAAGAAAAGA	AGAAAATATT	TGTCTTTTTG	540
	GAGCATCAAA	CAAAGGTCCT	AAAGAAAAGA	CATACTAAAG	AAAAAGTTCT	AAGGCGCGCC	600
	AAGAGAAGAT	GGGCTCCAAT	TCCTTGTTCG	ATGCTAGAAA	ACTCCTTGGG	TCCTTTTCCA	660
	CTTTTCCTTC	AACAGGTTCA	ATCTGACACG	GCCCAAAACT	ATACCATATA	CTATTCCATA	720
	AGAGGTCCTG	GAGTTGACCA	AGAACCTCGG	AATTTATTT	ATGTGGAGAG	AGACACTGGA	780
35	AACTTGTATT	GTACTCGTCC	TGTAGATCGT	GAGCAGTATG	AATCTTTTGA	GATAATTGCC	840
	TTTGCAACAA	CTCCAGATGG	GTATACTCCA	GAACTTCCAC	TGCCCCTAAT	AATCAAAATA	900
	GAGGATGAAA	ATGATAACTA	CCCAATTTTT	ACAGAAGAAA	CTTATACTTT	TACAATTTTT	960
	GAAAATTGCA	GAGTGGGCAC	TACTGTGGGA	CAAGTGTGTG	CTACTGACAA	AGATGAGCCT	1020
40	GACACGATGC	ACACACGCCT	GAAGTACTCC	ATCATTGGGC	AGGTGCCACC	ATCACCCACC	1080
40	CTATTTTCTA	TGCATCCAAC	TACAGGCGTG	ATCACCACAA	CATCATCTCA	GCTAGACAGA	1140
	GAGTTAATTG	ACAAGTACCA	GTTGAAAATA	AAAGTACAAG	ACATGGATGG	TCAGTATTTT	1200
	GGTCTACAGA	CAACTTCAAC	TTGTATCATT	AACATTGATG	ATGTAAATGA	CCACTTGCCA	1260
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4.5	TTACGAGTTA	CTGTTGAGGA	TAAGGACTTA	GTGAATACTG	CTAACTGGAG	AGCTAATTAT	1380
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	CAAATTGGTG	TAGTTAATGA	AGCTCCATTT	TCCAGAGAGG	PERCOCCUE	ATCAGCCATG	1620
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50	CCAATACAGA	ACCCAGAAAC	GAAAGAAAAT	GCAGAAGTGG	GRACALCARG	AMERICAN TALL	1740
30	AAAGCATATG	GGGTCACCAT	AAGAAGTAGC	AGTGGCATAA	MCD & BOTTOT	CACAACCCTG	1800
	CCAACAGGGT	CAGAGACCAT	CDADAMACCO	ACAGGATCAA	TTACAGTCCT	TECATCAGAC	1860
	Chagadaga	GAACATGTAC	CCCCACACAC	CCCATTATAC	TTCAAGACGT	GAATGATAAC	1920
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55	ATTOTTOTO	TTGATCCTGA	TGAGCCTATC	CATGGCCCAC	CCTTTGACTT	TAGTCTGGAG	2040
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	GATAGACTTG	GCATGTCTAG	TGTCACTTCA	TTGGATGTTA	CACTGTGTGA	CTGCATTACC	2220
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-	CTGGTCTGTG	GGGCTTCTGG	GACGTCTAAA	CAACCAAAAG	TAATTCCTGA	TGATTTAGCC	2400
	CAGCAGAACC	TAATTGTATC	AAACACAGAA	GCTCCTGGAG	ATGACAAAGT	GTATTCTGCG	2460
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65	TOGGAATCCT	GCCGGGGGGC	TGGCCACCAT	CACACCCTGG	ACTCCTGCAG	GGGAGGACAC	2640
	ACCCACCTCC	ACAACTGCAG	ATACACTTAC	TCGGAGTGGC	ACAGTTTTAC	TCAGCCCCGT	2700
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	GTCCTGACAT	ATAACTATGA	AGGAAGAGGA	TOGGTGGCTG	GGTCTGTAGG	TTGTTGCAGT	2820
70	GAACGACAAG	AAGAAGATGG	GCTTGAATTT	TTGGATAATT	TGGAGCCCAA	ATTTAGGACA	2880
70	CTAGCAGAAG	CATGCATGAA	GAGATGAGTG	TGTTCTAATA	AGTCTCTGAA	AGCCAGTGGC	2940
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75	TCTATCCAAG	GAGGTCTACA	GAGAAATTAA	AGTCTGCCTT	ATTTGTTACA	TTTGGGTATA	3180
75	ATGACAACAG	CCAATTTATA	GTGCAATAAA	ATGTAATTAA	TTCAAGTCCT	TATTATAGAC	3240
	TATTTGAAGC	ACAACCTAAT	GGAAAATTGT	AGAGACCTTG	CTTTAACATT	ATUTUCAGIT	3300
	AATTAAGTGT	TCATGTGGTG	CTTGGAAACT	GITGITITCC	TGAACATCTA	AAGTGTGTAG	3360
	ACTGCATTCT	TGCTATTATT	TTATICTTOT	AATGTGACCT	TTTCACTGIG	CANAGGAGA	3420
80	TTTCTAGCCA	GGCATTGACT	ATTACAATTT	CALL			

Seq ID NO: 617 Protein sequence Protein Accession #: NP_077740.1

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1 11 21 31 41 51 1 1 ERARAPSGSN MGALCRILLI TIAILIPASD ACKNYTHYD SKLDAEKIVO KVILKECPTA AKLHSSDED PQILEDGSVY TINTILLSSK KRSFTILLSN TENQEKKKIP VFLENQTKVL 85

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	KKRHTKEKVL	RRAKRRWAPI	PCSMLENSLG	PFPLFLQQVQ	SDTAQNYTIY	YSIRGPGVDQ	180
	EPRNLFYVER	DTGNLYCTRP	VDREQYESFE	IIAFATTPDG	YTPELPLPLI	IKIEDENDNY	240
	PIPTERTYTE	TIFENCRUGT	TVGOVCATOK	DEPOTMETEL.	KYSTIGOVPP	SPILESMHPT	300
	TOUTTTEEN	LDRELIDKYQ VEILRVTVED	LKTKVODMDG	OVEGLOTTST	CTINTDDVND	HIPTETRISY	360
5	rmorrament.	MOST DIMINED	SOLITOR STORE	VILABOLISI	MAIN TIME	CONDUIT CALL	420
,	ATSAFFMIAD	APITMATAPA	MUDITALIAN	WALLITHOUS	MODELLIATOR	CINEGUECOV	
	KAPWAERKÖÖ	MILQIGVVNE	APPSKEASPR	SAMSTATVTV	MARDODROBE	CUPPLIGITARM	480
	KENABVGTTS	NGYKAYDPET	RSSSGIRYKK	LTDPTGWVTI	DENTGSIKVP	RSLDREARTI	540
	KINGT VMTTVIT.	ASDOCCRTCT	CTLGTTLODY	NUNCERLEKK	TVTTCKPTMS	SARTVAVDDD	600
	RETHIRDS WOR	ST.RCSTSEVO	RMWRI-KATND	TAARLSYOND	PPPGSYVVPT	TVRDRLGMSS	660
10	IMOX DUM CD	CITENDCTHR DLAQQNLIVS HQTSESCRGA	UDBBICCCCU	OLCHWATTAT	LIGINIARCI	L.PTL.VCCA.CC	720
10	ATPROVIDED	CIIMBCIER	VDFKIGGGGV	Angrest for	moranomica	mianorinioa	780
	TEKQPKVIPD	DPWOONPIAR	NTEAPGOOKV	YSANGPTTOT	AGURNOGACO	TVGSGIKNGG	
	QETIEMVKGG	HQTSESCRGA	GHHHTLDSCR	GGHTEVDNCK	TTYSEWHSFT	Chkrosekaar	840
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		d Accession		040 1			
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	Coding sequ	ience: 202	2745				
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20	1	11	21	31	41	51	
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	CCCCABAGGA	AAAGCCCCTT	GGATGAGAGG	CAGGGGGCTTC	AGAGAAGCTA	AGAAAAGCAC	60
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	CICICCOCOC	GCCCCACCTC	C1CCGCC1CG	cocrected.	000000000	CTCCCCCCCCCCC	180
25	GCTCCGGCCG	CGGCCCTCGC	CCCGCGGAGC	CCTCCTACCC	COGCCCOMCG	CICOGCCCGC	
23	GACCTGCCCC	GAGCCCTCTC	CATGGAGGCA	GCCCGCCCCT	CCGGCTCCTG	GAACGGAGCC	240
	CTCTGCCGGC	TGCTCCTGCT	GACCCTCGCG	ATCTTAATAT	TTGCCAGTGA	TGCCTGCAAA	300
	AATGTGACAT	TACATGTTCC	CTCCAAACTA	GATGCCGAGA	AACTTGTTGG	TAGAGTTAAC .	360
	CTGAAAGAGT	GCTTTACAGC	TGCAAATCTA	ATTCATTCAA	GTGATCCTGA	CTTCCAAATT	420
	TOYCOACCATC	GCTTTACAGC GTTCAGTCTA	TACARCAAAT	ACTATTCTAT	TOTOCTOGGA	GAAGAGAAGT	480
30	TIGGAGGATG	TACTTTCCAA	CL CONCLUENT	COLUMN TOTAL	1010010001	TOTO TOTO	540
30	TTTACCATAT	TACTTTCCAA	CACTGAGAAAC	CAMBANANGA	WOMMANIALL	IGICITITIO	340
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	AAGAGAAGAT	GGGCTCCAAT	TCCTTGTTCG	ATGCTAGAAA	ACTCCTTGGG	TCCTTTTCCA	660
	CTTTTCCTTC	AACAGGTTCA	ATCTGACACG	GCCCAAAACT	ATACCATATA	CTATTCCATA	720
	AGAGGTCCTG	GAGTTGACCA	AGAACCTCGG	AATTTATTTT	ATGTGGAGAG	AGACACTGGA	780
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	MCI IOIAII	GIACICOICC	CONTRACTOR	CARCETTOCAC	TOTO CONTRACT	BATCABABUS	900
	TITGUAKKA	CICCAGAIGG	GIATACICCA	GAMCIICCAC	IGCCCCIMI	MICHANIA	
	GAGGATGAAA	ATGATAACTA	CCCAATITIT	ACAGAAGAAA	CTTATACTTT	TACAATTTT	960
	GAAAATTGCA	GAGTGGGCAC ACACACGCCT	TACTGTGGGA	CAAGTGTGTG	CTACTGACAA	AGATGAGCCT	1020
	GACACGATGC	ACACACGCCT	GAAGTACTCC	ATCATTGGGC	AGGTGCCACC	ATCACCCACC	1080
40	CTATTTTCTA	TGCATCCAAC	TACAGGCGTG	ATCACCACAA	CATCATCTCA	GCTAGACAGA	1140
	GAGTTAATTG	ACANGTACCA	GTTGAAAATA	AAAGTACAAG	ACATGGATGG	TCAGTATTTT	1200
	CCCCTACACA	ACAAGTACCA CAACTTCAAC	TTOTATCATT	AACATTGATG	ATVITABATVIA	CCACTTGCCA	1260
	GGICIACAGA	GTACTTCTTA	TIGITATORI.	CHICATE TOTAL	* TO CO COMPOS	TOTOCOADATO	1320
	ACATTTACTC	GIACITOTIA	TGTGACATCA	GIGGAAGAAA	MINCAGIIGA	10100MMIC	1380
45	TTACGAGTTA	CTGTTGAGGA AGGGCAATGA	TAAGGACTTA	GIGAATACIG	CTAACTGGAG	AGCTANTTAT	
45	ACCATTTTAA	AGGGCAATGA	AAATGGCAAT	TTTAAAATTG	TAACAGATGC	CAAAACCAAT	1440
	GAAGGAGTTC	TTTGTGTAGT	TAAGCCTTTG	AATTATGAAG	AAAAGCAACA	GATGATCTTG	1500
	CAAATTGGTG	TAGTTAATGA	AGCTCCATTT	TCCAGAGAGG	CTAGTCCAAG	ATCAGCCATG	1560
	AGCACAGCAA	CAGTTACTGT	TAATGTAGAA	GATCAGGATG	AGGGCCCTGA	GTGTAACCCT	1620
	CCAATACACA	CTGTTCGCAT	CAAAGAAAAT	GCAGAAGTGG	GAACAACAAG	CARTUGATAT	1680
50	CCANTACAGA	ACCCAGAAAC	***********	BOROGONTAN	COMMENSACINA	A TOTAL A CTICAT	1740
50	MAAGCATATG	ACCCAGAMAC	ANGRAGIAGE	AGIGGCAIAA	GGIAIAAGAA	ATTANCIONI	1800
	CCAACAGGGT	GGGTCACCAT	TGATGAAAAT	ACAGGATCAA	TCAAAGTTTT	CAGAAGCCTG	
	GATAGAGAGG	CAGAGACCAT	CAAAAATGGC	ATATATAATA	TTACAGTCCT	TGCATCAGAC	1860
	CAAGGAGGGA	GAACATGTAC	GGGGACACTG	GGCATTATAC	TTCAAGACGT	GAATGATAAC	1920
	AGCCCATTCA	TACCTAAAAA	GACAGTGATC	ATCTGCAAAC	CCACCATGTC	ATCTGCGGAG	1980
55	ATTYTTYTYT	TTGATCCTGA	TGAGCCTATC	CATGGCCCAC	CCTTTGACTT	TAGTCTGGAG	2040
	ACTICIACIT	CAGAAGTACA	CACAATCTCC	DEAGDTTOADA	CAATTAATGA	TACAGCAGCA	2100
	AGIICIACII	ATCAGAATGA	moomoo man	OCCUPANT TATO	TA CON COMPT	BACACTORCA	2160
	OGICITICUT	ATCAGAATGA	ICCICCATII	GGCTCATATO	INGIACCIAL	MCMSTQMSA .	
	GATAGACTTG	GCATGTCTAG	TGTCACTTCA	TTGGATGTTA	CACTGTGTGA	CTGCATTACC	2220
· ·	GAAAATGACT	GCACACATCG	TGTAGATCCA	AGGATTGGCG	GTGGAGGAGT	ACAACTTGGA	2280
60	AAGTGGGCCA	TCCTTGCAAT	ATTGTTGGGC	ATAGCATTGC	TCTTTTGCAT	CCTGTTTACG	2340
	CTGGTCTGTG	GGGCTTCTGG	GACGTCTAAA	CAACCAAAAG	TAATTCCTGA	TGATTTAGCC	2400
	CAGCAGAACC	TAATTGTATC	AAACACAGAA	GCTCCTGGAG	ATGACAAAGT	GTATTCTGCC	2460
	AATOOOTO	CAACCCAAAC	TOTOGGGGGG	TOTOCTOROS	GACTUTUTOG	CACCUTTGGGA	2520
	AAJGGCITCA	CONCCCOOLAC	TO LOGGCGC1	A TOTAL A TOTAL	MODEL FOR CO.	ACACCACACC	2580
65	TCAUGAATCA	AAAACGGAGG GCCGGGGGGC	TCAGGAGACC	ALCONATIO	10MMOUNDS	OCCUPACE OF C	2640
03	TCGGAATCCT	GCCGGGGGGC	TGGCCACCAT	CACACCCTGG	ACTUCTGUAG	GGGAGGACAC	2640
	ACCCACCTOC	ACAACTGCAG	ATACACTTAC	TCGGAGTGGC	ACAGTTTTAC	TCAGCCCCGT	2700
	CTTGGTGAAG	AATCCATTAG	AGGACACACT	CTGATTAAAA	ATTAAACAAT	GAAAGAAAGT	2760
	GTATCTGTGT	AATCCATTAG AATCAAGATG	ARARTCACAA	GCATGCCCAA	GACTATGTCC	TGACATATAA	2820
	COTA TYCK NOOR	AGAGGATOGG	reacreagere	POTROCTIVET	TOCADTONAC	GACAAGAAGA	2880
70	POPECCOURT.	CA ATTENTOC	ATRATTOGA	CCCCABATTT	ACCACACTAG	CAGAAGCATG	2940
, ,	MUMICOGCIT	GAATTTTTGG TGAGTGTGTT	MANAGE TOOM	OCCUPANTIT	NOONCHUING	TO CONTRACT O	3000
	CATGAAGAGA	TGAGTGTGTT	CTAATAAGTC	TCTGAAAGCC	AGTGGCTTTA	TGACTTTTAA	
	AAAAAATTAC	AAACCAAGAA	TTTTTTAAAG	CAGAAGATGC	TATTTGTGGG	GGTTTTTCTC	3060
	TCATTATTTG	GATGGAATCT	CTTTGGTCAA	ATGCACATTT	ACAGAGAGAC	ACTATAAACA	3120
	AGTACACAAA	TTTTTCAATT AATTAAAGTC	TTTACATATT	TTTAAATTAC	TTATCTTCTA	TCCAAGGAGG	3180
75	TCTACAGACA	AATTAAAGTC	TGCCTTATTT	GITACATTTO	GGTATAATGA	CAACAGCCAA	3240
	TTTT TACTO	AATAAAATGT	BATTABTTCA	VCACCALAN AM	ATAGACTATT	TGAAGCACAA	3300
	TATAGAGG	MINMARGI	UNIT TOWN TOWN	ALCOUNTY	CONCERNIA	a a construction	3360
	CCTAATGGAA	AATTGTAGAG	ACCTIGCTT	MACATTATCT	CAGTTAATT	ANGIGITCAT	3360
	GTGGTGCTTG	GAAACTGTTG	TTTTCCTGAA	CATCTAAAGT	GTGTAGACTG	CATTCTTGCT	3420
	ATTATTTAT	TCTTGTAATG	TGACCTTTTC	ACTGTGCAAA	GGGAGATITC	TAGCCAGGCA	3480
80	TTGACTATTA	CAATTTCATT					
	Seg ID NO:	619 Prote	n semieron				
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85							
83	1	11	21	31	41	51	
	1	1	1	1	1	1	
	MEAARPSGSW	NGALCRLLLL	TLAILIFASD	ACKNVTLHVP	SKLDARKLVG	RVNLKECFTA	60

5	ANLIHSSDPD KKRHTKEKVL EPRNLFYVER PIFTEBTYTF TGVITTTSSQ VTSVEENTVD KPLNYEEKQQ KENAEVGTTS KNGIYNITVL EPIHGPPPDF	DTGNLYCTRP TIPENCRVGT LDRELIDKYQ VEILRVTVED MILQIGVVNB NGYKAYDPET ASDQGGRTCT SLESSTSEVO	VDREQYESFE TVGQVCATOK LKIKVQDMDG KDLVNTANWR APFSREASPR RSSSGIRYKK GTLGIILQDV EMWRLKAIND	IIAPATTPDG DEPDTMHTRL QYFGLQTTST ANYTILKGNE SAMSTATVTV LTDPTGWVTI LTDPTGWVTI NDNSPFIPKK TAARLSYOND	TENQEKKKIF SDTAQNYTIY YTPELPLPLI KYSIIGQVPP CIINIDDVND NGNPKLVTDA NVEDQDEGPE DENTGSIKVF TVIICKPTMS PPFGSYVVPI LLGIALLFCI VGASAQGVCQ	IKIEDENDNY SPTLFSMHPT HLPTFTRTSY KTNEGVLCVV CNPPIQTVRM RSLDREAETI SAEIVAVDPD TVRDRLGNSS	120 180 240 300 360 420 480 540 600 660 720
15	QETIEMVKGG GHTLIKN Seq ID NO:	HQTSESCRGA	GHHHTLDSCR equence	GGHTEVDNCR	VGASAQGVCG YTYSEWRSFT	TVGSGIKNGG QPRLGEESIR	780 840
	Coding sequ	d Accession	718	343.1			
20	1] ABACTGATCT	11 TCAATGCACT	21 	31 -	41 CCAAAAATGA	51 CCTGGAGGCA	60
25	CCATGTCAGG CTATCAAAGA GCACCGACAG CGAGGGCTGG	CTTCTGTTTA GAGAAACATA TCACCGCTCA GGGCCGGAGG CGCTGCTGCA	CGGTCAGTTT ACGGCGGTAG ACTGGACCTC AGCCGCTCCC	GGCATTACAG AGAGGAAGTC CAGTCATTTC CTACTCCCGG TACCTGCGTG	ATCATCAATT ACCAAGGTTG GGAGAGGTGA GCTTTCGGAG CTGGGCAGCT	TGGGAAACAG CCACTCAGAA CTGGGAGCGC AGGGTGCGTC TCTGCGTGTG	120 180 240 300 360 420
30	CCTGCACTGC	CTCCCCCTCC	AGACGCCTGA	CCCCAGCCTG	AGGCGCAGTG TGCAGGTGCA CCGAAAGACT CTACTCTTGC CCTCGGTCCC CTTGGGCATC	TGCCGGGCCTC	480 540 600 660 720
35	TTCTATGTTG	TAAATAATAG	ATGTGTTTAG	TTTACCGTAA	GCTGAAGCAC AAAAAAAAAA	TGGGTGAATA	780 840
40	Seq ID NO: Protein Acc	621 Protes	in sequence P_115934.1				
	ì	11	21	31	41	51	
45 .	VTGSAEGWGP	REPLPYSRAF	GEGASARPRC CIPGALHCLP	CRNGGTCVLG	VATOKHROSP SPCVCPAHFT DPLASHAHGP HRL	GRYCEHDQRR	60 120 180
50	Seq ID NO: Nucleic Ac: Coding sequ	622 DNA se id Accession mence: 13	a #: FGENES	H predicted	1		
	1	11	21	31	41	51	
55	GAACCATGGC	TGTGCCAGCC	GGCACCCAGG	TGTGGAGACA	GGAGTGTGCT TCATCGCTCC AGATCTACAA CCCGCCAATG CCTTTGGCCT GCCACTCATC	TGGTCCCCCC	60 120 180 240 300
60	agtaaatgtg	AAAGAGGCCG	GATATGTTAG	AATTCCCAGT	GCCACTCATC	TECCATETEE	360
	Seq ID NO: Protein Ac	623 Prote: cession #: 1	In sequence PGENESH pred	iicted			
65	1	11	21	31	41	51	
70	MRFSVSGMRT QCCYMDAIVS SKCERGRIC	 DYPRSVLAPA LSETROCGPP	YVSVCLLLLC CTFWPCFELC	PREVIAPAGS CLDSFGLTND	i epwlcqpapr fvvklkvqgv	NSOCHSSBIS CCDKIANAFE	60 120
70		624 DNA se id Accession mence: 51	a #: M18728	1			
75	GGAGCTCAAG	11 CTCCTCTACA	21 AAGAGGTGGÁ	31 CAGAGAAGAC	41 AGCAGAGACC GGTCCTGCTC	51 ATGGGACCCC ACAGCCTCAC	60 120
80	ATGTCGCAGA GTTACAGCTG TAGGAACTCA	GGGGAAGGAG GTACAAAGGC ACAAGCTACC	GTTCTTCTAC GAAAGAGTGG CCAGGGCCCG	TCGCCCACAA ATGGCAACAG CATACAGTGG	CCTGCCCCAG TCTAATTGTA TCGAGAGACA	AATCGTATTG GGATATGTAA ATATACCCCA	180 240 300 360 420
85	TCATAAAGTC TGCCCAAGCC CCTTCACCTG	AGATCTTGTG CTCCATCTCC TGAACCTGAG	AGCAACAACT GTTCAGAACA	CAACCGGACA CCAACCCGT CAACCTACCT	GTTCCATGTA GGAGGACAAG GTGGTGGGTA CATGACCCTC	TACCCGGAGC GATGCTGTGG AATGGTCAGA	480 540 600 660

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	GCGTCAAAAG	GAACGATGCA CCCAGTCACC	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720 780
	CCTCAAAGGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
5	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
3	CACCCACTCC	CAACATCACT	BCCACACACA	GCGGATCCTA	TATGTGCCAA	ACTOCTOCTO	960 1020
	TOCTCTCAGC	TGTGGCCACC	GTCGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGTATT	TTCGATATTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCCT	1140
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10	ACCCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAACTAGAGA	CAGTCAAACT	1320
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		TTTAAATGTC					1980
	CCCCCCAATT	ACDADACTCA.	CACAAAATCTC	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
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	1	11	21	31	41	51 .	
	1	!	1	<u></u>			
40	MOPPSAPPCR	LHVPWKEVLL ERVDGNSLIV	TASLLTPWNP	PTTAKLTIES	TPPNVAEGKE	NUTONDTORY	60 120
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	MCOST.DVCDD	TOT CHOWNETT	MT T CHHONEN				240
		DANSWOM! IT	LPPRAKTONDY	GSYECETONE	MANNKSDEVI	TWATIGEDAS	240
	TISPSKANYR	PGENLNLSCH	AASNPPAQYS	WFINGTFQQS	ASANRSDPVT TQBLFIPNIT	VNNSGSYMCQ	300
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45	Seq ID NO: Nucleic Ac:	TTVTMITVSG 626 DNA se id Accession	SAPVLSAVAT equence a #: M18728	VGITIGVLAR	TQELFIPNIT VALI	VNNSGSYMCQ	300
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50	AHNSATGLNR Seq ID NO: Nucleic Ac: Coding sequ GGAGCTCAAG CCTCAGCCCC TTCTAACCTT	626 DNA se id Accession sence: 1355 11	SAPVLSAVAT equence #: M187281657 21 AAGAGGTGGA TTGCATGTCC CCCACCACTG	VGITIGVLAR 1.1 31 CAGAGAAGAC CCTGGAAGGAC CCTAGGATGACCCACC	41 AGCAGAGACC GGTCCTGCTC TATTGAATCC	51 ATGGGACCCC ACAGCCTCAC ACGCCATTCA	60 120 180
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50	AHNSATGLNR Seq ID NO: Nucleic Ac: Coding seq	626 DNA se id Accession Lence: 1355 11 i CTCCTCTACA TCCCTGCAGA TCGGAGAAGGAG GTACAAAGGC ACAAGGTACACAAAGGC ACAAGGTACCA	SAPVLSAVAT equence #: M18728 .1657 21 AAGAGGTGGA TTGCATGTCC CCCACCACTG GTATATCTAC GRAAGAGTGG CCAGGGCCG CCAGGCCC GCAGGCCCC CCAGCCC CCAGCCC CCAGCCC CCACCC CCCACC CCACCC CACCC CCACCC CCACCC CCACCC CCACC CCACCC CCAC	VGITIGVLAR 31	41 	51 	60 120 180 240 360
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50 55	AHNSATGLNR Seq ID NO: Nucleic Ac: Coding sequ GGAGCTCAAG CCTCAGCCCC TTCTAACCTT ATGTCGCAGA GTTACAGCTG ATGCACTCA ATGCATCCT TAGGAACTCA ATGCATCCT TCTATAAGTC	626 DNA set d Accession Lence: 1355 11	SAPVLSAVAT quence a #: M187261657 21 AAGAGGTGGA TTGCATGTC CCCACCACTG GTTCTTCTAC GAAAGAGTGGA CCAGGGCCG AACGTCACAA	31 	41 	51 ATGGGACOCC ACAGCCTCAC ACGCCATTCA AATGGTATTG GGATATOTAA ATATACCCCA ACCCTACAAG TACCCGGAGC	60 120 180 240 300 420 480
50	AENSATGLNR Seq ID NO: Nucleic Ac: Coding sequ GGAGCTCAAG CCTCTAACCTT ATGTGCAGA GTTACAGCTG TAGGAACTCA ATGCATCAGTT TCCTAAAGTT TCCCAAAGCT TCCCAAAGCT TCCCAAAGCT TCCCAAAGCT TCCCCAAGCC TCCTTAACTT	626 DNA set id Accession sence: 1355 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SAPVLSAVAT quence a #: M18726 .1657 21 AAGAGGTGGA TTGCACCACTG GTTCTTCTAC CCACACTG GAAAGAGTGG CAAGGGCCGG AACGTCACCAC AACGACAACAACT GTTCAGAACAACAACT GTTCAGAACAACAACT GTTCAGAACAACAACT GTTCAGAACAACAACT GTTCAGAACAACAACT	VGITIGVLAR 31 CAGAGAAGAC CCTGGAAGGA CCAGACTCAC TCGCCCACAA ATGGCACCAGA AGGAATGACAC CAACCGGGAC CAACCGGGAC CCAACCCCAT CAACCTGCACAC	41 	51 ATTOGGACCCC ACAGCCTCAC ACAGCCATTCA AATCGTATTG GGATATOTAA ACTATACCCCA ACCCTACAAG GATCCTOTGG GATCCTOTGG GATCCTOTGG	50 120 180 240 300 360 420 480 540 600
50 55	AENSATGLNR Seq ID NO: Nucleic Ac: Coding sequ GGAGCTCAAG CCTCTAACCTT ATGTGCAGA GTTACAGCTG TAGGAACTCA ATGCATCAGTT TCCTAAAGTT TCCCAAAGCT TCCCAAAGCT TCCCAAAGCT TCCCAAAGCT TCCCCAAGCC TCCTTAACTT	626 DNA set id Accession sence: 1355 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SAPVLSAVAT quence a #: M18726 .1657 21 AAGAGGTGGA TTGCACCACTG GTTCTTCTAC CCACACTG GAAAGAGTGG CAAGGGCCGG AACGTCACCAC AACGACAACAACT GTTCAGAACAACAACT GTTCAGAACAACAACT GTTCAGAACAACAACT GTTCAGAACAACAACT GTTCAGAACAACAACT	VGITIGVLAR 31 CAGAGAAGAC CCTGGAAGGA CCAGACTCAC TCGCCCACAA ATGGCACCAGA AGGAATGACAC CAACCGGGAC CAACCGGGAC CCAACCCCAT CAACCTGCACAC	41 	51 ATTOGGACCCC ACAGCCTCAC ACAGCCATTCA AATCGTATTG GGATATOTAA ACTATACCCCA ACCCTACAAG GATCCTOTGG GATCCTOTGG GATCCTOTGG	60 120 180 240 300 360 420 480 540 660
50 55	AHNSATGLNR Seq ID NO: Nucleic Ac: Coding seq GGAGCTCAAG CCTCAGCCCC TATGACCTT ATGTGGCAGA GTTACAGCTT AAGGACTCA ATGCAATCCAT TCATAMGTT TCCCAAGCC CCTTCCACTG GCCTCCCGGT GCGTCCCAGGAAAAG	626 DNA set did Accession tence: 1355 11 11 11 12 CTCCTCTACA TCCCTGCAGA GAGGAAGGAG GAGG GTACAAGGC ACAGGTACCAG GAGCATACCAG AGATCTATC CTCCATCTC TGAACCTAGTCCAGA GATCCTAGA GATCCTAGA GATCCTAGA GATCCTAGA GATCCTAGA GATCCTAGA GATCCTAGA GATCCTAGA GATCCTAGA GATCCCAGG GAACGATGCA	SAPVLSAVAT quence 2 H: M187261657 21 ARGAGGTGGA TTGCATGTC CCCACCACTG GTTCTTCTAC GAAGAGGTGGA ACGTCACCC AATGAAGAGG ATGAAGAGTG GCAGGGCCG AATGAAGAAGA GCAACAACT GTTCAGAACA CTGCAGCTGT GTTCAGACA CTGCAGCTGT GTTCAGACA CTGCAGCTGT GGATCCTATG	JI CAGAGAAGAC CCTGGAAGGA CCTGGAAGGA ATGGCACAC CAACCAGGA CAACAGGGA CAACCAGGA CAACCAGGA CAACCAGGA CAACCAGGAC CCAACCAGGAC CCAACCAGGAC CCAACCAGGAC CCAACCAGGAC CCAACCAGGAC CCAACCAGGAC CAACCAGGAC CAACCAGGAC CAACCAGGAC CAACCAGGAC CAACCAGGAC CAACCAGGAC CAACTACCT CCAATGGCAA ATGTGAAAT	41	S1 ATGGGACCCC ACAGCCTCAC ACGCCATTCA ANTGGTATTG GGATATOTAA ATATACCCCAA ACCCTACAAG TACCCGGAGC GATGCTOTGG AATGGTCAGA ACCTTACTCA ACGGAGTCAGA GCGAGTGCCA	60 120 180 240 360 420 540 660 660
50 55 60	AENSATGLINR Seq ID MO: Nucleic Ac: Coding sequ GAGGCTCAAG GCTCAGCCC TICTAACCTT TATTGCGAGA GTACAGCTC TAGTAAGTC TAGTAAGTC TGCTCAAAAGTC GCTCCAAAAGAC TGCCAAAAGAC TGCCAAAAGAC TGCCAAAAGAC TGCCAAAAGAC TGCCAAAAGAC TCTCAAAAGAC	626 DNA set did Accession tence: 1355 11 11 11 12 CTCCTCTACA TCCCTGCAGA GCAGGAGGAG GAG GTACAAGCTACCAGCAGCTACCATCCC GCGAACCACCCCCCCCCC	SAPVLSAVAT quence 2 H: M187261657 21 ARGAGGTGGA TTGCATGTCC CCCACCACTG GTTCTTCTAC GAAGAGGTGGA ACGTCACCC GAAGAGGTGGA ACGTCACCC GAAGAGAGGA ACGTCACCC GTTCACCC CTCAGGGGAAA CCCCAGGGGAAA CCCCAGGGGAAA	JI GAGAGAAGAC CAGAGAAGAC CAGAGAAGAC CAGAGAAGAC CAGACCACA ATGGCACACA CAACCAGAC CAACCAGAC CAACCAGAC CAACCAGAC CAACCAGC CAACTACC 41 AGCAGAGACC GGTCCTGCTC CCTGCCCCAG TCTATTGAATCC CCTGCCCCAG TCGAGAGACCA AGGATTCATT GTTCCATGTA GGAGGACAAG GTGCTGGGTA CATGAACCCA AGATTTCCAC AGATTTCCAC CCTCCTGCCAC AGATTTCCCC CCTCCTGCCCCC CTCCTGCCCCC CTCCTGCCCCC CTCCTGCCCC	51 ATGGGACCCC ACACCATICA ACGCCATICA ACGCCATICA ACCCTACAAG ACCCTACAAG ACCCTACAAG ACCCTACAAG ACCCTACAAG ACCTTACACA ACCATTACCCA ACCATTACCA ACCATTACCA ACCATTACCA ACCATTTCCC	50 120 180 240 300 420 480 540 600 660 720	
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50 55 60 65 70 75	AMPSANTULME Seq ID NO) Nucleic Acc Coding seq 1 GAGCTCAAG COTTACACC COTTACACC COTTACACC ACC COTTACACC OTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC COTTACACC	26 DNA 9. 26 CNA 9. 26 NNA 9. 26 NNA 9. 21 1 11 1	SAPVLSAVAT SQUENCE B H NETZE B H NETZE L 1657 21 11 ARGAGGTGGA ARGAGGTGGA ARGAGGTGGA ARGAGGTGGA GAMAGGAGGGG ANTGAAGGAG GAMAGGAGGGG ANTGAAGAG GATGCTATTA ARGAGGAGGG COAGGGGAAA TGGTTATAGGA ARGAGGAGGAG TGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1.1 31 11 CAGRANGIAGO COTOGORÍO CATROCAGO ATOGOCOAGO	41 AGCAGRAGACC AGCAGCACA GOTOCTOCTC GOTOCTC GOTTC	51	60 120 160 240 360 480 480 480 600 860 860 860 100 100 1200 1200 1200 1200 1200 1200
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50 55 60 65 70 75	AMPISATOLIAR Seq ID NO. Nucleic As: Coding seq 1 1 1 1 1 1 1 1 1	226 DNA 91 240 Accession 195 11 11 11 11 11 11 11 11 11 11 11 11 11	SAPVLSAVAT (quence a #: NH8726 a #: NH8726 21 1	I.1 CAGAGAAGAA CAGAGAAGAAGAA TOGOCOLOLA ATOGOCOLOLA CACTATOGOC CACTATOGOC AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA TOG	41 AGGAGAGACC GOTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOC	51 1 ATGGGACCCC ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACGCCCCCCCCCC	300 120 120 180 300 240 300 420 480 540 660 780 960 960 1020 1140 1200 1140 1200 1140 1200 1150 1150 1150 1150 1150 1150 115
50 55 60 65 70 75 80	AMPISATOLIAR Seq ID NO. Nucleic As: Coding seq 1 1 1 1 1 1 1 1 1	626 DNA 91 626 DNA 92	SAPVLSAVAT (quence a #: NH8726 a #: NH8726 21 1	I.1 CAGAGAAGAA CAGAGAAGAAGAA TOGOCOLOLA ATOGOCOLOLA CACTATOGOC CACTATOGOC AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA AGAGTATOCOC TOGOCOLOLA TOG	41 AGGAGAGACC GOTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOC	51 1 ATGGGACCCC ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACG ACGGCTGACGCCCCCCCCCC	300 60 120 180 300 240 420 420 540 540 560 660 660 780 900 1020 1130 1130 1130 1130 1130 1130 1130 1130 1140 1150

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	CCITCCITAG	GACCIGGGGG	CCAGGCIGAC	######################################	and a community	200000000000000000000000000000000000000	840
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-	GCCCCCCAPACO	ATTGTTTCAT ATGAATACAA	CONTROL OF THE	20000000000	COMMISSION	BARCCTTCAC	1800
	TICICIOGCA	TACAAGAGAT	DAMOIO IOCC	ACTOCOMITO	CTTTOTOTO	MODE & BOOCCOT	1860
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5	AAAGTTTAAT TGTGTATATA	AATAGGTTTA	TTAACTGAAT AATACAACAT	ACTAAAAATT TTCATTAGTT TTACAATAAA	TTTTAAAAGT	GTTTTTGGTT	3720 3780 3840
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10	PYSKQVSYVI EGVHNSSIAL	QAEGKEHIIH SDCFGLRGLL	LERNKOLLPE HLENASYGIE	31 RPGFQQTSHL DFVVYTYNKE PLQNSSHFEH TRYVELPIVV	GTLITDHPNI IIYRMDDVYK	LTRERREAPR QNHCHYRGYV EPLKCGVSNK	60 120 180 240
15	LLANYLDSMY AQLVLKKGFG RDCSCGAKSC LVDAGEBCDC DVPEYCNGSS	IMLNIRIVLV GTAGMAFVGT IMNSGASGSR GTPKECELDP OFCOPDVFIO	GLEIWTNGNL VCSRSHAGGI NFSSCSAEDF CCEGSTCKLK NGYPCONNKA	INIVGGAGDV NVFGQITVET EKLTLNKGGN SFAECAYGDC YCYNGMCOYY	LGNFVQWREK FASIVAHELG CLLNIPKPDE CKDCRFLPGG DAOCOVIFGS	FLITRRHDS HNLGMNHDDG AYSAPSCGNK TLCRGKTSEC KAKAAPKDCF	300 360 420 480 540
20	HEVNSKGDRF WGVDFQLGSD NCHCENGWAP DOLWRSYFRK	UNDERGREE	TKCGAGKICR SVDSGPTYNE KNOANPSROP	MPQCVDASVL MNTALRDGLL GSVPRHVSPV	IDADGIADAI	HOHOVONSNK	600 660 720 780
25	Seq ID NO: Nucleic Act	634 DNA se ld Accession lence: 56!	equence				
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55	Seq ID NO: Nucleic Ac: Coding sequ	636 DNA se id Accession mence: 265.	a#: NM_01€	522.1			
60	1	11	21	31	41	51	
	CTGGCAAAAG	CCGAGGCTGG	ATTTGGGGGA	GCCGTCCTCC GGAATATTAG CGGGTTCACC	ACTCGGAGGA	GCGCCCCCCC	60 120 180
65	CCGCACCCCA TCGGGGAAGT TGCCTCGTGG AGCGGAGATG GCCACCCTCA	CCCACTTCCT TGTGGCTGTC TCGTGTCTCT CCACCTTCCC GGTGCACTAT	GTGCTCGCCC GAGAATGGGG CAGGCTGCTG CAAAGCTATG TGACAACCGG	GGGGGGCGTG GTCTGTGGGT TTCCTTGTAC GACAACGTGA GTCACCCGGG	TGCCGTGCGG ACCTGTTCCT CCACAGGAGT CGGTCCGGCA TGGCCTGGCT	CTGCCGGAGT GCCCTGGAAG GCCCGTGCGC GGGGGAGAGC AAACCGCAGC	240 300 360 420 480
70	ACCATCCTCT AACACCCAAA TACACCTGCT	ATGCTGGGAA CGCAGTACAG CGGTGCAGAC	TGACAAGTGG CATCGAGATC AGACAACCAC	TGCCTGGATC CAGAACGTGG CCAAAGACCT TCAGATATCT	CTCGCGTGGT ATGTGTATGA CTAGGGTCCA CCATTAATGA	CCTTCTGAGC CGAGGGCCCT CCTCATTGTG AGGGRACAAT	540 600 660 720 780
75	CGGGAACAGT CGGAGAGTAA GTCCCCGTGG	CAGGGGACTA AGGTCACCGT GACAAAAGGG	GAGTGCAGT GAGACTATCCA GACACTGCAG	CCATACATTT	CAGAGGCCAA CAGCAGTCCC	GCCCGTGGTA GGGTACAGGT CTCAGCAGAA	840 900 960 1020
80	AACAGACCTT TACACTTGCG CCAGGCGCCG	TCCTCTCAAA TGGCCTCCAA TCAGCGAGGT	ACTCATCTTC CAAGCTGGGC GAGCAACGGC CCTGCTTCTC	TTCAATGTCT CACACCAATG ACGTCGAGGA AAATTTTGAT	CTGAACATGA CCAGCATCAT GGGCAGGCTG GTGAGTGCCA	GAAAGTGGAA CTATGGGAAC GCTATTTGGT CGTCTGGCTG CTTCCCCACC CCGACAGCAA	1140 1200 1260 1320 1380
85	GGGAGGGGAA	CARAGRATAC	GAAATTAGAA	GAAACACAGC	AAAAAAGAAA	AGAAATTTGA TTGAAAATTG ACACAGCACA	1440 1500 1560

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5	GGCTCAGCCT AAATTCAATC CCGGCCCAAG	CTCTGCCCAC AGTCCATAGA CGTGGCGCTG	AGCTGCATCG AGACTGCCCC GACGAACAGA CGGGCACTTT CAAAAAAAA	CACGTGGAAC ATGAGACCTT GGTAGACTGT	ATTCTGGAGC CCGGCCCAAG	TGGCCATCCC	1620 1680 1740 1800
	Seq ID NO: Protein Acc	637 Protei	in sequence P_057606.1	•			
10	1	11	21	31	41	51	
15	NRVTRVAWLM NHPKTSRVHL SEDEYLEIQG LQCEASAVPS	RSTILYAGND IVQVSPKIVE ITREQSGDYB AEFQWYKDDK	LLFLVPTGVP KWCLDPRVVL ISSDISINEG CSASNDVAAP RLIEGKKGVK NGTSRRAGCV	LSNTQTQYSI NNISLTCIAT VVRRVKVTVN VENRPFLSKL	GRPEPTVTWR YPPYISEARG IFFNVSEHDY	GPYTCSVQTD HISPKAVGFV	60 120 180 240 300
20	Seq ID NO: Nucleic Ac: Coding seq	638 DNA se id Accession Lence: 203.	#: NM_012	261.1			
	1	11	21	31	41	51	
25	1	I CONTROL	GTCGGTGCCG	CGCTCGACAC	CACTCCTAG	CTAGGGGGCTC	60
	ACAGAATACG	CCCTCCCTCC	CTCCCCCTTC	TCTGTCCCCC	GCCTCTCGCT	CACCCCGGCC	120
	CACTCATTCGG	GCGACTTTGA	GGGATTCCCT GTATGGATCT TGTTCCATAC	CTCTGGCGGC	GGGGTCCCCA	GCACAGCCGG	240
30	ACTTCGAGTT	CTCCTGATGT	TGTTCCATAC	AATGGCTCAA	ATCATGGCAG	AACAAGAAGT	300
30	TGGGACGACG	TGTCTCATGG	CAGAGTTTGC TGATCACAGA	AGCCAAATTT	ATTOTACCTT	ATGATGTGTG	420
	GGCCAGCAAC	TACGTAGATC	TGATCACAGA	ACAGGCCGAT	ATCGCATTGA	CCCGGGGAGC	480 540
	CGCATATGCA	CTCAAAATGC	GCCACAGCCA TCTTTGTAAA AAGTGCAGTT	GGAAAGCCAC	AACATGTCCA	AGGGACCTGA	600
35	GGCGACTTGG	AGGCTGAGCA	AAGTGCAGTT	TGTCTACGAC	TCCTCGGAGA	AAACCCACTT	660 720
	CACCCCCCCCC	GGGAAGTCCT	GGAAGCACAC ATGAGTGTCA	AGCTCAACAG	ACCATTTCAC	TGGCCTCTAG	780
	TGATCCGCAG	AAGACGGTCA	ATGAGTGTCA CCATGATCCT	GTCTGCGGTC	CACATCCAAC	CTTTTGACAT	900
40	GGAAGAAACC	TIGCCCCTGA	GTGAAGAGCA TTTTGGGGCT	CATCTTGGGC	CTCGTCATCA	TGGTAACACT	960
	CGCGATTTAC	CACGTCCACC	TTTTGGGGCT ACAAAATGAC	TGCCAACCAG	GTGCAGATCC	CTCGGGACAG	1020
	CCAACTGGAT	CAGGTAGAAC	GCTAGAGGCC	CTTTTCCATC	TTGTACACGA	GATACACCAA	1140
45	CATAGCTACA	ATCAAACAGG	AACAAAAGCA CCTGGGTATC	TGAGGCTTGC	TTGGCTTGTG	TCCATGCTTA	1200
43	ATGCTGGGA	AGGGGGAGAC	TCTTTCGGAT	ACAGCTTTCG	TGCTCATGGT	GGCTTGGCTT	1260 1320
	TGACTCTCCA	AAGAGCAATA	AATGCCACTT	GGAGCTGTAT	CTGGCCCCAA	GGCTTGGCTT AGTTTAGGGA	1380
	TTGAAAACAT	GACACAGCTG	GGAGGAAACC	TACAGTTGTC	AATGCACACA	GAATACAACC	1500
50	TCATGCTCCC	TGCAGCAAGA	GCTTATCCTA CCCCTGAAAG	TGATTCATGC	TTCTGGCTGG	CATTCTGCAT	1560 1620
	AAAACGACTA GGGGGACCTG	ATGTAACTAT	ATGTTTCACT GCAGAGTTGT CTGTGTGAGT	TTGGACTTCT	TCCTGTGCCA	GGTCCAAGTC	1680 1740
55	TTCTCTCCC						
	Seq ID NO: Protein Ac	639 Protes cession #: 1	in sequence P_036393.1				
60	1	11	21	31	41	51 1	
00	MDLQGRGVPS	IDRLEVILML	PHTMAQIMAE	OEVENLSGLS	TWPEKDIFVV	RENGTTCLMA	60
	EFAAKPIVPY	DVWASNYVDL	ITEQADIALT VQFVYDSSEK	RGAEVKGRCG	HSQSELQVFW WUTANGUUT.C	VDRAYALKML	120 180
	ECOACOTISL	ASSDPORTVT	MILSAVHIOP	FDIISOFVFS	EEHKCPVDER	EQLECTLY	240
65	TOPITCEAIW	VTLAIYHVHH	KMTANQVQIP	RDRSQYKHMG			
	Seq ID NO: Nucleic Ac	640 DNA se id Accession uence: 64	n #: NM_002	1993.1			
70							
	1 GGCACGAGCC	l AGTOTOGOG	21 CCTCCACCCA	31 CCTCAGGAAC	41 CCGCGAACCC	51 TCTCTTGACC	60
75	ACTATGAGCC	TCCCGTCCAG	CCGCGCGGCC	CGTGTCCCGG	GTCCTTCGGG	CTCCTTGTGC	120
75	GCGCTGCTCG	CGCTGCTGCT	CCTGCTGACG	CCGCCGGGGC	CCCTCGCCAG	GAGAGTAAAC	180 240
							300
	GTGGTAGCCT	CCCTGAAGAA	CGGGAAGCAA TTTGGACAGT	GCAAACAAGA	ACCCGGAAGC	CCCTTTTCTA	360 420
80	ACCATGCATC	ATAAAATTGC	CCAGTCTTCA	GCGGAGCAGT	TTTCTGGAGA	TCCCTGGACC	480
-	CAGTAAGAAT	AAGAAGGAAG	GGTTGGTTTT	TTTCCATTTT	CTACATGGAT	TCCCTACTTT TAATGAAGTA	540 600
	CTAATATAGT	ATTTCCACTA	TTTACTGTTA	TTTTACCTGA	TAAGTTATTG	AACCCTTTGG	660
05	CARTICACCA	TATTOTCACC	BABGAATCAC	TGGTTATTAG	TCTTTCAATG	AATATTGAAT	720 780
85	ATTTCCCTATC	GARATARTGT	CTATCATACA TTTATTAGTG	TGCTGTTGAG	GGAGGTATCC	TGTTGTTCTT	780 840
	ACTCACTCTT	CTCATAAAAT	AGGAAATATT	TTAGTTCTGT	TTTCTTGGGG	AATATGTTAC	900

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5	TTATCTGTGC CTAATATATT CATGATTTAC ATTCTGGTCA TGATTGCTAA	AGGATGCTAT AGAATATATT CTCTTCCTAT TCATTAAACT CTAAATATAC TTTACATAGA	TCCTTATTCA GGTTTTAGAT TTGATTTTGT ACTTTAGATA AATGTATTCT	GAATTTCTAA GTTTGATGTC ATGCTATTTT GATGAAGAAG CTTGGTTTTT	AAATTTAAGT TTCTTAGTAT TTCACTATAG CCCAAAAACA TAAATAAAAG	TCTGTAAGGG GGCATAATGT GATGACTATA GATAAATTCC CAAAATTAAC	960 1020 1080 1140 1200 1260
10	CATTTAGTCC TTTAAAGGTT AAATTGCACT	GCTCTGCAAA TCAAAATATA TTGACCATTT TTTATTTTTT ATAAAAGATT	TACAGCATTG TGTTATGAGG CCTGTGTGTC	CTAAGATTTT AATTATACAT ATGTTGGTTT	CAGATATCTA GTATCACATT TTGGTACTTG	TTGTGGATCT CACTATATTA	1320 1380 1440 1500
15	Seq ID NO: Protein Acc	641 Protei cession #: 1	in sequence IP_002984.1	31	41	51	
20	MSLPSSRAAR	VPGPSGSLCA AGPQCSKVEV	LLALLLLLTP	 PGPLASAGPV	 SAVLTELECT	 CLRVTLRVNP	60
	Seq ID NO: Nucleic Ac: Coding sequ	642 DNA se ld Accession mence: 27	1 #: NM_013	271.1			
25	1 TCCGGAGCCA CCGGGGGCGT	11 GGCTCGCTGG CGGCCTTTTG	21 GGCAGCATGG GTGCTGCTGC	31 CGGGGTCGCC TGCTCGGCCT	41 GCTGCTCTGG GTTTCGGCCG	51 GGGCCGCGGG CCCCCCGGCGC	60 120
30	AGACTGGCGC	GCCGGTAAAG TCCTCGCCGC GGCGCGGGCG GCAGGAGGCT CCCCCGCAAC GCTCGCTCGC	TTCCGGCGGT	CAGTGCCCCG	AGGTGAGGCG	GCGGGGGGGG	180 240 300 360 420
35	CCCAGCTTGT ACGACGGCCC	CCCCGCGCCCC	GTCCCCGCCG GATGCTGAGG	AGGCAGGCGA	ACCCCGGCCC CGAGACACCC	GACGTGGACC TCCGAGGGGG	480 540 600 660 720
40		GCGCCGCTC GCTGGGGGCG CCGCCTCTTG CCGGCCATCC CAGCCAGCCC					780 840 900 960
45		643 Protes	₹P_037403.1				
50	Protein Act		P_037403.1 21 LLLGLFRPPP HLLEAERQER LRARLDPAAL	31 ALCARPVKEP ARAEAQEAED AAQLVPAPVP	QQARVLAQLL AAALRPRPPV	RVWGAPRNSD YDDGPAGPDA	60 120 180 240
50	Protein Act	11 RAGGVGLLVL AVQELARALA APAAQLARAL DPELLRYLLG	NP_037403.1	31 - ALCARPVKEP ARAEAQEAED AAQLVPAPVP GVAAPRRLRR	 RGLSAASPPL QQARVLAQLL AAALRPRPPV	AETGAPRRFR RVWGAPRNSD YDDGPAGPDA	120 180
50	Protein Act Magspllwgp RSVPRGEAAG PALGLDDDPD RVKRLETPAP Seq ID NO: Nucleic Ac: Coding sequ CCCAGAGCGG CTGCCGGACTT	11	P_037403.1 LLLGLFRPPP HLLEAERGER LRARLDPAAL ERLAGSADSE Quence 1 #: NM_002 2990 21 TGCTGGCAT TGCTGGCAT	31 ALCARPVKEP ALCARPVKEP ARABEAGEAED AAQLVPAPVP GVAAPRELER 214 31 CCCGAGGCTTC AGACCGGGGT	GCAAAGCTGC	AETGAPRRFR RYMGAPRISD YDDGPAGPDA PPEGVLGALL 51 AGCCAGGACG AACTAATGGT	120 180 240
50	Protein Act	11	P_037403.1 21	31 ALCARPVKEP ARAEAQEAED ARAUVFAPVP GVAAPRRIAR 214 31 CCCGAGCTTC AGACGGGCT CTGCGCTGAT CAGATCCAGC TGTTTGGGT CGGCTGARAA GAGCCCTC GAGCCTGARAA GAGCCCTCTGARAC	GLSAASPPL QQARVLAQLL AAALRPRPPA AADRDVGSEL 41 CTCCCTTGCC GCAAAGCTGC GCAAAGCTGC TGATGGCGCA ATCACCCAGT TGATGTGTT GAAACAAAGA TCCAGTGTTT GAAACAAAGA	AETGAPRER RVHGAPRISD TODGE AGED AGED AGED AGED AGED AGED AGED A	120 180 240 60 120 180 240 300 360 420
50 55 60	Probein Act Name	11 11 12 RAGGVGLLVIL RAGGVGLLVIL RAGGVGLLVIL RAGGVGLLVIL RAGGVGLLVIL RAGGVGLLVIL RAGGVGLLVIL STAPPACHARAL STAPPACHARAL STAPPACHARAL STAPPACHARAL STAPPACHARAL STAPPACHARA RAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RP_037403.1. 21 1 LLIGITARPPA HILEAREGER LEARIDPAIL RILAGASDE QUIENCE A # NM_002 291 1 TTGCTGGCAT GCTGGTCCCC GTGGAGCCAT AACCCTTCCA CTTGCGGCAT GAAGCCCTAC GAAGCCCTAC GAGCCCAC GAGCCCAC GGCGAGCCAC GGCGAGCCAC GGCCAGCCA	31 ALCARPUREP ARAEA(BEADE AND ANGLERA PUREP GWAAPRELER 2214 11 COCCAMACTEC COCCAMACT	FRISANSPEL QOARVLAQUL AVALREPERP AADLEPPRP ADLEPPRP AADL	S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S	60 120 240 240 120 240 300 360 420 480 660 660 6720
50 55 60 65	Protein Aci Acidotte	BERGOUGLAVI. AVGELARALA AVAGLARALA AVAGLARALA BERLEYILG GVARRELIDE 644 DIN. 644 DIN. 644 DIN. 644 DIN. 647 DIN	IP_037403.1. 1 LIJOILPREPP HLIERBERGER LLIAGISABSE PRIMERS A 1 % INM_002.2990 21 TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL OF TOTAL CONTROL CONTR	31 I ALCAD PWEEP ALCAD P	BILISANSPEL QQARVLAQLL ANALREPEPY AADHEDVOSEL 11 CTOCCTTGCC TOATCGCC TOATCGCC GCAAAGCTCG GCAAAGCTCG GCATCGCC CCTGCGCGC GCTTACTCGCC CCTGCGCAGC GCTTACTCCC CCTGCGCAGC GCTACCACC GCGCACCAGC TTTTTTTTCC TTTTTTTCC GCGCACCAGC GCACCAGC GCACCAGC GCACCAGC GCACCAGCAGC GCACCAGC GC GCACCAGC GCACCACCACCAC GCACCACCAC GCACCACCACCAC GCACCACCACCACCAC GCACCACCACCACCACCACCAC GCACCACCACCACCACCACCACCACCACCACCACCACCAC	APTOAPREPR RVHCAPREPS TO TOO PROPERTY OF THE P	120 180 240 240 120 180 360 420 420 420 660 660 6720 780 960 960 960
50 55 60 65 70	Protein Act MAGSPLLMGP RSVPRGEAG PALGLODDPI MAGSPLLMGP RSVPRGEAG RSVPRGEAG Seq ID No Nucleic Ac Codin FOR COMMISSION COMMI	mension B: 1 AGGOVGILVIL AVGELARIAA AVAQLARIA BPELLERTILIA GURARELLEP 644 DNA B: 14 Accession Encore 681. 11 1 CCTCCCCCTA TOTATICACEO TOCCTCACC TOCCCACCAC TOCCCACCAC TOCCCACCAC TOCCCACCAC TOCCCCACCAC TOCCCCACCAC TOCCCCACCAC TOCCCCCACCAC TOCCCCCACCAC TOCCCCCACCAC TOCCCCCCACCAC TOCCCCCCACC TOCCCCACCAC TOCCCCCCACC TOCCCCCCCACC TOCCCCCCCCC TOCCCCCCCCC TOCCCCCCCC	RP_017403.1. ILLIGITPPPP HILERARGER LERARIDPARI, RELAGISADE GUERCE S 9: NN_002 21 I I I I I I I I I	31 ALCARPVKEP ALCARPVKEP ARABAGISTAN ANGARPATER ANGARPATER 214 31 CCCARGCTTCA CRISTICATE COGARGCTTCA ANGARCGGGGC CGGGAAACGT CGGGGGGGGGGGGCC CGGGAAACGT CGGGCCTGTGCT ACCGCGGGAC CGGGCCTGTGCT ACCGCGGGAC CGCCCTGCT ACCGCGGGAC ACCGCGGGAC ACCGCGGGAC ACCGCGGGAC ACCGCGGGAC ACCGCGGGAC ACCGCGGAC ACCGCGAC ACCGCGGAC ACCGCGGAC ACCGCGGAC ACCGCGGAC ACCGCGGAC ACCGCGGAC ACCGCGAC ACCGCGGAC ACCGCGAC ACCGCAC ACCGCGAC ACCGCGAC ACCGCAC ACCCCAC ACCGCAC ACCGCAC ACCCCAC ACCGCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCCAC ACCCAC ACCCCAC ERGLEARSPEL QQARVLAQLIA ANALERPERY ANALERPERY ANDIENVOSEL 11 CTCCCTTGCC GCAAGCTCC TRATCGCCAAC TRATCGCCAAC TRATCGCCAC GCAAGCTCC TTGATTGCTGT GAACAAAAA CCCAGT TTTTTTTAC GCGCACCAGC GCGACCAGC TTGTTTTTTAC GGGCACCAGC GGGACCTAG	STATION PRINTED TO THE PROPERTY OF THE PROPERT	60 120 120 120 120 120 180 360 420 480 600 720 780 840 900	

	CCOUNTIGGC	GACAACCATG	CAACACCCC	CACTACCCCA	ACTORNO	ARATTANTAC	1680
	ACCICABATE	MA ANCHORIO	TTTCCACCCCI	AACCAAAACA	ATTTCATTCA	TATAAGGATC	
	TECHNOLICAT	CTTCCCACCC	ACCATTCCTC	CTCAAATACA	ATCABACCCT	CCABACCTCA	1000
5	11CIACCCC1	CITOCOAGGC	MARCACIA ACC	DOS MONTON	ACTORNACET	GCAAACCTCA CAGGTGGAAA TCCAGAAAGC	1060
,	ATACTTIGGT	AG1GGAAGCC	TATCAGAAGC	COCCOCATORC	TOCAGATOGG	TCCACAAACC	1020
							1980
	TTACAATCAA	A A A A TOTO A T	CTCACACCAC	CARAGATOR	TGCABTABTC	AAACCTATTG TGTGAGGACA TGTTTCCAGT	2040
	TTACAATGAA	AMMIGIGAT	ATTICATION OF THE	PCPCPPPCIA	CACCINITION	TOTOROGRACE	2100
10	DOLONGO	TARRECTARA	TOTOTACATO	ALAGORACIG	ACATTCCARG	TOTOTOCACT	2160
10	ACAGAGGACC	TAAATGTCAT	TOTGTAGATG	AMACITITCI	TECTCACACT	TOTALCE	2220
	GIGNIGNAN	IAAAIGICAI	TITGATGAAG	AICHOITTIC	mromooda a a	MORROR TOTAL	2280
	ACAAGGATCA	GCCTGTTTGC	AGTGGTCGAG	GAGITIGIGI	TIGIGGGGGGG	TGTTCATGTC TTTTCTTGTC AGATGCCAAT	2340
	ACAAAATTAA	GCTTGGAAAA	GIGIATGGAA	AATACTUTGA	AAAGGATGAC	TTTTCTTGTC	
15	CATATCACCA	TGGAAATCTG	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
13	GCTTCAGTGG	CTGGGAAGGT	GATCGATGCC	AGTGCCCTTC	AGCAGCAGCC	CAGCACTGTG	2460
	TCAATTCAAA	GGGCCAAGTG	TGCAGTGGAA	GAGGCACGTG	TGTGTGTGGA	AGGTGTGAGT	2520
	GCACCGATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
	GCAAGGAAAA	CTGGAATTGT	ATGCAATGCC	TTCACCCTCA	CAATTTGTCT	CAGGCTATAC	2640
20	TTGATCAGTG	CAAAACCTCA	TGTGCTCTCA	TGGAACAACA	GCATTATGTC	AGGTGTGAGT TATACAGCCT CAGGCTATAC GACCAAACTT	2700
20	CAGAATGTTT	CTCCAGCCCA GTTGCTTAAA	AGCTACTTGA	GAATATTTTT	CATCATTTTC	ATAGTTACAT	2760
	TCTTGATTGG	GTTGCTTAAA	GTCCTGATCA	TTAGACAGGT	GATACTACAA	TGGAATAGTA	2820
	ATAAAATTAA	GTCCTCATCA	GATTACAGAG	TGTCAGCCTC	aaaaaaggat	AAGTTGATTC	2880
	TGCAAAGTGT	TTGCACAAGA	GCAGTCACCT	ACCGACGTGA	GAAGCCTGAA	GAAATAAAAA	2940
~-	TGGATATCAG	CAAATTAAAT	GCTCATGAAA	CTTTCAGGTG	CAACTTCTAA	AAAAAGATTT	3000
25	TTAAACACTT	AATGGGAAAC	TGGAATTGTT	AATAATTGCT	CCTAAAGATT	AAGITGATTC GAAATAAAA AAAAGATTT ATAATTTTAA ACACTCGAAC TTTTCAGGAG GTAATATATA	3060
	AAGTCACAGG	AGGAGACAAA	TTGCTCACGG	TCATGCCAGT	TGCTGGTTGT	ACACTCGAAC	3120
	GAAGACTGAC	AAGTATCCTC	ATCATGATGT	GACTCACATA	GCTGCTGACT	TTTTCAGAGA	3180
	AAAATGTGTC	TTACTACTGT	TTGAGACTAG	TGTCGTTGTA	GCACTTTACT	GTAATATATA	3240
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							3720
	TACTGCCATA	AAAAACTAAT	AATACAATGT	CACTITATCA	GAATACTAGT	TTTAAAAGCT	3780
	GAATGTTAA						
40	Sea TD NO.	645 Prote	n gemience				
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	1	11	21	31	41	51	
	ī	T-	1		i	,	
45	MCCONTARRE	T-	1		OGEDNECASS	,	60
45	MCGSALAFFT	T-	1		QGEDNRCASS	,	60
45	 MCGSALAFFT LGPECGWCVQ	T-	1		QGEDNRCASS YPSVHVIIPT	,	120
45	MCGSALAFFT LGPECGWCVQ GEVSIQLRPG	AAFVCLQNDR EDFISGGSRS ARANPMI.KVH	RGPASFLWAA ERCDIVSNLI PLEKYPUOLY	WVFSLVLGLG SKGCSVDSIE YLVDVSASMH	QGEDNRCASS YPSVHVIIPT NNIEKLMSVG	NAASCARCLA ENEINTQVTP NDLSRKMAFF	120 180
45	MCGSALAFFT LGPECGMCVQ GEVSIQLRPG SRDFRLGFGS	AAFVCLQNDR EDFISGGSRS ARANPMI.KVH	RGPASFLWAA ERCDIVSNLI PLEKYPUOLY	WVFSLVLGLG SKGCSVDSIE YLVDVSASMH	QGEDNRCASS YPSVHVIIPT NNIEKLMSVG PHGYIHVLSL	NAASCARCLA ENEINTQVTP NDLSRKMAFF	120 180 240
	VHROKISGNI	AAFVCLQNDR EDFISGGSRS AEANFMLKVH YVDKTVSPYI DTPEGGFDAN	RGPASFLWAA ERCDIVSNLI PLKKYPVDLY SIHPERIHNQ LQAAVCESHI	WVFSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL	LVMTDQTSHL	NAASCARCLA ENBINTQVTP NDLSRKMAFF TENITEPEKA ALDSKLAGIV	120 180 240 300
45 50	VHROKISGNI	AAFVCLQNDR EDPISGGSRS AEANPMLKVH YVDKTVSPYI DTPEGGFDAM	RGPASFLWAA ERCDIVSNLI PLKKYPVDLY SIHPERIHNQ LQAAVCESHI EHPSLGOLSE	WVFSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNNINVI	LVMTDQTSHL	MAASCARCLA ENEINTQVTP HDLSRKMAFF TENITEPEKA ALDSKLAGIV YKOLLPLLPG	120 180 240 300 360
	VHROKISGNI	AAFVCLQNDR EDPISGGSRS AEANPMLKVH YVDKTVSPYI DTPEGGFDAM	RGPASFLWAA ERCDIVSNLI PLKKYPVDLY SIHPERIHNQ LQAAVCESHI EHPSLGOLSE	WVFSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNNINVI	LVMTDQTSHL	MAASCARCLA ENEINTQVTP HDLSRKMAFF TENITEPEKA ALDSKLAGIV YKOLLPLLPG	120 180 240 300 360 420
	VHRQKISGNI VPNDGNCHLK TIAGEIESKA NVTSNDEVLP	AAFVCLQNDR EDFISGGSRS AEANFMLKVH YVDKTVSPYI DTPEGGFDAM NNVYVKSTTM ANLINILVVEA NVTVTMKKCD	RGPASFLWAA ERCDIVSNLI PLKKYPVDLY SIHPERIHNQ LQAAVCESHI EHPSLGQLSE YQKLISEVKV VTGGKNYAII	WVFSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWREAKRLL KLIDNNINVI QVENQVQGIY KPIGFNETAK	LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ	NAASCARCLA ENEINTQVTP HDLSRKMAFF TENITEFEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGK	120 180 240 300 360 420 480
	VHRQKISGNI VPNDGNCHLK TIAGEIESKA NVTSNDEVLP CVDRTFLDSK	AAFVCLQNDR EDPISGGSRS AEANFMLKVH YUDKTVSPYI DTPESGFDAM MNVYVKSTTM ANLINILVVEA NVTVTMKKCD CFOCDENKCH	RGPASFLWAA ERCDIVSNLI PLKKYPVDLY SIHPERIHNQ LQAAVCESHI EHPSLGQLSE YQKLISEVKV TOGKNYAII FDEDOFSSES	WVPSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNNINVI QVENQVQGI KPIGFNBTAK CKSHKDOPVC	LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK	NAASCARCLA ENBINTOUTP HDLSRKMAFP TENITEFEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGR CSCHKIKLGK	120 180 240 300 360 420 480 540
50	VHRQKISGNI VPNDGNCHLK TIAGEIBSKA NVTSNDEVLF CVDETFLDSK VYGKYCKKDD	AAFVCLQNDR EDFISGSSS ABANFMLKVH YVDKTVSPYI DTPESGFDAN NNVYVKSTTM ANLINILVVEA HVTVTMKKCD CFQCDENKCH FSCCPYHIGNL	RGPASFLWAA ERCDIVSNLI PLKKYPVDLY SIHPERIHNQ LQAAVCESHI EHPSLGQLSE YQKLISEVKV VTGGKNYAII FDEDQFSSES CAGHGECEAG	WYPSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNNINVI QVENQVQGIY KPIGFNBTAK CKSHKDQPVC RCOCFSGWEG	LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK DRCOCPSAAA	I NAASCARCLA ENBINTQVTP MDLSRKMAFF TENITEPEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGK CSCHKIKLGK OHCVNSKGOV	120 180 240 300 360 420 480 540 600
	VHRQKISGNI VPNDGNCHLK TIAGEIBSKA NVTSNDEVLF CVDETFLDSK VYGKYCKKDD	AAFVCLQNDR EDFISGSSS ABANFMLKVH YVDKTVSPYI DTPESGFDAN NNVYVKSTTM ANLINILVVEA HVTVTMKKCD CFQCDENKCH FSCCPYHIGNL	RGPASFLWAA ERCDIVSNLI PLKKYPVDLY SIHPERIHNQ LQAAVCESHI EHPSLGQLSE YQKLISEVKV VTGGKNYAII FDEDQFSSES CAGHGECEAG	WYPSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNNINVI QVENQVQGIY KPIGFNBTAK CKSHKDQPVC RCOCFSGWEG	LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK DRCOCPSAAA	I NAASCARCLA ENBINTQVTP MDLSRKMAFF TENITEPEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGK CSCHKIKLGK OHCVNSKGOV	120 180 240 300 360 420 480 540 600
50	SRDFRLGFGS VHRQKISGNI VPNDGNCHLK TIAGEISSKA NVTSNDEVLF CVDETFLDSK VYGKYCEKDD CSGRGTCVCG CALMEOOHYV	AAFVCLQNDR EDFISGSRS AEANFMLKVH YUDKTVSPYI DTPEGGPDAM NNVYVKSTIM ANLINILVVEA NVTVTMKKCD CFQCDENKCH FSCPYHHGNL RCECTDPRSI DOTSECFSSP	RGPASFLWAA ERCDIVSNLI PLKKYPVDLY SIHPERIHNQ LQAAVCESHI EHPSLGQLSE YQKLISEVKV VTGGKNYAII FDEDQFSSES CAGHGECEAG GRFCEHCPTC SYLRIFPIIF	WYPSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNNINVI QVENQVQGIY KPIGFNBTAK CKSHKDQPVC RCQCFSGMEG YTACKENMINC IVTFLIGLLK	PHGITHVISE LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ	NAASCARCLA ENBINTOUTP HDLSRKMAFP TENITEFEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGR CSCHKIKLGK	120 180 240 300 360 420 480 540 600
50	SRDFRLGFGS VHRQKISGNI VPNDGNCHLK TIAGEISSKA NVTSNDEVLF CVDETFLDSK VYGKYCEKDD CSGRGTCVCG CALMEOOHYV	AAFVCLQNDR EDFISGSSS ABANFMLKVH YVDKTVSPYI DTPESGFDAN NNVYVKSTTM ANLINILVVEA HVTVTMKKCD CFQCDENKCH FSCCPYHIGNL	RGPASFLWAA ERCDIVSNLI PLKKYPVDLY SIHPERIHNQ LQAAVCESHI EHPSLGQLSE YQKLISEVKV VTGGKNYAII FDEDQFSSES CAGHGECEAG GRFCEHCPTC SYLRIFPIIF	WYPSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNNINVI QVENQVQGIY KPIGFNBTAK CKSHKDQPVC RCQCFSGMEG YTACKENMINC IVTFLIGLLK	PHGITHVISE LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ	I NAASCARCLA ENBINTQVTP MDLSRKMAFF TENITEPEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGK CSCHKIKLGK OHCVNSKGOV	120 180 240 300 360 420 480 540 600
50	SRDFRLGFGS VHRQKISGNI VPNDGNCHLK TIAGEISSKA NVTSKDEVLF CVDETFLDSK VYGKYCEKDD CSGRGTCVCG CALMEQQHYV DYRVSASKKD	AAFVCLQNDR AAFVCLQNDR EDPISGGRS AEANFMLKVH YVDRIVSFYI DTPEGGFDAM NNVYVKSTIM ANIANILAVEA NIVTYMRKCC CFQCDENKCH PSCPYHHGNL RCECTDPRSI DOTSECPSSP KLILQSVCTR	RGPASFLWAA ERCDIVSMLI PLRKYPVDLY SIHEERIENQ LGAAVCESHI EHPSLGQLSE YQKLISEVKV VTGGRNYAII FDEDQFSSES CAGGECEAG GRFCEHCPTC SYLRIFFIIF AVTYRREKPE	WYPSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNNINVI QVENQVQGIY KPIGFNBTAK CKSHKDQPVC RCQCFSGMEG YTACKENMINC IVTFLIGLLK	PHGITHVISE LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ	I NAASCARCLA ENBINTQVTP MDLSRKMAFF TENITEPEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGK CSCHKIKLGK OHCVNSKGOV	120 180 240 300 360 420 480 540 600
50 55	SRIPFILIGIGS VHROKISGNI VPNDGNCHLK TIAGEIBSKA HVTSNDEVLF CVDETFILDSK VYGKYCEKDD CSGRGTCVCG CALMEQQHYV DYRVSASKKD Seg ID NO:	AAFVCLQNDR EDPISGGRS AEANFMLKVH YVDKTVSFYI DTPEGGFDAN NNYVKSTTM ANIANLVVEA NVTVTMKKCD CFQCDENKCH RCECTDPRSI DOTSECPSS KLILGSVCTR 646 DNA 22	RGPASFLWAA ERCDIVSMLI PLKKYPVDLI PLKKYPVDLI SIHEERIUM LQAAVCESHI EHPSLGQLSE YQKLISEVV VTGGGNYAII FDEDQFSSES GRFCEHCPTC SYLRIFFIIF AVTYRREKPE	WYPSLYLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNINWI KPIGFNETAK CKSHKDQPVC YTACKEMNC YTACKEMNC IVTFLIGLLK BIKMDISKLN	PHGITHVISE LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ	I NAASCARCLA ENBINTQVTP MDLSRKMAFF TENITEPEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGK CSCHKIKLGK OHCVNSKGOV	120 180 240 300 360 420 480 540 600
50	SRIPFILIGIGS VHROKISGNI VPNDGNCHLK TIAGEIESKA NVTSNDEVLP CVDETFILDSK VYGKYCEKDD CSGRGTCVCG CALMEQOHYV DYRVSASKKD Seq ID NO: Nucleic Ac:	AAFVCLQNDR EDPISGGSRS AEANFMLKVH YVDKIVSFYI DTPEGGFDAN NNYVYKSTIM ANLNNLVVEA NVTVTMKKCD CFQCDEJMKCH FSCPYHHGNL RCECTDPRSSP KLILQSVCTR 646 DNA as dd Accession	RGPASFLWAA ERCDIVSMLI PLKKYPUDLY SIHBERINNQ LQAAVCESHI EHPSLGQLSE YQKLISEVKV VTGGKNYAII FDEDQFSSES CAGGGCSAG GRFCEHCPTC SYLRIFFIIF AVTYRREKPE pquence n #: NM_003	WYPSLYLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNINWI KPIGFNETAK CKSHKDQPVC YTACKEMNC YTACKEMNC IVTFLIGLLK BIKMDISKLN	PHGITHVISE LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ	I NAASCARCLA ENBINTQVTP MDLSRKMAFF TENITEPEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGK CSCHKIKLGK OHCVNSKGOV	120 180 240 300 360 420 480 540 600
50 55	SRIPFILIGIGS VHROKISGNI VPNDGNCHLK TIAGEIESKA NVTSNDEVLP CVDETFILDSK VYGKYCEKDD CSGRGTCVCG CALMEQOHYV DYRVSASKKD Seq ID NO: Nucleic Ac:	AAFVCLQNDR EDPISGGRS AEANFMLKVH YVDKTVSFYI DTPEGGFDAN NNYVKSTTM ANIANLVVEA NVTVTMKKCD CFQCDENKCH RCECTDPRSI DOTSECPSS KLILGSVCTR 646 DNA 22	RGPASFLWAA ERCDIVSMLI PLKKYPUDLY SIHBERINNQ LQAAVCESHI EHPSLGQLSE YQKLISEVKV VTGGKNYAII FDEDQFSSES CAGGGCSAG GRFCEHCPTC SYLRIFFIIF AVTYRREKPE pquence n #: NM_003	WYPSLYLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNINWI KPIGFNETAK CKSHKDQPVC YTACKEMNC YTACKEMNC IVTFLIGLLK BIKMDISKLN	PHGITHVISE LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ	I NAASCARCLA ENBINTQVTP MDLSRKMAFF TENITEPEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGK CSCHKIKLGK OHCVNSKGOV	120 180 240 300 360 420 480 540 600
50 55	SRIPFILIGIGS VHROKISGNI VPNDGNCHLK TIAGEIESKA NVTSNDEVLP CVDETFILDSK VYGKYCEKDD CSGRGTCVCG CALMEQOHYV DYRVSASKKD Seq ID NO: Nucleic Ac:	AAFVCLQNDR EDFISGGSRS AEANFMLKVH YVDKTVSSYI DTPEGGFDAM NNVYVKSTYI NILANLVVEA NVTVTMKKCD CFGCDEMKCH FSCSYHHGNL RCECTDFRSS KLILQSVCTR 646 DNA se id Accession sence: 12:	RGPASFLMAA ERCDIVSNLI PLKKYPUDLY SINBERINNQ LQAAVCSSHI ENPSLGQLSE YQKLISEVKV VTGGKNYAII FDEDQFSSES CAGHGECSAG GRFCEHCPTC SYLRIFFIIF AVTYRREKPE EQUENCE ##: NM_003	WYPSLVLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLU KLIDDNINU QVENQVQGIY KPIGFNETAK CKSHKDQPVC RCQCPSGMEG YTACKEBMC IVTFLIGLLK BIKMDISKLN	PAGTIRVISI LYMTOOTSHL PAVQGKQFHM FNITAICPDG HIHIRNCSCQ SGRGVCVCGK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ AHETFRCNF	AMASCARCLA ENEINTQUTP HDLSRKMAFF HDLSRKAFF YRDLLPLLPG SRKPGMEGCR CEDNRGPKGK CEDNRGPKGK QHCUNSKGQV QAILDQCKTS WNSNKIKSSS	120 180 240 300 360 420 480 540 600
50 55	SRIPFILIGIGS VHROKISGNI VPNDGNCHLK TIAGEIESKA NVTSNDEVLP CVDETFILDSK VYGKYCEKDD CSGRGTCVCG CALMEQOHYV DYRVSASKKD Seq ID NO: Nucleic Ac:	AAFVCLQNDR EDPISGGSRS AEANFMLKVH YVDKIVSFYI DTPEGGFDAN NNYVYKSTIM ANLNNLVVEA NVTVTMKKCD CFQCDEJMKCH FSCPYHHGNL RCECTDPRSSP KLILQSVCTR 646 DNA as dd Accession	RGPASFLWAA ERCDIVSMLI PLKKYPUDLY SIHBERINNQ LQAAVCESHI EHPSLGQLSE YQKLISEVKV VTGGKNYAII FDEDQFSSES CAGGGCSAG GRFCEHCPTC SYLRIFFIIF AVTYRREKPE pquence n #: NM_003	WYPSLYLGLG SKGCSVDSIE YLVDVSASMH CSDYNLDCMP GWRKEAKRLL KLIDNINWI KPIGFNETAK CKSHKDQPVC YTACKEMNC YTACKEMNC IVTFLIGLLK BIKMDISKLN	PHGITHVISE LVMTDQTSHL FAVQGKQFHW FNITAICPDG IHIHRNCSCQ SGRGVCVCGK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ	I NAASCARCLA ENBINTQVTP MDLSRKMAFF TENITEPEKA ALDSKLAGIV YKDLLPLLPG SRKPGMEGCR CEDNRGPKGK CSCHKIKLGK OHCVNSKGOV	120 180 240 300 360 420 480 540 600
50 55 60	SRDFRIDGES VERQNISCHI VPNDONCHLK TIAGEIESKA NVTSNDEVLF CVDETFLDSK VYGKYCEKDD CSGRGTCVCG CALMEQQHYV DYRVSASKKD Seq ID NO: Nucleic Ac: Coding sequ 1	AAFVCLQNDR AAFVCLQNDR EDPISGGRSS AEANFMLKVH YVDKTVSPYI DTPEDGFDAM KNYVVKSTM ANIANILVVEA NVTVTMKCC CFQCDEMKCH RCECTDFRSI KOTSECTSPSS KLILQSVCTR 646 DNA as id Accession ence: 12	RGPASFLWAA RCCDIVSNLI PLKKYPVOLY SIHDERIUM LQAAVCESHI LQAAVCESHI EHFSLGQLSE YQKLISEVKV VTGGRNYAII FDEOGFSSES SYLEIFFIIF AVTTRREKPE EQUENCE 1 %: NM_00: 574	WYPSLVLGLG SKGCSVDSIE SKGCSVDSIE SKGCSVDSIE SKGCSVDSIE SKGCSVDSIE SUNTDCMS GUNKEAKHD KLIDNINVI QVERQVQCIY KYIGFNSTAK CKSHKODPVC TYTFLIGLLK BIKMDISKLM 318.1	PRISTINUES LIMITO/TSHL FAVQUKQFHM FNITAICPDG IHIHRNCSCQ SGRGVCVGIK DRCQCPSAAA MQCLHPHNLS VLIIQVILQ AHSTFRCNF	MAASCARCLA ENELITOVEN ENELITOVEN BULGENKAP TENITEPEKA ALDEXLAGY YROLLPLLPG SRKYGMEOGR GEONRGPKGK CSCHKIKIGK WNSNKIKSSS	120 180 240 300 420 480 540 600 720
50 55	SRDFRIDGES VERQNISCHI VPNDONCHLK TIAGEIESKA NVTSNDEVLF CVDETFLDSK VYGKYCEKDD CSGRGTCVCG CALMEQQHYV DYRVSASKKD Seq ID NO: Nucleic Ac: Coding sequ 1	AAFVCLQNDR AAFVCLQNDR EDPISGGRSS AEANFMLKVH YVDKTVSPYI DTPEDGFDAM KNYVVKSTM ANIANILVVEA NVTVTMKCC CFQCDEMKCH RCECTDFRSI KOTSECTSPSS KLILQSVCTR 646 DNA as id Accession ence: 12	RGPASFLWAA RCCDIVSNLI PLKKYPVOLY SIHDERIUM LQAAVCESHI LQAAVCESHI EHFSLGQLSE YQKLISEVKV VTGGRNYAII FDEOGFSSES SYLEIFFIIF AVTTRREKPE EQUENCE 1 %: NM_00: 574	WYPSLVLGLG SKGCSVDSIE SKGCSVDSIE SKGCSVDSIE SKGCSVDSIE SKGCSVDSIE SUNTDCMS GUNKEAKHD KLIDNINVI QVERQVQCIY KYIGFNSTAK CKSHKODPVC TYTFLIGLLK BIKMDISKLM 318.1	PRISTINUES LIMITO/TSHL FAVQUKQFHM FNITAICPDG IHIHRNCSCQ SGRGVCVGIK DRCQCPSAAA MQCLHPHNLS VLIIQVILQ AHSTFRCNF	MAASCARCLA ENELITOVEN ENELITOVEN BULGENKAP TENITEPEKA ALDEXLAGY YROLLPLLPG SRKYGMEOGR GEONRGPKGK CSCHKIKIGK WNSNKIKSSS	120 180 240 300 350 420 480 600 720
50 55 60	SRDPRLIGGS VERGALSCAI VPHOCHCILK TIAGEISEKA NTISIDEULE CVDETFLDSK VYGKYCEKDD CSGRGTCVCG CALMBOGHYV DYRVSASKKD Seq ID NO: Nucleic Ac: Coding seq	AAFVCLQNDR EDPISGGRSS AEANFMLXVH YVDKTVSFYI DTPEGGFDAM NNVYVKSTM ANIANIAVEA KOTOTHERS FSCPYHENL RCECTDFRSI EJGTSECTS	RGPASFLWAA RCCDIVSHLI PLKKYPYDLY 91HPERIUMO LQAAVCESHI EHFSLQQLSE YQKLISEVKV VTGGKNYAII FDEOGFSSES SYLRIFFIIF AVTYRREKPE PQUENCE 1 %! NM_00:574	WYPSLVLGLG SKGCSVDSIE SKGCSVDSIE KLVDVSASMH CSDVNLDCMP GWRKEAKRLU KLIDENINVI QVERQVQGIY KPIGFNSTAK CKSIKHODPVC TYTFLIGLLK BIKMDISKLN 318.1 TTGACAATTG	PRISTINUSSI LIMITOOTSHL FAVQUKQFHM FNITAICPDG IHIHRNCSCQ SGRGVCVGIK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ AHSTFRCNF	MAASCARCLA ENELITOVIP MILGERKAL ENDLSEKHAL MULGERKAL ALDSKLAGIV YKOLLELLPG SEKFGMEGGE GENNEGPKIK CSCHKIKIGK WHINTER WHINTER MILGER STEPLEN S	120 180 240 300 350 420 480 540 600 660 720
50 55 60	SRDPRLIGGS VERGALSCAI VPHOCHCILK TIAGEISEKA NTISIDEULE CVDETFLDSK VYGKYCEKDD CSGRGTCVCG CALMBOGHYV DYRVSASKKD Seq ID NO: Nucleic Ac: Coding seq	AAFVCLQNDR EDPISGGRSS AEANFMLXVH YVDKTVSFYI DTPEGGFDAM NNVYVKSTM ANIANIAVEA KOTOTHERS FSCPYHENL RCECTDFRSI EJGTSECTS	RGPASFLWAA RCCDIVSHLI PLKKYPYDLY 91HPERIUMO LQAAVCESHI EHFSLQQLSE YQKLISEVKV VTGGKNYAII FDEOGFSSES SYLRIFFIIF AVTYRREKPE PQUENCE 1 %! NM_00:574	WYPSLVLGLG SKGCSVDSIE SKGCSVDSIE KLVDVSASMH CSDVNLDCMP GWRKEAKRLU KLIDENINVI QVERQVQGIY KPIGFNSTAK CKSIKHODPVC TYTFLIGLLK BIKMDISKLN 318.1 TTGACAATTG	PRISTINUSSI LIMITOOTSHL FAVQUKQFHM FNITAICPDG IHIHRNCSCQ SGRGVCVGIK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ AHSTFRCNF	MAASCARCLA ENELITOVIP MILGERKAL ENDLSEKHAL MULGERKAL ALDSKLAGIV YKOLLELLPG SEKFGMEGGE GENNEGPKIK CSCHKIKIGK WHINTER WHINTER MILGER STEPLEN S	120 180 240 300 350 420 480 540 600 660 720
50 55 60	SRDPRLIGGS VERGALSCAI VPHOCHCILK TIAGEISEKA NTISIDEULE CVDETFLDSK VYGKYCEKDD CSGRGTCVCG CALMBOGHYV DYRVSASKKD Seq ID NO: Nucleic Ac: Coding seq	AAFVCLQNDR EDPISGGRSS AEANFMLXVH YVDKTVSFYI DTPEGGFDAM NNVYVKSTM ANIANIAVEA KOTOTHERS FSCPYHENL RCECTDFRSI EJGTSECTS	RGPASFLWAA RCCDIVSHLI PLKKYPYDLY 91HPERIUMO LQAAVCESHI EHFSLQQLSE YQKLISEVKV VTGGKNYAII FDEOGFSSES SYLRIFFIIF AVTYRREKPE PQUENCE 1 %! NM_00:574	WYPSLVLGLG SKGCSVDSIE SKGCSVDSIE KLVDVSASMH CSDVNLDCMP GWRKEAKRLU KLIDENINVI QVERQVQGIY KPIGFNSTAK CKSIKHODPVC TYTFLIGLLK BIKMDISKLN 318.1 TTGACAATTG	PRISTINUSSI LIMITOOTSHL FAVQUKQFHM FNITAICPDG IHIHRNCSCQ SGRGVCVGIK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ AHSTFRCNF	MAASCARCLA ENELITOVIP MILGERKAL ENDLSEKHAL MULGERKAL ALDSKLAGIV YKOLLELLPG SEKFGMEGGE GENNEGPKIK CSCHKIKIGK WHINTER WHINTER MILGER STEPLEN S	120 180 240 300 350 420 480 540 600 660 720
50 55 60 65	SRDPRLIGGS VERGALSCAI VPHOCHCILK TIAGEISEKA NTISIDEULE CVDETFLDSK VYGKYCEKDD CSGRGTCVCG CALMBOGHYV DYRVSASKKD Seq ID NO: Nucleic Ac: Coding seq	AAFVCLQNDR EDPISGGRSS AEANFMLXVH YVDKTVSFYI DTPEGGFDAM NNVYVKSTM ANIANIAVEA KOTOTHERS FSCPYHENL RCECTDFRSI EJGTSECTS	RGPASFLWAA RCCDIVSHLI PLKKYPYDLY 91HPERIUMO LQAAVCESHI EHFSLQQLSE YQKLISEVKV VTGGKNYAII FDEOGFSSES SYLRIFFIIF AVTYRREKPE PQUENCE 1 %! NM_00:574	WYPSLVLGLG SKGCSVDSIE SKGCSVDSIE KLVDVSASMH CSDVNLDCMP GWRKEAKRLU KLIDENINVI QVERQVQGIY KPIGFNSTAK CKSIKHODPVC TYTFLIGLLK BIKMDISKLN 318.1 TTGACAATTG	PRISTINUSSI LIMITOOTSHL FAVQUKQFHM FNITAICPDG IHIHRNCSCQ SGRGVCVGIK DRCQCPSAAA MQCLHPHNLS VLIIRQVILQ AHSTFRCNF	MAASCARCLA ENELITOVIP MILGERKAL ENDLSEKHAL MULGERKAL ALDSKLAGIV YKOLLELLPG SEKFGMEGGE GENNEGPKIK CSCHKIKIGK WHINTER WHINTER MILGER STEPLEN S	120 180 240 300 350 420 480 540 600 660 720
50 55 60	SEDPHLIGHES VIRIQUISCNI VENDONCHILK TIAGEISEKA NYTSKDEVLE CVDETFILDSK VYGKYCEKDD SEQ ID NO: Nucleic Ac- DOMINICATE ATTICTICA AATTICTICAT AACCOAGAGA GANGACATTA AATTICTICAT	AAPVCLQNDR EDPISGGSS AAPVCLVQNDR EDPISGGSSA AAPVCLVA TOPTOSGGSSA ANTOTYMSKCD CCPQCBMKCA AVIANIAVESTTM ANIANIAVEST AVIANIAVEST 646 DNA mid d Accessio sunce 1	REPASTIMAA ERCDIVANILI PIKKYPOULS SIHBERING LOANVCESHI EMPSIGQLES VOGLISSEVE VOGGRAVAILI PEDOPESSES CAGHGECEAG GRECEHOPE SYLARFPILF AVTYREREE EQUENCE 1 NM_001 TAACATGAGAA TAAAAATGAA TAAAAATGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA	WYPSLVIJGLO SKGCSVDSTE YLVDVBASME CSDYNLDCMP GRIKEARRIL KLIDNINVI QVENYQGIY KPIGPNETAK KPIGPNETAK TYTACKBIMNOP 1VTFLIGLLK 31 1TCACAATTG GACCTACTG AAACTGACAA	LIMIDOTSEL PAVGGGGTHM FNITAICPDG IHIERNCSCO RCCCPSANA MCCLHPHNLS VLITROVILO AHETYRCNP 41 ATTCCATAAT ATGAACTAAG AAATTATGAT CAATTGAACT CAATTGA	MAASCARCLA EMEINTOUTP BIOLERICARY TENTIFERS ALDERAGATY YELLELIGE SERREGRESSE SERREGRESSE SERREGRESSE SI GROWNERGOV OALLDOCKTS WASHKIKSSS SI GACAMGTG GRACAMGTG GTTGATTAMA GATGGCAMG	120 180 240 300 420 480 540 600 720
50 55 60 65	SEDPHLIGHES VIRIQUISCNI VENDONCHILK TIAGEISEKA NYTSKDEVLE CVDETFILDSK VYGKYCEKDD SEQ ID NO: Nucleic Ac- DOMINICATE ATTICTICA AATTICTICAT AACCOAGAGA GANGACATTA AATTICTICAT	AAPVCLQNDR EDPISGGSS AAPVCLVQNDR EDPISGGSSA AAPVCLVA TOPTOSGGSSA ANTOTYMSKCD CCPQCBMKCA AVIANIAVESTTM ANIANIAVEST AVIANIAVEST 646 DNA mid d Accessio sunce 1	REPASTIMAA ERCDIVANILI PIKKYPOULS SIHBERING LOANVCESHI EMPSIGQLES VOGLISSEVE VOGGRAVAILI PEDOPESSES CAGHGECEAG GRECEHOPE SYLARFPILF AVTYREREE EQUENCE 1 NM_001 TAACATGAGAA TAAAAATGAA TAAAAATGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA TAACATGAGAA	WYPSLVIJGLO SKGCSVDSTE YLVDVBASME CSDYNLDCMP GRIKEARRIL KLIDNINVI QVENYQGIY KPIGPNETAK KPIGPNETAK TYTACKBIMNOP 1VTFLIGLLK 31 1TCACAATTG GACCTACTG AAACTGACAA	LIMIDOTSEL PAVGGGGTHM FNITAICPDG IHIERNCSCO RCCCPSANA MCCLHPHNLS VLITROVILO AHETYRCNP 41 ATTCCATAAT ATGAACTAAG AAATTATGAT CAATTGAACT CAATTGA	MAASCARCLA EMEINTOUTP BIOLERICARY TENTIFERS ALDERAGATY YELLELIGE SERREGRESSE SERREGRESSE SERREGRESSE SI GROWNERGOV OALLDOCKTS WASHKIKSSS SI GACAMGTG GRACAMGTG GTTGATTAMA GATGGCAMG	120 180 240 300 420 480 540 600 720
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50 55 60 65 70 75	SHOPHUJESS SHOPHUJESS WEDGELESS WEDG	ARPVCLQNDR EDPISGGSS ARPVCLQNDR EDPISGGSS ARRAYMLKWIN DIPESGFDAN MINIVISTA M	REPASPLWAR ERCDIVENTI PINKYEPULI ERPASPLWAR ERCDIVENTI ERPASPLWAR ERPASPLWAR I DANAYCESHI ERPASIQLES YOKULSENIKY YOUGHNAIL PDENOFASS GREGEICPTA GREGEICPTA TOGOAGAGAN TOGOAGAGAN TOGOAGAGAN TOGOAGAGAN TOTOTUCTO GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTITIOCT GAGTIGAN ACCACAGAM	WYSILVIGIO SKOCHYDSIE YLDYDANSE WYSILVIGIO GRIEBRARILI KULDENINE CHERRICH KULDENINE CHERRICH KULDENINE CHERRICH	PARTIAN SELL PROVINCES OF THE PROVINCES	MARGARCLA BREINTQVTP BARACARCLA BREINTQVTP BARACARCLA BREINTQVTP BARACARC BREINTERITERS BREINTERITERS BREINTERITERS BREINTERITERS BREINTERITERS GREINTERITER GREINTER GREINTERITER GREINTER GREINTERITER GREINTER GREINTERITER GREINTERITER GREINTER GREIN	120 180 300 420 480 600 720 600 120 120 120 120 120 120 120 120 120 1

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	TTGTCAACAC	CTTATGGCCA	ACCTGCCTGT	TTCCAGCAGC	AACAGCATCA	AATACTTGCC	1500
	ACTCCACTTC	AAAATTTACA TTTATTCCAT	GGTTTTTAGCA	TCTTCTTCAG	CAAATGAATG	CATTTCGGTT	1560 1620
5		ATGAAAAGAA					1680
-	GATAACCAAA	CTCTTGATAG	TTACCGGAAC	GAAATAGCTT	ATTTGAATAA	ACTACAACAA	1740
	CACAGTGATA	AGATCATCCG	ACTITATGAT	TATGAAATCA	CGGACCAGTA	CATCTACATG	1800
	GTAATGGAGT	GTGGAAATAT	TGATCTTAAT	AGTTGGCTTA	AAAAGAAAAA	ATCCATTGAT	1860
10	CCATGGGAAC	GCAAGAGTTA	CTGGAAAAAT	ATGTTAGAGG	TCATACTTCA	TGGAATGCTA	1920 1980
10		ATTTTGGGAT					2040
	GATTCTCAGG	TYGGCACAGT	TAATTATATG	CCACCAGAAG	CAATCAAAGA	TATGTCTTCC	2100
	TCCAGAGAGA	ATGGGAAATC	TAAGTCAAAG	ATAAGCCCCA	AAAGTGATGT	TTGGTCCTTA	2160
1.5	GGATGTATTT	TGTACTATAT	GACTTACGGG	AAAACACCAT	TTCAGCAGAT	AATTAATCAG	2220
15	ATTTCTAAAT	TACATGCCAT	AATTGATCCT	AATCATGAAA	TTGAATTTCC	ACAGAGGATA	2280 2340
	GAGAAAGATC	AGCTCCTGGC	GTTAAAGTGT	TGTTTAAAAA	BAACTCATCC	ACAGAGGATA	2400
	ATGGGGAAGG	GAACCACTGA	AGARATGRAA	TATCTTCTGG	GCCAACTTGT	TGGTCTGAAT	2460
	TCTCCTAACT	CCATTTTGAA	AGCTGCTAAA	ACTITATATG	AACACTATAG	TGGTGGTGAA	2520
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30	ETATANIATO	KKOTTSEEEK	KNLSASTVLT	AOESPSGSLG	HLONRINGCO	SRGOTTKARF	240
	LYGENMPPQD	AEIGYRNSLR	QTNKTKQSCP	FGRVPVNLLN	SPDCDVKTDD	SVVPCFMKRQ	300
	TSRSECRDLV	VPGSKPSGND	SCELRNLKSV	QNSHFKEPLV	SDEKSSELII	TDSITLKNKT	360
	essllaklee	TKEYQEPEVP	ESNOKOWOSK	RKSECINQNP	AASSNHWQIP	ELARKVNTEQ	420
35	KHTTPEOPVP	SVSKQSPPIS FQQQQHQILA	TSKWFDPKSI	CKTPSSNTLD	DYMSCFRTPV	VKNDFPPACQ	480 540
55	ONLYBERROLA	PUCCOUNTERS	DNOTLDSVEN	ELVINKTOO	HEDKITETING	YEITDQYIYM	600
	VMECGNIDLN	SWLKKKKSID	PWERKSYWKN	MLEAVHTIHO	HGIVHSDLKP	AMPLIVEGML	660
	KLIDPGIANO	MOPDTTSVVK	DSQVGTVNYM	PPEAIKDMSS	SRENGKSKSK	ISPKSDVWSL	720
40	GCILYYMTYG	KTPFQQIINQ	ISKLHAIIDP	NHEIEFPDIP	EKDLQDVLKC	CLKRDPKQRI	780
40	SIPELLAHPY SHNSSSSKTF	VQIQTHPVNQ	MAKGTTEEMK	AAFGÖFAGEN	SPNSILKAAK	TLYEHYSGGE	840
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50	Nucleic According sequences of the control of the c	id Accession uence: 241 11 GCCTCGGCCA GCGTGCCTG GGAGGACCC GGCGCCCTCC CCTGGAGCCT CCAGTGCAAG	n #: NM_015 .1902 21 GGCTAGCCAG GCCTCCCCTC AGCGCTGAG CAAGGGGGGC TGCGCTCCCG GCATCACGGG	31 GGCGCCCCCA CCAGACTGCA GAGAGAGGAG TCAGGAGGAG CTGCTGCTCT	GCCCTCCCC GGGACAGCAC GCGGCGGCTT GAAGGAGGAC CCTGGGTGGC CGGCACGTCA	AGGCCGCGAG CCGGTAACTG AGCTGCTACG CCGTGCGAGA AGGTGGTTTC GCCTGGGGTC	120 180 240 300 360
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50	Nucleic According sequences of the control of the c	id Accession uence: 241 11	n #: NM_015 .1902 21	31 	GCCCTCCCC GGGACAGCAC GCGGCGGCTT GAAGGAGGAC CCTGGGTGGC CGGCACGTCA GAAGAAACAG GCGTGGGACC	AGGCCGCGAG CCGGTAACTG AGCTGCTACG CCGTGCGAGA AGGTGGTTTC GCCTGGGGTC CAAGGGAGTC AAACAAATGC	120 180 240 300 360 420 480
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50	Nucleic Ac Coding sequilibrian concentration of the	id Accession uence: 241. 11 GCCTGGCCA GCGGTGCCTG GGAGGACCG GGCGCCTCC CCTGGAGCCT CCAGTGCAG GAACTAAACT CATGGAAAC CATGCAAC ACAGGATACAC ACAGGATACAC ACAGGATACAC ACAGGATACAC	n B: NM_015 .1902 21	31 GGCGCCCCCA CCAGACTGCA GAGAGAGGAG TCAGGAGGAG CTGCTGCTCT TTGTTAGCAT TACGCTGGA TTTGGTGAGT TGCAGTCAAG AATACACACG	GCCCTTCCCC GGGRCAGCAC GCGGCGGCTT GAAGGAGGAC CCTGGGTGGC CGGCACGTCA GAAGAAACAG GCGTGGGACC ATGTGAATGA AAGGTACAA AACTCTAAGGA	AGGCCGCGAG CCGGTAACTG AGCTGCTACG CCGTGCGAGA AGGTGGTTTC GCCTGGGGTC CAAGGAGTC AAACAAATGC GTGTGGAATG GTGCTTTTGC ATGTGCCATG	120 180 240 300 360 420 480
50	Nucleic Ac. Coding sequence COCCAGAGGA COCCCTGCC CGAGTGGAGCA ATGCTCTGCC GGGAAGGCGA TGTCACTATG TGTGAAGCTA AGATGCTTTC AAACCCCGGC CTCAGTGGCC ATAAACTGTC	id Accession uence: 241 11 GCTCGGCCA GCGGTGCCTG GGAGGACCG CCTGGAGCC CCATGCAGG GAACTAAACT CATGGAACA ACATGCTAA ACATGCTCAT AGGATACAC ACATGCTCAT AGGATACGCTG	n B: NM_015 .1902 21 gGCTAGCCAG GGCTCCCCTC AGCGGCTGAG CGAGGGGGG GGCTCCCG GGATCACGGG GGCTCCTG CGGGAAAACC CAGATGTTAG GCCAGATGTT GGAGATGCT TGAAGACACA	31 GGGGCCCCA CCAGACTGCA GAGAGAGGAG TCAGGAGGAG CTGCTGCTT TTGTTAGCAT TGCAGTCAAG AATACACACG ACGTGTGTGA	GCCCTTCCCC GGGACAGCAC GCGGCGGCTT GAAGGAGGAC CCTGGGTGGC GGGCACGTCA GAAGAAACAG GCGTGGGACC ATGTGAATGA ACTCTAAGGAC CACAGTGCCT	AGGCCGCGAG CCGGTAACTG AGCTGCTACG CCGTGCGAGA AGGTGGTTTC GCCTGGGGTC CAAGGGAGTC AAACAAATGC GTGTGGAATG GTGTGTTTGCCATG	120 180 240 300 360 420 480 540 600 660 720
50	Nucleic Ac. Coding sequence of the control of the c	id Accession uence: 241 11	n B: NM_015 .1902 21 j GGCTAGCCAG GGCTTGAGCCAG GGCGCTTGAG CGAGGGGGGG GGCTCCCG GGATCACGG GGCTTGCTGC TGGATGTTAG CGGAAAAACC CAGATGTTTG GCCAGATGCT TGAAGACACA AAATGGAAGA	31 GGGGCCCCCA CCAGACTGCA GAGAGAGGAG TCAGGAGGAG TCAGGAGGAG TTGGTTAGCAT TAGGGCTGGA TTTGGTTAGAT TGCAGTCAAG AATACACAG GACGTGTGTAG GAGAAGGGG GACATCTTAG	GCCCTTCCCC GGGACAGCAC GCGGCGGCTT GAAGGAGGAC CCTGGGTGGC CGGCACOTCA GAAGAAACAG GCGTGGACC ATGTGAATGA ACTCTAGGAC CACAGTGCACT ATATTGATGA	AGGCCGCGAG CCGGTAACTG AGCTGCTACG CCGTGCGAGA AGGTGGTTTC GCCTGGGGTC CAAGGGAGTC AAACAAATGC GTGTGGAATG GTGGTCATCG ATGTGCCATCG ATGTGCCATCG ATGTGCCATCG ATGTCCATCCT	120 180 240 300 360 420 480 540 600 660 720 780
50	Nucleic Ac. Coding sequence COCCAGAGGA COCCAGGCA COCCAGGCA COCCAGGCA COCCAGGCA COCCAGGCA COCCAGGCA COCCAGGCA COCCAGGCA COCCAGGCA COCCAGGCA COCCAGGCA COCCAGGACTCC COCCAGGACTC COCCAGGAC	id Accession uence: 241 11 12 GCCTCGGCCA GCGGTGCCTG GGAGGACCG CCTGGAGCC CCATGCAAG GAACTAAACT CATGGAACA CATGCCAAC ACATGCTCA ACATGCTCAT GCTGGCCCC CCTGGGCCCC CCTTGGCCCCC CCTTGGCCCCC	n B: NM_015 .1902 21 21 GGCTAGCCAG GGCTCCCCTC AGCGGCTGAG CGAGGGGCT GGACTCCCG GCATCACGGG GGCTCCTGC TGGATGTAG GCCAGATGTT GGCAGATGTT TGAAGAAAC AAATGGAAGA AAATGGAAGA	31 GGGGCCCCA CCAGACTGCA CAGACAGCAG CTAGGAGGAG CTGCTGCTCT TAGTGAGCAT TACGCTGGA TTTGGTGAGT TGCAGTCAAG AATACACACG GACTGTGTAG GACAGAGGGC GACTGTCTAG GA	GCCCCTCCCC GCGCACACAC GCGGCGCTT GAAGGAGCAC CCTGGGGTGGC CGGCACGTCA GAAGAAACAG GCGTGGACC ATGTGAATGA GAAGCTACAA ACTCTAGGAC CACAGTGCCT ATATTGATGA CATTTGAGAA CATTTGAGAA CATTTGAGAA	AGGCCGCGAG AGGCGCTAACTG AGCTGCTACG AGCTGCTACG GCCTGGGGTC CAAGGGAATG AGACAAATGC GTGTGGAATG GTGCTTTTGC ATGTGCCATG GTGTGCATC ATGTGCCTCT CTACTACCTGC	120 180 240 300 360 420 480 540 600 720 780 840
50 55 60	Nucleic Ac. Coding sequence of the control of the c	id Accession elence: 241 11	n B: NM_015 1992 21	31 GGGGCCCCCA CCAGACTGCA GAGAGAGGAG TCAGGAGGAG TCAGGAGGAG TTGGTTAGCAT TAGGAGCTGAG TTGGTTGAGT GACAGCACG ACGTGTGTAA GACAGCAGG GACTGTCTAG TGTGTGAACA TGTGTGAACA	GCCCCTCCCC GGGACAGCAC GCGGCGCTT GAAGGAGGAC CCTGGGTGGC CGGCACTCA ATGTGAATGA ACTCTAGGAC CACAGTGCCT ATATTGATGA CATTTGATGA	AGGCCGCGAG AGGCGCGCAG AGGTGCTACG CCGTGCGAGA AGGTGGTTTC GCCTGGGGTC CAAGGGAGTC AAACAATGC GTGTGGAATG GTGTGCATG GTGTGCCATG GTGTGCCATC ATGTGCCATC ATGTGCCTCT CTACTACTGC TATAGATATA	120 180 240 300 360 420 480 540 600 660 720 780
50	Nucleic Ac. Coding sequence Coding sequence COCCAGAGGA COCCAGCA COCCACAC COCCAGCA COCCAGCA COCCAGCA COCCAGCA COCCAGCA COCCAGCA COCCACAC COCCAGCA COCCACAC	id Accession elence: 241 11 GCCTGGCCA GGGGTGCCTG GGAGGACCGG GGCCCCCC CCTGGAGCCT CATGGCAG GAACTAAACT CATGCAAG GAACTAAACT CATGCAACA CATGCCACA AGTACACC TCTGTCCTA AGTACACC TTGGTTTGGA CTATGGTTAGA CTATGGTTAGA	n B: NM_015 1992 21	31 GGGGCCCCA CCAGACTGCA CCAGACTGCA CCAGACTGCA TCAGGACGAG CTCCTCTTTTAGCAT TTAGGACTGGA TTTGGTGAG TTGCAGTGAA AATACACACG GACTGTGTGA GACTGTGTGA GACTGTGTGA TGTGTGACGA TGTGTGACA TGTGTGACA TGTGTGACA TGTGTGACA TGTGTGACA TGTGTGACA	GCCCCTCCCC GGGACAGCAC GGGGCGCTT GAAGGAGGAC CCTGGGTGGC CGGCACCTCA GAAGAACAG GCTTGGGACG ATGTGAATGA ACTCTAGGAC CACAGTGCCT ATATTGATGA CATTTGGAATG CATTTGGAATG CATATTGGATG CCAATTTGCT CCAATTGCTT CCAATTGCTT CCAATTGCTT CCAATTGCTT	AGGCCGGAG CCGTAACTG AGGTGGTTAC CCGTGCGAGA AGGTGGTTTC CAAGGGGTC CAAGGGAGT CAAGCAATGG GTGTGGAATG GTGTCCATCG ATGTGCATG GTGTCCATCC TATGTACTGC TATGTACTGC TATGATATC CAATACCCAA GTGTCTGCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50 55 60	Nucleic Actoding sequility of the control of the co	id Accession eence: 241 11	n B: NM_015 1992 21	31 	GCCCTCCCC GGGACAGCAC GCGGCACTCA GAAGGAGGAC CCTGGGTGGC CGGCACGTCA GAAGGAACCAC ATGTGAATGA GAAGCTACAA ACTCTAGGAC CACAGTGCCT ATATTGGAAG GATATTGGAAG GATATTGCTT ATGGAACTTCCT ATGGAACTTCCT ATGGAACTTCCAATTGCTT ATGGAACTTCCA GTACCACTCAA	AGGCCGGAG CCGGTAACTG AGCTGCTACCG CCGTGCGAGA AGGTGGTTC CAAGGGAGT CAAGGAGTC ATGTGGAATG GTGTGGAATG GTGTGGAATG GTGTGCATC GTGTCCATC CTACTACTGC TATAGATATA GTGTCTCTCT TATAGATATA GTGTCTCTCATC AGACAGAATC	120 180 240 300 360 420 480 540 660 720 840 900 960 1020
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80	AACCACTTAC	AGTTGCTTAT	ACCTTTCTCA	TIAACITTIG	1 TTCTTAACA	TTTAGAATAT	3300
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Seq ID NO: 651 Protein sequence Protein Accession #: NF_003497.1

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-	VILTITWELA	AGRKWSCEAI	EOKAVWPHAV	AWGTPGFLTV	MLLALNKVEG	DNISGVCFVG	360
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10	LMTLIVGISA	VPWVGSKKTC	TEWAGPFKRN	RKRDPISESR	RVLQESCEPP	TCD PECCHONIC	540 600
10	KKHYKPSSHK	LKVISKSMGT	STGATANHGT PAASISRLSG	SAVAITSHDY	DOCUMENTED	DICORCUITO	660
	TOT ACCUMEN	UDCCCCPDCCI.	KGSTSLLVHP	POADGROOM	CCHSOT	MISE MODELLO	
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	TIGIGAATAT						
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	1	11	21	31	41	51	
	1	I TOTAL STORE OF THE STORE OF T	CENTRAL VOIL	TI TOPMIN TH	TMDWWT GOD	LDDIKTEIFA	60
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                                                                                                                                                                                                                                                                                                                             200
                           СМЕМАТИТЕ ТЯССИССКИЕ ФИССТТЕСЯ, АПТАМПТСЯ АСДАМАССЯ ТОАССЛОЯТО 
ДОПОТАТТИТО АКТИГИАНИЯ ТОАТИТИТЕ СНЯТОВКОЕ ОССОБОЛЕТС СНЯТОВЛЕТО 
АКСИЛСТЕТО АТОМІТОМА ТОАСКТОМИ ОПІТОТИСЬ ВОТЕТОМИТЯ СПІТОВСТОВ 
ТЕТОМИТАМІ ТОМІТОМИ ОПІТОМИ                                                                                                                                                                                                                                                                                                                              360
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                                                                                                                                                                                                                                                                                                                             720
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                           GTUTTAGACC COMANGTAN GGANGAGAT ANACACCTON ANTTCOTAT TICTOCNTAN TIMENTAGEN CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CONTINUENT CON
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                           ATAACATITI ATGICACTAI AATCITTIGI TITITAAGIT AGTGTATATI TIGTIGTUGAT TAATCITTITA TCHTGATGT AATAAGATI TGGTGGGTAA AAATCITTITA TCHTGATGT AATAAGAATI TGGTGGTGTAATAATAAACAATAAC CITITITACT
                                                                                                                                                                                                                                                                                                                       1200
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25
                             Seq ID NO: 655 Protein sequence
                             Protein Accession #: NP_000573
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30
                           MRIAVICFCL LGITCAIPVK QADSGSSEEK QLYMKYPDAV ÄTMLNEDPSQ KQMLLARQTL PSKANSSIDE MODMODEDDD DHVDSQOSID SMODOVDDT DOSKGSGSSE MISDSDELVT DPTDLPATE YFPVPVPTVD THORKOROSVY VGLASKSKKE REPUQYPDA TUBDITSNE SEELMGAKKA IPVAQDLAAP SDMOSKGNS YETSQLDQS ARTHSKKGS LYKRANDES MISDSDELVT MISDSDELVT MISDSDELVT SKEET SKANSKE SKANSKE KYRRANDES
                                                                                                                                                                                                                                                                                                                             120
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35
                             Sea ID NO:
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                             Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401
40
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                             GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA
45
                             GOCCTICAAC GGATCATGGT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCCC CGGGGAGGGCC TGACACCGGA GGAGGCGGAA TTCATGGGCTT GCAGCCGGT GGCCCTTGAAC GAGAGGGGAC CAGACTGGTG CCAGCTGGAC CGAGAGGGACC CAGACTGGTG CAGAGAGGGCC TGGGGCCACA TCACACCGG
                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                              240
                             GARANCGARCC САВАСТОВТЯ СМАВСОВОЙ ТОХВІССКОГ ТОМАВСОВСЕ В АТКАНСКОГА ТОКТОТОВТА О ВОТСАТАВТА САВАССКІЙ В АТКАНСКОГА КАСОСТИВНЯ ТЕТСТОТОВТЯ В ОБТСОВАВЛЕ ОСТОВОВАЛЬ ТОСТОВАВЛЕ ТОТСОВАВЛЕ ОСТОВОВАЛЬ ТОСТОВАВЛЕ ТОСТОВАВЛЕ ТО
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                             CAGAGCCCAG AGAGAGGGC CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCCGCGGGCC
GCGGGGCGCA AGCGGGCGCC GGGCAAGGAG CCCAGTCCG GGGACTACGG CCCGCGGGCC
                                                                                                                                                                                                                                                                                                                              660
                             GACGACTACO TGCTGGGCAC CTGCGCGTG AGCGGCTCGG GCGGGGCGG CGCGGGCAG
ACGGTCAAGT GCGTGTTTCT GGATGAGGAC ACGACGACGA CGACGAGCTG
55
                                                                                                                                                                                                                                                                                                                              720
                              CAGCTGCAGA TCAAACAGGA GCCGGACGAG GAGGACGAGG AACCACCGCA CCAGCAGCTC
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                             CHOCAGO COGOGORAGO ACCORDADA PROPERTADA COCCADA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA CONTROLA 
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                              AMBANCATCA COANCIANCA COGGCGCGC CTGGGGCAGC CGGGGCTGTC GCCGGGTCC
TGGGGCTGG TGTCCACCTC CTGGTCAGC ACCAGGGAG GCAGCAGGG GAGCAGGG
GAGGAGGG ACGACCTGAT GTTGAACCTG AGCTGAATT TCTCTCAAAG GGGGCACAGC
                                                                                                                                                                                                                                                                                                                         1080
                                                                                                                                                                                                                                                                                                                          1140
                              GCCAGCGAGC AGCAGCTGGG GGGCGGCGG GCGGCCGGGA ACCTGTCCCT GTCGCTGGTG
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65
                             GATANGGATT TGGATTCGTT CAGCGAGGGC AGCCTGGGCT CCCACTTCGA GTTCCCCGAC
TACTGCACCC CGGGGGTGAG CGAGATGATC GCGGGGGGACT GGCTGGAGGC GAACTTCTCC
                                                                                                                                                                                                                                                                                                                         1320
                              GACCTGOTGT TCACATATTG AAAGGCGCCC GCTGCTCGCT CTTTCTCTCG GAGGGTGCAG
                                                                                                                                                                                                                                                                                                                         1440
                              AGCTGGGTTC CTTGGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG
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                             ACCIDENTIC TOTTGATGET GGCGGTGGTA GGGTGGAGGG GAGAGAAGA TATGATTGATA GATTGATAGT TTGATAGTT TTTAATGTT TTTAATGTT TTTAATGTT TTTAATGTT TTTAATGTT TTTAATGTT TTTAATGTT TTTAATGTA ATGTTTATGT TTTAATGTGA ATGGTAATGT TTTAATGATAT TTTGATGTT TTTAATGTGA ATGGTAATGT TTTAATGTGA COCCCTCCCT
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70
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                             TCCTTTATCG TGTCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCAA
AAAATGTGTT TTTGTAATTA CTATTCTTT TTCCTGAATAT TCGTGATTGC AACAAGGCA
GAGGGGGGG CGCGGGGAG GGGAGGTAGG ACCGGCTCG GAAGGGGCTG TTTGAAGGT
                                                                                                                                                                                                                                                                                                                          1740
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75
                              GTCGGTCTTT GAAGTCTGGA AGACGTCTGC AGAGGACCCT TTTGGCAGCA CAACTGTTAC
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                              TCTAGGGAGT TGGTGGAGAT ATTTTTTTT CTTAAGAGAA CTTAAAGAAC TGGTGATTTT
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                              Seq ID NO: 657 Protein sequence
80
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                              MVQQAESLEA ESNLPREALD TEEGEFMACS PVALDESDPD WCKTASGRIK RPMNAFWVWS
 85
                              KIERRKIMEQ SPOMENAEIS KRLGKRNEML KOSEKIPPIR EAERLRLKHM ADYPDYKYRP
                                                                                                                                                                                                                                                                                                                                120
                              RKKPKMDPSA KPSASQSPEK SAAGGGGSA GGGAGGAKTS KGSSKKCGKL KAPAAAGAKA
GAGKAAOSCD YGGACDDYVL GSLRVSGSGG GGAGKTVKCV FLDEDDDDDD DDDELQLQIK
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	OEDDEEDEED	PHOQLLQPPG	OOPSOLLEPY	NVAKVPASPT	LSSSAESPEG	ASLYDEVRAG	300
	ATSGAGGGSR LMFDLSLNFS	LYYSFKNITK QSAHSASEQQ EANFSDLVFT	QHPPPLAQPA LGGGAAAGNL	LSPASSRSVS	TSSSSSSGSS	SGSSGEDADD	360 420
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	Nucleic Act	658 DNA se d Accession ence: 123	:#: NM 001	719			
10	1	11	21	31	41	51	
	CTCCCACCTC	GGGCGGTCT GGGCGGTGCG	GGCCCGGAGC	CCGGAGCCCG	GGTAGCGCGT	AGAGCCGGCG	60 120
16	CONTROL	OCCUTCACTO	CONCURRENCE	CGCCGCACAG	CTTCCTGGCG	CTCTGGGCAC	180 240
15	GCTTCATCCA	GCTGCGCTCC CCGGCGCCTC	CGCAGCCAGG	AGCGGCGGGA	GATGCAGCGC	GAGATCCTCT	300
	CCATTTTGGG	CTTGCCCCAC GCTGGACCTG	CGCCCGCGCC	CGCACCTCCA	GGGCAAGCAC	AACTCGGCAC	360
	CCATGTTCAT	GCTGGACCTG	TACAACGCCA	TGGCGGTGGA	GGAGGGCGGC	GGGCCCGGCG	420 480
20	COCKECT POR	TROCCA TTTC	CTCACCCACC	COCACATOCT	CATGAGCTTC	GTCAACCTCG	540
20	TGGAACATGA	CAAGGAATTC	TTCCACCCAC	GCTACCACCA	TCGAGAGTTC	CGGTTTGATC	600
	TTTCCAAGAT	CCCAGAAGGG	GAAGCTGTCA	CGGCAGCCGA	ATTCCGGATC	TACAAGGACT	660 720
	ACATCCGGGA	ACGCTTCGAC CAGGGAATCG	GATCTCTTCC	TECTCGACAG	CCGTACCCTC	TGGGCCTCGG	780
25							840
	GGCACAACCT	GGGCCTGCAG CCTGATTGGG	CTCTCGGTGG	AGACGCTGGA	TGGGCAGAGC	ATCAACCCCA	900 960
	AGTTGGCGGG	CACGGAGGTC	CGGCACGGGC	CCCAGAACAA	CACCCCCTTC	AAACAGCGCA	1020
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30	AGAACAGCAG	CAGCGACCAG	AGGCAGGCCT	GTAAGAAGCA	CGAGCTGTAT	GTCAGCTTCC	1140 1200
	GAGACCTGGG	CTGGCAGGAC	TGGATCATCG	PCATGRAGG	CACCAACCAC	GCCATCGTGC	1260
	AGACGCTGGT	TGCCTTCCCT CCACTTCATC	AACCCGGAAA	CGGTGCCCAA	GCCCTGCTGT	GCGCCCACGC	1320
25							1380
35	ACAGAAACAT	GGTGGTCCGG	GCCTGTGGCT	GCCACTAGCT	GCCAGGAACC	AGCAGACCCA	1500
	CTGCCTTTTG	GTTTTTCTGG TGAGACCTTC	CCCTCCCTAT	CCCCAACTTT	AAAGGTGTGA	GAGTATTAGG	1560
	AAACATGAGC	AGCATATGGC	TTTTGATCAG	TTTTTCAGTG	GCAGCATCCA	ATGAACAAGA	1620 1680
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40	TTATGAGGGG	CTACCAGCCA	GGCCACCCAG	CCGTGGGAGG	AAGGGGGCGT	GGCAAGGGGT	1800
	GGGCACATTG	GTGTCTGTGC	GAAAGGAAAA	TTGACCCGGA	AGTTCCTGTA	ATAAATGTCA	1860
45	CAATAAAACG Seq ID NO:	659 Prote	in sequence				
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	1	11	NP_001710	31 i	41	51 j	
50	1 MHVRSLRAAA	11 j phspvalwap	NP_001710 21 LFLLRSALAD	FSLIDNEVHSS	PIHRRLRSQB	RREMORBILS	60
50	1 MHVRSLRAAA	11 PHSFVALWAP	NP_001710 21 J LFLLRSALAD MEMILILYNAM	j PSLDNEVHSS AVERGOGPGG	PIHRRLRSQB OGFSYPYKAV	RREMORBILS PSTOGPPLAS	120
50	1 MHVRSLRAAA ILGLPHRPRP LQDSHFLTDA	11 PHSFVALWAP HLQGKHNSAP DMVMSFVNLV	NP_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR	FSLDNEVHSS AVEEGGGPGG YHREFRFDL LDSRTLWASE	PIHRRLRSQB QGFSYPYKAV SKIPEGEAVT EXWLVFDITA	RREMORBILS FSTOGPPLAS AAEPRIYKDY TSNHWVVNPR	120 180 240
	1 MHVRSLRAAA ILGLPHRPRP LQDSHFLTDA	11 PHSFVALWAP HLQGKHNSAP DMVMSFVNLV	NP_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR	FSLDNEVHSS AVEEGGGPGG YHREFRFDL LDSRTLWASE	PIHRRLRSQB QGFSYPYKAV SKIPEGEAVT EXWLVFDITA	RREMORBILS FSTOGPPLAS AAEPRIYKDY TSNHWVVNPR	120 180 240 300
50 55	1 MHVRSLRAAA ILGLPHRPRP LQDSHFLTDA IRBRFDNETF HNLGLQLSVE OND SKTDKNO	11 phspvalwap HLQSKHNSAP DMVMSFVNLV RISVYQVLQE TLDGQSINPE TLDGQSINPE EALRMANVAE MHATMHAIVQ	21 J LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDOROAC	FSLDNEVHSS AVEEGGGPGG YHHREFRPDL LDSRTLWASE QNKQPPMVAF KKHELYVSFR	PIHRRLRSQB QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHFRS DLGWQDWIIA	RREMORBILS FSTOGPPLAS AAEFRIYKDY TSHHWVVNPR IRSTGSKORS PBGYAAYYCE	120 180 240
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	1	11	P_001710 21	FSLDNEVHSS AVEBGGGPGG YHHREFRFDL LDSRTLWASE ONKOPFMVAF KKHELYVSFR VPKPCCAPTQ	PIHRRLRSQB QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHFRS DLGWQDWIIA	RREMORBILS FSTOGPPLAS AAEFRIYKDY TSHHWVVNPR IRSTGSKORS PBGYAAYYCE	120 180 240 300 360
55	1	11 PHSFVALWAP PHLQGKHNSAP DMVMSFVNLV RISVYQVLQE TLDOQSINPK EALRMANVAE MWATNHAIVQ H 660 DNA se id Accessio	P_001710 21	FSLDNEVHSS AVEBGGGPGG YHHREFRFDL LDSRTLWASE ONKOPFMVAF KKHELYVSFR VPKPCCAPTQ	PIHRRLRSQB QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHFRS DLGWQDWIIA	RREMORBILS FSTOGPPLAS AAEFRIYKDY TSHHWVVNPR IRSTGSKORS PBGYAAYYCE	120 180 240 300 360
55	HVRSLRAAA HIJGDHRPRP LQDSHELIDA IRREPINETF HHLGLQLSVE GREAKTPKNQ GECAPPLNSY RRMVVRACGO Seq ID NO: Nucleic Ac Coding seq	11 PHSFVALMAP HLQGKINSAP DMVMSFVALV RISVYQVLQE TLDOQSIMPK EALRMANNAE MHATNHAIVQ H 660 DNA si id Accession uence: 211.	P_001710 21 LFLLRSALAD MFMLDLYNAM MFMLDLYNAM MFMLSFHIFR HLGRESDLFL LAGLIGRED NSSSDQRQAC TLVHFINPBT equence m #: Eos se 1895 21	FSLDNEVH9S FSLDNEVH9S	PHHRRRSOB QGFSYPYKAV SKIPEGEAVT SKIPEGEAVT SHATEVHFRS DLGMQDWIIA LMAISVLYFD	RREMORBILS FSTQSPPLAS AABERIYKDY TSHIMWUNPR IRSTGSKQRS PEGYANYYCE DSSNVILKKY	120 180 240 300 360
55	HVRSLRAAA HIGLHERPRE LQDSHELTDA HERREFNETF HNLGLULSVE GREAKTPKNO GECAPPLNSY RNMVVRACGC Nucleic Ac Coding seq	11 PHSFVALMAP HLQGKINSAP DMVMSFVALW RISVYQVUQE TLDOQSIMFK EALRMANVAE MATNHAIVQ H 660 DNA si id Accession uence: 211. 11 GGCGCCCAGT	PP_001710 21 LFLURSALAD MFMLDLYNAM EIDKEFFHER HLGRESDLFL LAGLIGRIGP NSSSDGRQAC TLVHEINPET equence n #: Eos sc .1895 21 CACTICCTCC	PSLDNEVH9S PSLDNEVH9S	PIHRRLRSOB QGFSYPYKAV SKIPEGEAVT EGMLVPOITA FKATEVHFRS DLGWQDWIIA LMAISVLYFD	RREMOREILS PSTGGPPLAS AABERIYKDY TSHIMVUNPR IRSTGSKORS PEGYANYYCE DSSNVILKKY 51 AGGAGGGGAT TTGGGTCGGA	120 180 240 300 360 420
55	MHYRSLRAAA ILGLEHREPE LODSHET/TDA IRREFUNETF HNLGLOEFF HNLGLOEFF KNMCVEACCC Seq ID NO: Nucleic Ac Coding seq 1	11 PHSFVALWAP PHOGKENSAP PLOGGENSAP RISVYQVLQE TLDOGSINE EALRMANVAE MENATNHAIVQ 660 DNA se dd Accession uence: 211.	PP_001710 21 LPLURSALAD MPMLDLYNAM EHDKEFFHFR HLGRESDIFL LAGLIGRIGP NSSSDQRQAC TLVHFINPET EQUENCE n #: Eos sc .1895 21 CACTICCICC CTCTCCAGTC	PSLDNEVHSS AVEEGGGGGG YHHREFRFDL LDSRTLWASE ONKOFPWAF KKHELYVSFR VPKPCCAPTQ Guence 31 ACGITICICGI CCTATCCACC	PHERLESOE QUESTPYKAV SKIPEGEAVI SKIPEGEAVI SKIPEGEAVI FARTUHFES LIGNQDWIIA LINAISVLYFD LINAISVLYFD	RREMOREILS PSTOGPPLAS AABERIYKDY IRSTGSKORS PEGYAAYVE DSSNVILKKY 51 AGGAGGGGGAT TTGGSTCGGA	120 180 240 300 360 420
55 60 65	1	11 PHSFVALWAP HLQGKHNSAP HLQGKHNSAP HLQGKHNSAP EISVYQVUQB RISVYQVUQB HCATHANANVAE MMATNHAIVQ H 660 DNA m 1d Accession Lence: 211. 11 GGCCCCAGT AGGCAGCCTG CTGATARAAT	P_001710 21 j LFLURSALAD MFMLDLYNAM HDMKSFFHFR HLGRESDLFL LAGLIGRIGP NSSSDGRGA TLVHFINPST equence n #: Eos se 1895 21 j CACTICCTCC TCCTGGGTTA	J PSLDNEVHSS AVEEGOGPGG YHRREFRFDL LDSRTLWASE ONKOPFMVAF KKHELYVSFR VPKPCCAPTQ dquence 31 J ACSTITCTGST ACGTITCTGST ATGCTTGGACC	PIHRRLRSOB QGPSYPYKAV SKIPEGEAVT SKIPEGEAVT PKATEVHPRS LIGNGDWIIA LNAISVLYFD 41	RREMOREILS FSTOGPPLAS AAEFRIYKDY TSHIMVUNPR IRSTGSKORS PEDYANYYCE DSSNVILKKY 51 AGGAGGGGAT TITIGAATA AACCAGCATA	120 180 240 300 360 420
55	MIVESLEAAA ILGLEHERPH LODSHELTDA IERFENNETS GREATPINGO GREATPLINGY REMOVERACIO Seq ID NO: Coding seq I GRATCHGAGG GGGGCTTGGG GAGGATTTAT TOATTITITI GTGCTTTTTG CACAGGTTCC	11 PHSFVALWAP HLQGKENSAP HLQGKENSAP HLQGKENSAP HLQGSHPK EISWYQVUQB MMATNHAIVQ H 660 DNA m dd Accession uence: 211. 11 GSCGCCCAGT AGGCAGCCTG CTGATARAT TCTTCTCTTC TTGAACAGCTT	AP_001710 21 LFLLRSALAD MFMLDLYNAM HDMEFFHER HLGRESDLFL LAGLIGHNER NSSSDQRQAC TLVHFINPET equence n H: Eos se 1895 21 CACTECTICC CACTECTICC TCCTGGGTTA TGACCTTTT TTTTTCTAGG GGATTCTGAT	J PSLDNEVHSS AVESCOGEGG YHHREPRPDL LDSRTLWASE QNKOFFMVAF KKHELYVSFR VPKPCCAPTQ SQUENCE 31 J ACGTTCTCGT CCTATCCACC ATATITITAA ATAATGANA ATAATGANA AGGACCATTA	PIHRRLRSOB QGPSYPYKAV SKIEEGEAVT SKIEEGEAVT PKATEVHERS LINGIGOPMIIA LINAISVLYFD 41 GCTGGGCGGG CACAGGTTTT AAACGGAGAG GCAGTTTGTC GCATTCTTC CTATAGAGGA	RREMORE ILS FSTGSPILAS FSTGSPILAS AABERITKDY TSNINNVNPR IRSTGSKORS PEGYANYYCE DSSNVILKKY 51 AGGGGGGAT TTTTANANA AACCAGCATA AAGAANAGT GCAGATTATG	120 180 240 300 360 420 60 120 120 180 240 360
55 60 65	MINTERIARA HIGHERPRE LODSHELTDA HEREFUNET GREATPINGO GREATPLING GREATPLING Seq ID NO: Nucleic Ac Coding seq GGATCTGAGG GGGATTAT TOATTITTT GTOCOGTICO	11 PHSFVALWAP HLQGKENSAP HLQGKENSAP KISYYQVUQE KISYYQVUQE KNATNHAIVQ H 660 DNA si dd Accession uence: 211. OCCCCCAGT AGGCACCAGT CCCTCGRANA TITTCTCTC TTGAACAGCT TAGGAACAGCT TTGATAANAT	NF_001710 21 1	J FSLDNEVHSS AVEEGOGIGG VEHREEPROL LDSRTLWASE ONKOPPWASE KKHELYVSFR VPKPCCAPTQ GUERCE 31 J ACGITICTGT CCTATCCACC ATATITITA ATGCTTCGTA ATGCTTCTGT ATATITITA ATGATAGAAA GGCACCATTA GTCAACATTA	PIHRRLRSOB QGPSTPYRAV SKIPEGEAVT EGHLVFDITA FYATEVHEN DLGRQDWIIA LNAISVLYFD 41 GCTGGGCGGG GCAGGTTTGTC GCATTCTTC CGATTCTTC CGATTCTTC CTATAGAGGA	RREMOREILS FSTGGPPLAS AABERIYAS TSHIMVUNDR IRSTGSKOR PBGYANYYCE DSSNVILKKY 51 AGGAGGGGAT TTGGGTCGGA TTTTTTAAAAA AACCAGCATA AAGAAAAAG GCAGATTNTC CCAGGAGGGA	120 180 240 300 360 420 60 120 180 240 360 420
55 60 65	HEVERLEAAA ILGLEHERPE LODSHEUTDA ILBERTONETE GREATPINGOLSVE GREATPLEST REMVERCOSC Seq ID NO: Nucleic Ac Coding seq Coding seq GGATCTGAGG GGGGTTGGG GGAGGAATTAT TGATTTTTT TGTGCTTTTC CACAGGTTCC CTTGTGCTGA	11 PHSFVALWAP HLOKENSAP HLOKENSAP HLOSIMFK RISVYOVLOR FEALMRANVAE H 660 DNA # id Accession dence: 211. 11 GGCGCCCAGT AGGCAGCCT CTGATARAT CCTTGATARAT TTTTCTTC TTGAACAGCT TGAACAGAT AGGCAAAGT	NF_001710 J LFLLRSALAD LFLLRSALAD LFLLRSALAD LFLLRSALAD LFLRSESDLEV LAGLIGHEF NSSSONGNO TUVHFINPST CHUMPINPST CH	J PSLDNEVHSS AVESCAGNOG VHIREPRIDL LDSRTUMASE CONKOPPMVAF KKHELYVSFR VPKPCCAPTQ EQUENCE 31 ACGITCICAT CCTATACACC ATATITITAA ATGATACACC ATAATITITAA ATGATACACC ATAATITAAA ATGATACACC ATAATITAAA ATGATACACC CCTCAACACCA ATAAATGAAA GGCACCATTA	PHERERSOB QGPSTPYEAV SKIPEGEAVT EGHLVPDITA FKATEVHPS DLGWQDWIIA LNAISVLYPD 41	RREMORE ILS FSTOGPPLAS AABERI YKDY TSHIRMVINPT IRSTGSKORS PEGYANYYCE DSSNVILKKY 51 AGGGGGGGA TITTIANAN ANCAGGTA ANCAGATA ANGANANAGG	120 180 240 300 360 420 60 120 120 180 240 360
55 60 65 70	MEVERLAAA ILGIDHIRPRE LQOSHFUTA IRBUDETF RINGULSE QMISTPOOL QCAPPAIG RINGULSE REQUITA REQUITA RINGULSE REQUITA REQUITA RINGULSE REQUITA RINGULS REQUITA REQUITA REQUITA REQUITA	11 PHSFVALMAP HLOGKBINSAP HLOGKBINSAP BLOGKBINSAP RISVYQVLOZ TLOOGSINIX ELADANWAS RISVYQVLOZ H 660 DNA m 660 DNA m 660 DNA m 660 DNA m 71 AGCAGCTO CONGRACA CONGRACA TITTECTOT TUGACAGCTO TU	F_001710 LPLLESALAD MPHLDLUNAM LEDIKEFHER HIGHESDLFL LAGLIGHER NSSEDONQAC TIVMFINPH CACTICTAC CACTTCCTCC CACTTCCTCC CACTTCCTCC GAGTTCCTACT GACATTTT TTTCTCAG GAGTTCTAAA ACAGGATGAA ACCAGGATGAA	FILINEVISS AVERGOOPG FILINEVISS AVERGOOPG	PHIRELESOR OPESTPYKAV SEXIPEGEAV ESHLESOR OFFICE SEXIPEGEAV ESHLESOR DIAGODHIA LNAISVLYPD 41 1 1 1 1 CACAGGTTTT AAACOGAGAG GCATTGTC GCATTTCTTC CTATAGAGGC CACCCTATAC TATAGAGGT TCATACACTTATACACT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACT TCATAGAGGT TCATAGA	FREMOREILS FSTUGPPLAS	120 180 240 3360 420 60 120 180 240 360 420 420
55 60 65	MEVERLAAA ILGIDHIRPRE LQOSHFUTA IRBUDETF RINGULSE QMISTPOOL QCAPPAIG RINGULSE REQUITA REQUITA RINGULSE REQUITA REQUITA RINGULSE REQUITA RINGULS REQUITA REQUITA REQUITA REQUITA	11 PHSFVALMAP HLOGKBINSAP HLOGKBINSAP BLOGKBINSAP RISVYQVLOZ TLOOGSINIX ELADANWAS RISVYQVLOZ H 660 DNA m 660 DNA m 660 DNA m 660 DNA m 71 AGCAGCTO CONGRACA CONGRACA TITTECTOT TUGACAGCTO TU	F_001710 LPLLESALAD MPHLDLUNAM LEDIKEFHER HIGHESDLFL LAGLIGHER NSSEDONQAC TIVMFINPH CACTICTAC CACTTCCTCC CACTTCCTCC CACTTCCTCC GAGTTCCTACT GACATTTT TTTCTCAG GAGTTCTAAA ACAGGATGAA ACCAGGATGAA	FILINEVISS AVERGOOPG FILINEVISS AVERGOOPG	PHIRELESOR OPESTPYKAV SEXIPEGEAV ESHLESOR OFFICE SEXIPEGEAV ESHLESOR DIAGODHIA LNAISVLYPD 41 1 1 1 1 CACAGGTTTT AAACOGAGAG GCATTGTC GCATTTCTTC CTATAGAGGC CACCCTATAC TATAGAGGT TCATACACTTATACACT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACACTT TCATAGAGGT TCATACT TCATAGAGGT TCATAGA	FREMOREILS FSTUGPPLAS	120 180 240 360 420 60 120 120 180 360 420 480 480 660
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55 60 65 70 75	HURSLEAM, INCLEMENT INCLEM	11 PHSPVALHAP PHSPVALHAP PHSPVALHAP PHDGRIBSHP DWMSFVMLW RESVYOVLOS TLDOGSINPR EALRHANVAN EALRHANVAN EALRHANVAN EALRHANVAN EALRHANVAN EARRHALTO T EAGCCCCACT TOMACAGCCT OMACAGCCT TOMACAGCCT TOMACAGCCT TOMACAGCCT TOMACAGCCT TOMACAGCC TOMACAGCCT TOMACAGCC TOMACAGCCT	FP_001710 21 LIFLERSALAD MEMLDLYNAM EIDNEFHER HUGHESDLER HUGHESDLER HUGHESDLER HUGHESDLER TLVHFINPH EQUADE CTCVCCAGT TCVTGCTCC CTCCCAGT TCCTGGGTAT TCCTGGGTAT TCCTGGTAT TCCTGCTAT TCCTGGTAT TCCTGCTAT TCCTGGTAT TCCTGCTAT TCCTGCTAT TCCTGCTAT TCCTGCTAT TCCTGCTAT TCCTGCTAT TCCTGTAT TCCTGCTAT TCCTG	FILDINEWISS AVESCOGNOG STATEMENT OF STANDARD S	PHIRELESOB QUESTPYNAV SEXTERESOR SULFRESOR ESTATEMENTS LIANESON 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	REMORBILS REMORB	120 180 240 300 420 420 60 120 180 240 300 420 420 540 660 720 720 840 840 900
55 60 65 70	PRIVELIEARA PRIVELIEARA LOSSIFITTA REBETORET BRIEGOLSTE GROUPS GR	11 PREVALWAP HIGGEORGA PRISONER PRISONE	F_001710 21 LEFLESALAD MPMLDLVNAM ESHOREFIER ESHORE	FILDINEWISS AVESCOORDED	PHIRELESOB QUESTPERAV SIL PEGRAVI- PRATEVIPES PRATEVIPES BLOGGODII I. LINAISVLYPD 41 1 1 1 1 1 1 1 1 1 1 1 1 1	REMORETLS FATGEPELS AMERITAN STATE FATGEPELS F	120 180 240 300 360 420 60 120 240 300 360 420 480 540 660 660 660 660 672 720 780
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55 60 65 70 75	I HURSLEAAA ILGURERER LOSSIFUTDA ILGURERER LOSSIFUTDA ILGURERER IMUGULSVE CONCENTRAL INCLUDIO	11 PHEFVALWAP HIGOGORSA DAWNSFYNLV RISVYOVLOS RISVYOVLOS HIGOGORSA HIGORSA HIGOGORSA HIGORSA HIGOGORSA HIGORSA HIGOGORSA HIGOR	F_001710 21 LEFLESALAD MEMBLICHMAN MEM	FILDINEWISS AVESCOOPED	PHIRELESOB QUESTPERAV SIL PEGGATY PARAMETER PERA PARAMETER PERAMETER PE	STATEMENT STATEM	120 180 240 360 420 60 120 180 240 360 420 480 660 720 720 780 840 960 960 960 910 910 910 910 910 910 910 910 910 91
55 60 65 70 75	PRIVELEARA HOUSELEARA LOBSETTIMA LOBSETTIMA HOUSELEARA COMMITTEE COMMIT	11 PHSFVALWAP HLOGRIMSAD DAVISIEVALVA DAVISIEVALVA HLOGRIMSAD HOSPICA GEO DIA n. GEO DI	P_001710 21	FILDINEVIES AVESCOORD	FIRELESOR GOFFEFEAV FIRELESOR GOFFFEAV FIRELESOR GOFFFEAV FIRELESOR GOFFFEAV FIRELESOR FIRELESOR GOFFFEAV GOFFF	PROPERTY PROPERTY	120 180 240 360 360 420 120 120 120 240 360 420 420 420 420 660 720 720 720 780 840 960 960 960 1020 1040 1140 1220
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	GTATGCCTGC	CTCACTCCTT	CACTGGGCTC	GGGTGGGAGA	TCCGCATGCA	CANTOGAGCTC	1440
	GTTCAGGCAG	ACCTGAAGAA	GATGTGGAGT	CCCCCCAATC	TCTCCGTGGA	CTGGAAAAGG	1560
_	ACACCGCCAT	AGGTGAAGAA GTGGCAGCCG	CAGATGCGGC	TCAGTGCTCA	CCACCGTGAC	GCACAGCACC	1620
5	AGCAGCCAGT	CACAGGTGGC	GGCCAGCACA	CGCATGGTGC	TTATCTCTGG	CAAAGCTGCC	1680 1740
	TCAGAGCAGG	GCAGACAGCC ACTGCCTGCC	ACACTCTTTC	CACGAGGAGA	CCAAGGAAGA	TAGTGGGAGG	1800
	CAGGGAGATG	ATATTCTAAT	GGAGAAGCCT	TCCAGGCCTA	TGGAATCTAA	CCCAGACACT	1860
10	GAAGGATGCC	AAGGAGAAAC	TGAGGATGTT	CTCTGA			
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15	1	11	21	31	41	51	
13	MI neer ever	VLFLFSSFST	THECTCOMP	PDET.POT.DED	CTITIFECIA	I.VI.KAKVOCE	60
	LNITAOLORG	EGNCPPEWDG	LICWPRGTVG	KISAVPCPPY	IYDFNHKGVA	FRHCNPNGTW	120
	DPMHSLNKTW	EGNCPPEWDG ANYSDCLRFL	OPDISIGKOE	PFERLYVMYT	VGYSISFGSL	AVAILIIGYF	180
20	RRIHCTRNYI	HMHLFVSPML VVMPIYPLAT	RATSIFVKDR	VVHAHIGVKE	LESLIMODDP	ONSIEATSVD	240 300
20	PVARWAVADA	TLADARCWEL	SACDIKMIYO	APILANIGIN	PILPLNTVRV	LATKIWETNA	360
	MOUNTOVOVO	ST APOTTATA	LUPCULIVIUP	UCT. DUSPING.	CWRIDMHCEL.	PENSFOCIETY	420
	SITYCYCNGE	VQAEVKKMWS KLASRQPDSH	RWINLSVDWKR	TPPCGSRRCG	SVLTTVTHST	SSQSQVAAST	480 540
25	RMVLISGKAA	KIASRQPDSH EGCOGETEDV	ITLPGYVWSN	SECOCLIPHSIA	HEETKEDSGR	OGDDITMSKL	540
23	SKPMESAPDI	EGCOGLEDA					
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30	courag sequ	uence: 143.	. 1795				
	1	11	21	31	41	51	
	!	CCGGGCCCGA	<u> </u>	<u></u>	1	1	60
	TOGGCCAGCC	AAGTTGGCAA	CTTGGAAGCT	TCTCCCGGGC	TCTGGAGGAG	GGTCCCTGCT	120
35	TCTTCCTACA	GCCGTTCCGG	GCATGGCCGG	GCTGGGGGGG	TCGCTCCACG	TCTGGGGTTG	180
	GCTAATGCTC	GGCAGCTGCC	TCCTGGCCAG	AGCCCAGCTG	GATTCTGATG	GCACCATTAC	240 300
	TATAGAGGAG	CAGGAGGGAG	AAGGTAATTG	AGCGAAAGTA	TOGGATGGAC	TCATCTTCAC	360
	GCCCAGAGGA	ACAGTGGGGA	AAATATCGGC	TGTTCCATGC	CCTCCTTATA	TTTATGACTT	420
40	CAACCATAAA	GGAGTTGCTT	TCCGACACTG	TAACCCCAAT	GGAACATGGG	ATTTTATGCA	480
	CAGCTTAAAT	AAAACATGGG AAGCAAGAAT	CCAATTATTC	AGACTGCCTT	CGCTTTCTGC	AGCCAGATAT	540 600
	CATCTCTTTT	GGTTCCTTGG	CTGTGGCTAT	TCTCATCATT	GGTTACTTCA	GACGATTGCA	660
4.5	TTGCACTAGG	AACTATATCC	ACATGCACTT	ATTTGTGTCT	TTCATGCTGA	GAGCTACAAG	720
45	CATCTTTGTC	AAAGACAGAG GATGACCCAC	TAGTCCATGC	TCACATAGGA	GTAAAGGAGC	TGGAGTCCCT	780 840
	TATOGGGTGC	AAGATTGCTG	TTGTGATGTT	TATTTACTTC	CTGGCTACAA	ATTATTATTG	900
	GATCCTGGTG	GAAGGTCTCT	ACCTGCATAA	TCTCATCTTT	GTGGCTTTCT	TTTCGGACAC	960
50	CAAATACCTG	TGGGGCTTCA GCACGAGCAA	TCTTGATAGG	CTGGGGGTTT	CCAGCAGCAT	TTGTTGCAGC	1020 1080
50	CATCARGIGG	ATTTATCAAG	CACCGATCTT	AGCAGCTATT	GGGCTGAATT	TTATTCTGTT	1140
	TOTGRATACG	GTTAGAGTTC	TAGCTACCAA	AATCTGGGAG	ACCAATGCAG	TTGGGCATGA	1200
	CACAAGGAAG	CAATACAGGA	AACTGGCCAA	ATCGACACTG	GTCCTGGTCC	TAGTCTTTGG	1260 1320
55	CCCCATCCAC	ATCGTGTTCG TGTGAGCTCT	TCTTCAACTC	CTTTCAGGGT	TICTTTGTGT	CTATCATCTA	1380
••	CTGCTACTGC	AATGGAGAGG	TTCAGGCAGA	GGTGAAGAAG	ATGTGGAGTC	GGTGGAATCT	1440
	CTCCGTGGAC	TGGAAAAGGA CACAGCACCA	CACCGCCATG	TGGCAGCCGC	AGATGCGGCT	CAGTGCTCAC	1500 1560
	TATCTCTCCC	AAAGCTGCCA	AGATOGOCAG	CAGACAGCCT	GACAGCACAC	TCACTTTACC	1620
60	TGGCTATGTC	TGGAGTAACT	CAGAGCAGGA	CTGCCTGCCA	CACTCTTTCC	ACGAGGAGAC	1680
	CAAGGAAGAT	AGTGGGAGGC	AGGGAGATGA	TATTCTAATG	GAGAAGCCTT	CCAGGCCTAT	1740 1800
	CATTTGTGGC	TGACTTTCAT	GOGGTGGTCC	AGGAGAAACT	TOTOTOTAGAG	GGCTTGGCTG	1860
	ATACTCCTAT	GCTTGAGTTC	AAAGGCTGAA	AATTCAGTTA	AGGTGTTACT	TAATAATAGT	1920
65	TTTTAGGCTC	CATGAATTGG	CTCCTGTAAA	TACTAACGAC	ATGAAAATGC	AAGTGTCAAT	1980
	GGAGTAGTTT	ATTACCTTCT	ATTGGCATCA	AGTTTTCCTC	AAAAAAAAATT	CAATTGCTTG	2100
	GCTGTAGCTT	TCTCTCATAT	ATATCACCCT	AAATATAATG	AAGATCTTTT	AGTGTGTATC	2160
70	ATTTTCCTTT	TAGAAACTAG	TATTCTCTTA	TTTCTTACTT	TAATGTACTT	CTATCACTGC	2220
70	ATTTATTTTG	CCTGTGCATA	GGAGCAATTA	GGATCTAAAA	AGATATATGG	BATRATICAT	2280
	TTATAACAAT	TACATGTGTT	TTTGGGAACA	AGGAAAATTT	CTCAAAAAAG	AATATTTCAC	2400
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75	TTCTTTGTAA	ACCATGTCAT	GTGGAAAGAT	TTCCTCAGTT	AGTGAGCTTG	TGTCTGCAAA	2520 2580
13	TTTGAGCTGT	TACTACATTG	TACATGGCAT	GTGGGATCAA	TTAAAAATTT	GTTTTAAAAA	2640
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-	LLOCULE AC		005059				
	1	11	21	31	41	51	
	Magraner ***	MONTH GEOT	LARACTORNO	TITIEROTVI	VIJKAKVOCET-	NITACLORGE	60
85	GNCFPEWDGL	ICWPRGTVGK	ISAVPCPPYI	YDFNHKGVAF	RHCNPNGTWD	nitaqlqege FMHSLNKTWA	120
	NYSDCLRFLO	PDISIGKQEF	FERLYVMYTV	GYSISPGSLA	VAILIIGYFR	RLHCTRNYIH	180
	MHLPVSPMLR	ATSIPVKDRV	VHAHIGVKEL	ESPINODDEO	NSIEATSVDK	SQYIGCKIAV	240

5	LADARCWELS LAKSTLVLVL OABVKKMWSR	AGDIKWIYQA VFGVHYIVFV WNLSVDWKRT	LHNLIFVAFF PILAAIGLNP CLPHSFTGLG PPCGSRRCGS EQDCLPHSFH	ILFLNTVRVL WEIRMHCELF VLTIVTHSTS	ATKIMBTNAV FNSPQGFFVS SQSQVAASTR	IIYCYCNGEV MVLISGKAAK	300 360 420 480 540
10	Seq ID NO: Nucleic Act Coding sequ	664 DNA se id Accession Lence: 43	1 #: NM_012	152			
	1	11	21	31	41	51 	
15	CTTCTTTAAA	TTTCTTTCTA	GGATGTTCAC TTATAATAGG	TTCTTCTCCA	CAATGAATGA	GTGTCACTAT	60 120
13	GGAACAAAGC	TTGTGATTGT	TTTGTGTGTT GGCAGTGATC	GGGACGTTTT	TCTGCCTGTT	TATTTTTTT	180
							300
20	ATGTTTAACA GGGCTTCTGG	CAGGCCCAGT	TTCAAAAACT GACTGCTTCC	TTGACTGTCA CTCACCAACT	ACCGCTGGTT TGCTGGTTAT	CGCCGTGGAG	360 420
							480 540
	TGGAATTGCC	TCTGCAACAT	CTCTGCCTGC	TCTTCCCTGG	CCCCCATTTA	CACACTGGGC CAGCAGGAGT TGTGGTGTAC	600 660
25	CTGCGGATCT	ACGTGTACGT	CAAGAGGAAA ACCCATGAAG CCCGGGCCTG	ACCAACGTCT	TGTCTCCGCA	TACAAGTGGG	720
	TCCATCAGCC	GCCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	CCTGAACTGC	780 840
	AGGCAGTGTG	GCGTGCAGCA	TGTGAAAAGG	TGGTTCCTGC	TGCTGGCGCT	GCTCAACTCC CATGAAGAAG	900 960
30	ATGATCTGCT	GCTTCTCTCA	GGAGAACCCA	GAGAGGCGTC	CCTCTCGCAT	CCCCTCCACA	1020
	GTCCTCAGCA GTCTGCAATA	GGAGTGACAC AAAGCACTTC	AGGCAGCCAG CTAAACTCTG	TACATAGAGG GATGCCTCTC	GGCCCACCCA	CCAAGGTGCA GGTGATGACT	1080 1140
	GTCTTAGG						
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	1	11	21	31	41	51	
40	WINECHADICHW	DFFYNRSNTD	THOOMYSTEE.	VIVLCVGTFF	CLFIFFSNSL	VIAAVIKNRK	60
	PHPPFYYLLA LVIAVERHMS	NLAAADFFAG IMRMRVHSNL	TKKRVTLLIL	LVWAIAIFMG	AVPTLGWNCL	SSLTASLTNL CNISACSSLA	120 180
	PIYSRSYLVE	WTVSNLMAFL	IMVVVYLRIY	VYVKRKTNVL	SPHTSGSISK	RRTPMKLMKT	240 300
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	l Name of the	I	TOGGGGTCGG	l I	Coormormer	TOCOGCOCCCC	60
	GCGCTCCGGT	GCCTCCGCCT	CCTGTGCCCG	CCGCGGAGCA	GTCTGCGGCC	CGCCGTGCGC	120
55							180 240
	CCATTGTCTT	CATCAAGCAG	CCGGGCCCGG	AGGATGCACT	GCAGGGGGGC	ACCCAGACAG CGGGCGCTGC	360 300
	CTGTCCAGGA	CACGGAGCGG	CGTTTCGCCC	AGGGCAGCAG	CCTGAGCTTT	GCAGCTGTGG ACTGGAGAAG CCTGTGGTCC	420
60	ACCEGCTECA	GGACTCTGGC	ACCTTCCAGT	GTGTGGCTCG	GGATGATGTC	ACTGGAGAAG	480 540
	resoccoons						
	TGAAGCATCC						600
65	ACATTGATGG	GCACCCTOGG GCACCCTOGG	GCTGAGATCC CCCACCTACC GTCAGCAGCA	AGCCACAGAC AATGGTTCCG AGGAGCGGAA	AGATGGGACC CCTGACGCTC	CCCCTTTCTG	600 660 720
-	ACATTGATGG ATGGTCAGAG GTCCTGAGCA	AGCCTCGGAA GCACCCTCGG CAACCACACA TAGTGGGCTG	GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT	AGCCACAGAC AATGGTTCCG AGGAGCGGAA GCGCCCACAG	AGATGGGACC CCTGACGCTC TGCTTTTGGC	CCCCTTTCTG CCGCCAGCTG CAGGCTTGCA	600 660 720 780
00	ACATTGATGG ATGGTCAGAG GTCCTGAGCA GCAGCCAGAA	AGCCTOGGAA GCACCCTOGG CAACCACACA TAGTGGGCTG CTTCACCTTG	GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG	AGCCACAGAC AATGGTTCCG AGGAGCGGAA GCGCCCACAG ATGAAAGCTT AGGCCATGTT	AGATGGGACC CCTGACGCTC TGCTTTTGGC TGCCAGGGTG CCATTGCCAG	CTTCGTTGCC CCCCTTTCTG CGGCCAGCTG CAGGCTTGCA GTGCTGGCAC TTCTCAGCCC	600 660 720 780 840 900
	ACATTGATGG ATGGTCAGAG GTCCTGAGCA GCAGCCAGAA CCCAGGACGT	AGCCTCGGAA GCACCCTCGG CAACCACACA TAGTGGGCTG CTTCACCTTG GGTAGTAGCGG	GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGAGG	AGCCACAGAC AATGGTTCCG AGGAGCGGAA GCGCCCACAG ATGAAAGCTT AGGCCATGTT AGGCCATGTT	AGATGGGACC CCTGACGCTC TGCTTTTGGC TGCCAGGGTG CCATTGCCAG	CTTOGITGCC CCCCTTTCTG CGGCCAGCTG CAGGCTTGCA GTGCTGGCAC TTCTCAGCCC AACCGCAGTC	600 660 720 780 840 900 960
70	ACATTGATGG ATGGTCAGAG GTCCTGAGCA GCAGCCAGAA CCCAGGACGT AGCCACCCCC GCCCCCCACA	AGCCTCGGAA GCACCCTCGG CAACCACACA TAGTGGGCTG CTTCACCTTG GGTAGTAGCG GAGCCTGCAG CCTCCGCAGA	GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGAGG TGGCTCTTTG GCCACAGTGT	AGCCACAGAC AATGGTTCCG AGGAGCGGAA GCGCCCACAG ATGAAAGCTT AGGCCATGTT AGGATGAGAC TTGCCAACGG	CCAGGTCACA AGATGGGACC CCTGACGCTC TGCTTTTGGC TGCCAGGGTG CCATTGCCAG TCCCATCACT GTCTCTGCTG	CTCGTTGCC CCCCTTTCTG CGGCCAGCTG CAGGCTTGCA GTGCTGGCAC TTCTCAGCCC AACCGCAGTC CTGACCCAGG	600 660 720 780 840 900 960 1020
	ACATTGATGG ATGGTCAGAG GTCCTGAGCA GCAGCCAGAA CCCAGGACGT AGCCACCCCC GCCCCCCACA	AGCCTCGGAA GCACCCTCGG CAACCACACA TAGTGGGCTG CTTCACCTTG GGTAGTAGCG GAGCCTGCAG CCTCCGCAGA	GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGAGG TGGCTCTTTG GCCACAGTGT	AGCCACAGAC AATGGTTCCG AGGAGCGGAA GCGCCCACAG ATGAAAGCTT AGGCCATGTT AGGATGAGAC TTGCCAACGG	CCAGGTCACA AGATGGGACC CCTGACGCTC TGCTTTTGGC TGCCAGGGTG CCATTGCCAG TCCCATCACT GTCTCTGCTG	CTCGTTGCC CCCCTTTCTG CGGCCAGCTG CAGGCTTGCA GTGCTGGCAC TTCTCAGCCC AACCGCAGTC CTGACCCAGG	600 660 720 780 840 900 960 1020 1080 1140
	ACATTGATGG ATGGTCAGAG GTCCTGAGCA GCAGCCAGAGAGT AGCACCCCC GCCCCCACA TCAGGCCACA TCAGGCCACG GGTGTTTAC AGCCCACGCACA	AGCTCGGAA GCACCTCGG CAACCACACA TAGTGGGCTG CTTCACCTTG GGTAGTAGGG GGTAGTAGGG CATCCGCAGA CATGCAGGG AGCCACACTT AGCTGCAGG GTGGTGGGAG CGACCTGTGGGAGG	GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGAGG TGGCTCTTTG GCCACAGTGT ATCTACCGCT CACCTAGCAG GAGGAGCGTG CACCGCGGAGG TTGGCCAATA	AGCCACAGAC AATGGTTCCG AATGGTCCGAAG AGGAGCGCACAG ATGAAAGCTT AGGCCATGTT AGGATGAGAC TTGCCAACGG GCATTGGCAA AGATTGACAC TGACCGCTTCCT TCCCGCTGCCT TTGCCAAAAG	CCAGGTCACA AGATGGGACC CCTGACGCTC TGCTTTTGGC TCCACGGTG CCATTGCCAG TCCCATCACT GTCTTCTCTG GGGGCAGAGG CATGCCGCTA TCCCCCCAAG CACCCATGGCTG TGATGCTGGT	CTTOGITIGCE CCCCTTTCTN CGGCCAGCTG CAGGCTAGCA CTTCTCAGCCC AACCGCAGTC CTGACCCAGG GGCCCACCCA TTTGAGCCAC GGTCTGCCAG AGGGTTACAC GTTTGAGCCAC GTTTAGACCCAG GTCTACACCT	600 660 720 780 840 900 960 1020 1080
	ACATTGATGG ATGGTCAGAG GTCCTGAGCA GCAGCCAGAAA CCCAGGAGGT AGCCACCACA TCCGGCCACA TCCGGCCACG GGGTGTTTAC AGCCCAGCGT AGAAGGGCCA	AGCTCGGAA GCACCTCGG CAACCACACA TAGTGGGCTG GTAGTAGCG GAGCTGCAG CCTCCGCAGA CAATGCAGGG AGCCACACTT AGCTGCAGC GTGGTGGGAG CGTGGTGGGAG	GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATTGCTG AGGTATTAGAG GCCACAGTGT ATCTACCGCT CACCTAGCAG GAGGAGCGTG CACCGGGAG TTGGCCAATA	AGCCACAGAC AGGACCGAA AGGACCGAAA GCGCCCACAG AGGACCACAG ATGANAGCT AGGCCATGTT AGGATGAGAC TTGCCAACAG GCATTGGCCA AGATTGACAA TGACCTGCCT TCCCGCTGCCT TCCCGCTGCAAAG CACAGATTGAAAAA CACAGATGAAAAA CACAGATGAAAAA CACAGATGAAAAA CACAGATGAAAAA CACAGATTAAAAAA CACAGATGAAAAA CACAGATGAAAAAA CACAGATTAAAAAA CACAGATTAAAAAAAAAA	CCAGGTCACA AGATGGGAC CCTGACGCTC TGCTTTTGGC TGCCAGGGTG CCATTGCCAG TCCCATCACT GGGGCAGAGG CATGCCGCTA TCCCCCCAAG CACCCCAAG CACCCATGCC	CTTOGITIGCE CCCCTTTCTN CGGCCAGCTG CAGGCTTGCA CTTCTCAGCCC AACCGCAGTC CTGACCCAG GGCCCACCCA TTTGAGCCAC GGTCTGCCAG AGGGTCTACC GTCTACACCT GTGTGCCACT	600 660 720 780 840 900 960 1020 1140 1260 1260 1320
70	ACATTGATGG ATGGTCAGAG GTCCTGAGCA GCAGCCAGAA AGCACCACCA TCAGCCACC TCATCCTGGA AGCCCACG TCATCCTGGA AGCCCACGGT AGCCCACGGT AGCCCACGGT AGCCCACGGT AGCCCACGGT TGCCTCCTG TGGATTGCCT TGGATTGCT TGGATTGCCT GGATTGCT TGGATTGCCT TGGATTGCCT TGGATTGCCT TGGATTGCCT TGGATTGCCT TGGATTGCCT TGGATTTCCT TGGATTTCCT TGGATTTCCT TGGATTTCCT TGGATTTCCT TGGATTTCCT TGGATTTCT TGGATTTCT TGGATTTCT TGGATTTCT	AGCCTGGAA GGACCACACA TAGTGGGCTG GGTAGTAGGG GGGCTGCAG AGCCTGCAG AGCCACACT AGCTGGCG AGCTGCAG CGAGGCAGA CGAGCTGGCG GGGGGGGGGG	GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGATTGCTG GCCACAGTGT ATCTACCGCT CACCTAGCAG GAGGAGCGTG CACGCGGGAG TTGGCCACTAGCAG GAGGAGCGTG CACGCGGAGAC CACCACAAAAC CCCACAAAAC CACCAAAAAC CACCAAAAAC	AGCACAGAC AGGACCACAGA AGGACCACAG AGGACCACAG AGGACCACAG AGGATGAC AGGATGAC AGGATGAC AGATTGACAA AGATTGACAA AGACTGAAAG ACAGGATGT TCCGGCTGCC TGCCTGAAAG GACAGGATGT ACAGGATGT ACAGGATGT ACAGGATGT ACAGGATTAC ACTACAGTTACA ACAGGATTAC ACTACAGTTAC AC	CCAGTCACA AGATGGGAC CCTGACGCTC TGCTTTTGGC TGCCAGGGTG CCATTGCCAG TCCCATGCCAG GGGCAGAGG CATGCCGCAAG CACCCCCAAG CACCCATGGC TGATGCTGGT CGACGTCAC TGCCCCAAG CACCCATGGC TGATGCTGGT CAACATCACT GGAGGGCAAA TTGGTACACA TTGCTACACA TTGGTACACA TTGCTACACA TTGGTACACA TTGGTACACA TTGCTACACA TTCACACA TTCACACACA TTCACACACA TTCACACACA	CTTOSTIGGE CCCCTTTCTG CGGCCACCTG CAGGCTTGCA GTGCTGGCAC ATCGCAGG GGCCACCCA AGGGTCTGCCAG GGCTGCCAG GGCTGCCAG GGTCTGCCAG GGTCTGCCAG GGTCTGCCAG GGTCTACCCT GTGGCCACTG CCGGCTACTA	600 660 720 780 840 900 960 1020 1140 1260 1320 1320 1440 1500
70	ACATTGATGG ATGGTCAGAG GCAGCAGAA CCCAGGACGT AGCACCCCC GCCCCCACA TCATCCTGGA GGGTGTTTTAG AGCCAGGGT AGAAGGGCA GCCACGGGT TGCCTCCTG TGCCTCCTG	AGCCTCGGAA GCACCATCAT TAGTGGCTG GTAGTAGCACTA GGTAGTAGCACTA GGTAGTAGCAC CATCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCGCAGA CCTCGCAGA CCACTTGGAGC CGTGGTGGGAG CGACCTGGGTG CACCTGGGTG CACCTGGGTG CACCTGGGTG CCTGAAGAAG GACCCAGGCC	GCTGAGATYC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGAGG GGCACAGTGT ATCTACCGCT CACCTAGCAG GAGGAGGTG CACCGGGAG TTGGCCAATA GGTCAGCGGA CCCCAAGACA ACACCCAAAAC	AGCCACAGAC AGGACCACAGA AGGACCACAG ATGANAGCTT AGGCCATCAT AGGACTAGACA TTGCCAACG GCATTGCCA AGATTGACA TTGCTGAAGA TGACCTGCT TCCTGAAG GACAGGATGT TCCAGGAGGATGT TCACAGGATGT TCACAGATTGT TCACAGATTGT TCAACAGATTGT ACAGATTT TCAACAGATTAACACACACACACACACACACACACACACA	CCAGTCACA AGATGGGAC CTGAAGCTC TGCTTTTGGC TGCAGGGTG CCATTGCCAG TCCCATCACT GTCTCTGCTG GGGCCAGAGG CACCCATGGC TACCCCCAAG CACCATGGC TGATGCTGGT GAACACACT TGATGCTGGT GGAGGGCAAA CTGGTACAGA ACCTTGGT	CTTG/TGCC CCCCTTTCTG CGGCCACTTG CAGCCTTGCA CTTCTCAGCCC AACCGCAGT CTGACCCAG GGCCACCCA AGGTTTGCAG GGTTTGCAG GGTTTGCAG GGTTTACACCT GTGGCACT AGGGTTAC ACCAGATGC CCCGGGTACT AACAGATGC ATCAACAGATGC	600 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500
70	ACATTRATISE ATOGRAGAG GTCCTGAGCA GCAGCAGGAG AGCCAGCAC AGCCACCAC TCGGGCAGG TCATCCTGGA AGCCACCAC AGCCACCAC AGCCACCAC TCATCCTGGA AGCCAGCGT TCATCCTGGA AGGAGGTCT TCATCTCCTGG TGGATTGCT TCATCTCAGA TGGAGGTTATAC TCATCTCAGA TGGAGGTTATAC TCATCTCAGA TGGAGGTTATAC TCATCTCAGA TGGAGGTTATAC TCATCTCAGA TGGAGGTTATAC TCATCTCAGA TGGAGGTTAC TGGAGGTTATAC TGATCTAGAA TGGAGGTTATAC TGGAGGTTATAC TGATCTAGAA TGGAGGTTAC TGATCTAGAA TGGAGGTTATAC TGATCTAGAA TGGAGGTTATAC TGATCTAGAA TGATCTAGAA TGGAGTTATAC TGATCTAGAA TGGAGTTATAC TGATCTAGAA TGATCAGAA TGATCTAGAA TGATCTAGAA TGATCTAGAA TGATCTAGAA TGATCTAGAA TGATCTAGAA TGATCTAGAA TGATCTAGAA TGATCAGAA TGATCAGAA TCAGAA TC	AGCCTOGGAN GANCCACACA TAGTOGGCTG GTAGTAGGCTG GTAGTAGGCGCG GAGCCTGGCAG CCTCCGCAGA CCATCGCAG CCTCGCAGA GCCACACTT AGCTGGCAG CGCACACTT GCTGGCAG CGAGCTGGTG CAACCTGGCAG CAACCTGGCA CAACCTGGCA CAACCTGGCA CAACCTGGCA CAACCTGGCA CAACCTGGCA CAACCTGGCA CAACCTGGCA CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGGCC CAACCAGCCC CAACCAGGCC CAACCAGCC CAACCACCACC CAACCACCACCACC CAACCACCAC	GCTGAGATICE CCCACCTACE TCAGCAGGA TATTCCTGCT AGCATTGCTG AGGTATGCTG TGGCTCTTTG GCCACAGTGT ATCTACCGCT CACCTAGCAG GAGGAGCGTG CACCGGGAG TTGGCCAATA CACCCAAAGCA ACACCAAACC TCGGGAGTCT TGGTACGGTT TGGTACGGTA	AGCCACAGAC AGGAGGGGAA ATGGATTCOG AGGAGGGGAA ATGGAAGGTT AGGCCACAG ATGGAAGGTT AGGCCATGTT TGCCAACAG GCATTGGAAG TGACTGCCA AGATTGAAGA TCAGCTGCCT TCCGGCTGCC TTGCTGAAAG GACAGGATGT GCCAGGTTGT TCAAGAATTGG TCAAGAATTGG TCAAGAATTGG TCAAGAATTGG TCAAGAATTGG GGCTAGAGTT TCAAGAATTGG GGCTAGAGTT TCAAGAATTGG GGCTAGAGTT TCAAGAATTGG GGCTAGAGTT TCAAGAATTGG GGCTAGAGTT TCAAGAATTGG GGCTAGAGTT TCAAGAGTTGG TGATGAGCAGT TCAAGAGTTGG GGCTAGAGTT TCAAGAGTTGG TCAAGAGTTGG GGCTAGAGTT TCAAGAGTTGG GGCTAGAGT TCAAGAGTTGG GGCTAGAGT TCAAGAGTTGG GGCTAGAGT TCAAGAGTTGG GGCTAGAGT TCAAGAGTTGG GGCTAGAGT TCAAGAGTTGG GGCTAGAGT TCAAGAGTTGG GGCTAGAGT TCAAGAGT T	CAGGTCACA AGATGGGAC CCTGAAGCTC TGCTTTGGGC TGCCATGCCA	CTTCSTTGCC CCCCTTTCTS CGGCCACTTG CAGGCTTGCA GTGCTGCA GTGCTGCA GTGCTGCAG GGCCACCCA GGTCTGCCAG GGCCACCCA GGTCTGCCAG GGTCTGCCAG GGTCTGCCAG GGTCTGCCAG GTCTGCCAG GTCTGCCAG AGGGTCTAC AGGGTCACCA ACCAGATGC GCCAGGCATCG GCCAGCCAC GCCAGCCAC GCCCAGCCAC GCCCAGCCAC GCCAGCCA	600 660 720 780 840 900 1020 1140 1260 1320 1320 1440 1500 1620 1680
70 75	ACATTGATGG ATGGTAGGA GCAGGAGGT AGCAGCAGGA TCGGGCAGA TCGGCCACA TCGGCCACA TCGGCCACA TCGGCCACA TCGGCCACG TCATCCTGGA AGGAGTTTAC AGCACGCCC TCATCCTGGA TGGATTTAC TGGATTGCT TGGATTGCCT TCATCTCAGA TGGATGGTTA AGGAGGTGTA AGGAGTGTA AGGAGGTGTA AGGAGGAGGTGTA AGGAGGTGTA AGGAGGTGTA AGGAGGAGGAGGAGGA AGGAGGTGTA AGGAGGAGGAGA AGGAGGAGGAGA AGGAGGAGGAGA AGGAGG	AGCCTCGGA GACCCACAC TAGTGGGCTG CTTCACCTTG GGTAGTAGCG GTGCTGCAG CATCCGCAGA AGCCACACTT AGCTGGCAG GGGTGGGAG CGAGCTGGTG CAACCTGGCT GACCTGGCG GACCAGGCC GACCTGGCT GACCAGGCC GACCAGGCC GACCAGGCC GACCTGGCT GACCAGGCC GACCAGGCC GACCAGGCC GACCAGGCC GACCAGGCC GACCAGGCC GACCAGGCC GACCAGGCC GACCAGGCC	GCTGAGATTCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTAGCAG AGGTATGAGG TGGCTCTTTG GCACAGTGT ATCTACCGCT CACCTAGCAG AGGAGGAGGAGAGGA	AGCCACAGAC AGGAGGGGAA AGGAGGGAA AGGACATGTT AGGACTAGAT AGGATGAGAC TTGCCAACAG GCATTGAC TGCCAACAG TGACCAGAG TGACCAGAG TGACCAGAG TGACCAGAG TGACAGATTGAAG TGACAGATTGA TGACAGATTGA TCAAGATTGT TCAAGATTGT TCAAGATTGA AGCTCAAGATTGA AGCTCAAGATTGA TCACAGTTGAT TCAAGATTGAT TCAAGATTGA AGCTCAAGATTGAT TGATGACCAG AGCTCAAGTTGT TCAAGATTGAT TCAAGATTGAT TGATGACCAG AGCTCAAGTTGT TGATGACCAG AGCTCAAGTTGT TGATGACCAG TGATGACCAG TGATGACCAG TGATGACCCTG TGGTCCACCTT TGGTCCCCTTG	CAGGTCAGA AGATGGGAC CTGAGGTCA TGCTATTGGC TGCCAAGGTG TCCCAACACAC GGGCCAGAGG CATCCCCAAG ACCCATCAC GACCATCAC GACCATCAC GACCATCAC GACCACCAC GACCACCAC CACCCACCAC CACCCACC	CTTOSTIGGE CCCCTTTCTG CGGCCACTTG CAGGCTTGCA CTGCTGCAC CTGCACCCA ACCGCAGTC CTGACCCAC TTTGAGCAC GGTCTGCCAG AGGGTCTACCA GGGTCTACCAG GGTCTACCAG AGGGTCTACC GTCGCCACTG CCCGGCTACT ACCAGANTG ATCAACAGCG CGCAGCATC CCCGAGCAC GGCCAGCAGCA GGCCAGCAGCA GGCCAGCAGCA GGCCAGCAGCA GCCCAGCACA CCCAGCAC GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCACACA GCCCCACAC GCCCACACA GCCCACACA GCCCACACA GCCCACACAC GCCCACAC GCCCACAC GCCCACACAC GCCCACAC GCCACAC GCCCACAC GCCCCACAC GCCCACAC GCCCACAC GCCCACAC GCCCACAC	600 660 720 780 840 900 1020 1140 1200 1320 1380 1440 1500 1620 1620 1680 1740
70 75	ACATTRATISE ATGGTCAGAG GTCTCAGCA GCAGCAGAA CCAGGACCT AGCACCCCC TCAGCACT TCAGCACAG GGTGTTTTAG AGCCAGGGT AGAGGGCACAG AGCACGGGT AGAGGGCACAG TCAGCTTCTGAA GCCACGGGT TGGATTGCCT TCATCTCAGA AGGCCACAG AGGAGGGTAGA AGGCCACAGAT AGCCCACTAT AGCC	AGCCTCGGA GAACCACACA TAGTGGGCTG CTTCACCTTG GGTAGTTAGCG GGTAGTTAGCG GGGCCTGCAG AGCCCACCTT AGCTGGCAG AGCCACCTT AGCTGGCAG CAACTGGCT GCTGAAGAAG GAACCAGGCC GAACTAGGCA GAACCAGGCC GAACTAGGCA GAACTAGGCA GAACTAGGCA GAACTAGGCA GAACTAGGCA CAA	GCTGAGATCC CCCAGCTACC GTCAGCAGGA TATTCCTGCT AGCATTGCTG AGGATTGCTG AGGATTGCTG TGGCCACAGTGT ATCTACCGCT ACCTAGCAG AAGGAGGTT ACCTAGCAG AAGGAGGTT TGGCCAATAA CCCCAAGACA TTCGAGGTCAAAAC TTCGAGGTCA TTCGAGGTCAAAAC TTCGAGGTCAAAAC TTCGAGGTCAAAAC CCCCAAGACAC TTCGAGGTCAAAAC CCCCAAGACAC TTCGAGGTCAAAAC CCCGAGGCACAT TGGTACCGTTAAAAC CCGCCACAGCAC CCGCCACAGCAC CCGCCACACAC CCGCCACACAC CCGCCCACACAC CCGCCACACAC CCGCCCACACAC CCGCCCACACAC CCGCCCACACAC CCGCCCACAC CCGCCCACAC CCGCCCACAC CCGCCCACAC CCGCCCACAC CCGCCCACAC CCGCCCACAC CCCCCACAC CCCCCCACAC CCCCCCACAC CCCCCC	AGCCACAGAC AGGAGGGGAA AGGAGGGGAA AGGAGGGGAA AGGAGG	CAGGTCAGA AGATGGGAC CCTGAGGCTC TGCTATTGGC TGCCAGGGTG TCCCATCACT GTCTCTCTCT GTCTCTCTCT GTCTCTCCCA ACCCCCAAG ACCCCCAAG ACCCCCAAG CACCCCCAAG CACCCCCAAG CACCCCCAGC CACCCCCAGC CACCCCAGC CACCCCAGGCCAAC CCCAGGGTGAC CCCAGGGTAC CCCAGGTCAC CCCAGGTCAC CCCAGGGTAC CCCAGGGTAC CCCAGGGTAC CCCAGGTCAC CCCAGCTCAC CCCAC CCCAC CC	CTTCSTTGCC CCCCTTTCTI COGCCLACTTG CAGGCTTGCA GTGCTGCAG TTCTCAGCC AACCGCAGTC TTTCAGCCA GGCCACCCA AGGGTTACC GGTTGCCAG GGTTGCCAG GTTGCAGC GTTTACACCT GTGGCCACT ACCAGGTTAC ACCAGGTACT ACCAGGTACT ACCAGGTACT CCCGGCTACT ACCAGGTAC ATCAACAGCA TGCAGCAGCA TGCAGCAGCAC TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA	600 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1620 1620
70 75	ACATTRATISE ATGGTCAGAG GTCCTGAGGA GCAGCAGAGAG CCAGGACGT ACGAGGACGT ACGAGGACGT ACGAGCAGAG TCATCCTGGA AGGAGTTTTAC AGGAGGGCAG GCACGAGGGCAG AGGAGTTTTAC AGGAGGGCAG GCAGGGGC TCATCTTGAG AGGAGGGCAG AGGAGGGCAG AGGAGGGCAG AGGAGGGCAAG AGGAGGCAAG AGGAGGCAAG AGGAGGCAAGC AGGAGGCAAGC AGCAGGCAAGC AGCAGCACAT	AGCCTCGGA CAACCACACA TAGTGGGCTG CTTCACCTTG GGTAGTAGCG GGTAGTAGCG GGTAGTAGCG GGTAGTAGCG AGCCACACTT AGCTGGCAGA CAATGCAGGG GGAGCTGGTG CAACCTGGTG CAACCTGGTG CGTGAAGAAG AGCCAGGCC GGATCTACCG GGATTTCACG GGATTTCACG CGAATTTCACG CAACTGCATTTCACG CAACTGCATTTCACG CGAATTTCACG CAACTGCATTTCACG CAACTGCATTTCACG CAACTGCACG TAATGGGAATTTCACG CAACTGCATTTTCACGCATTTTTCACGCATTTTTCACGCATTTTTCACGCATTTTTCACGCATTTTTCACGCATTTTTCACGCATTTTCACGCATTTTCACGCATTTTTCACCGCATTTTTCACGCATTTTTCACCGCATTTTTCACCGCATTTTTCACCGCATTTTTCACCGCATTTTTCACCGCATTTTTCACCCTCACGCATTTTTCACCCTCACGCATTTTTCACCCTCACGCATTTTTCACCCTCACGCACTCACCCACC	GCTGAGATTCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCAG AGGATTGCAG GGCACAGTTG ACCTAGCAG AGCACCAGTTG ACCTAGCAG AGGAGCGTG CACCCGAGCAG CCCCAAGACA ACACCAAAAC TTGGGCGAAT ACACCAAAAC TTGGGGGAAA AAGAGGGCTG TGGTGAGAAAA AAGAGAGCAGAGACA ACACCAAAAC ACACCAAAAAC ACACCAAAAC ACACCAAAAC AC	AGCCACAGAC AGGAGCGCA AGGAGCGCAA AGGATGTT AGGATGAGC AGGATGGCCACAG AGGATGACC AGGATGACC AGGATGACC AGGATGACC AGGATGACC AGGATGACC AGGATGACC AGGATGACC AGCACC CAGGTCACM AGATGGGAC CTGAAGGCTC TGCTTTTGGC TGCCAGGGTG TGCCATGCTG GGGCAGGGTG CATGCCAGGCAGGCC TGCCCCAAG CACCCAGGCC TGCAGGCGCAGGCC TCAGGCAGGCC TCAGGCAGGCC TCAGGCAGGCC TCAGGCAGGCC TCAGGCAGGCC TCAGGCAGGCC TCAGCCAGGCC TCAGCCAGGCC TCAGCCAGGCC TCAGCCAGGCC CCAGCCAGCCC TCAGCCAGCC CCAGCCCAGC	CTTCSTTGCC CCCCTTTCTI CGGCCAGCTG CAGGCTTGCA GTGCTGGCA ACCGCAGC GTGCTGCAGC GGCCACCA AGGCTGCCAG GGCCACCA AGGGCTTAC GGCCAGCAGCA CGGCTGCCAG GGCCACCA AGGGCTTAC ACCAGGATGC GGCCAGCA GGCCACGA GGCCACGA GGCCACGA GGCCACGA GGCCACGA GGCCACGA GGCCACGA GGCCACGA GGCCACGA GGCCACGA GGCCACGA GGCCACGA GGCCACGAC GGCCACGAC GGCCACGAC GGCCACGACA TACACCTTGCA TGACAGCAC TACACTTGCA TGCCAGGATT	600 660 720 780 840 900 960 1080 1140 1260 1320 1380 1440 1500 1620 1680 1740 1680 1740 1800 1800	
70 75	ACATTRATISG ACATTRATISG GTCAGAGA GTCAGAGAG GTCAGAGAG GTCAGAGAGA CCAGAGACAT ACCAGCACCAC GCCCCCACA ACCACCACCAC ACCACCACAC ACCACCAC	AGCCTOGGAN GCACCTCOSI CAACCCACCA TAGTISOGCTS CTTCACCTTS GGTAGTAGCS GGTAGTAGCS GGGCTGCAGA AGCCACACT AGCTGCAGA CAATGCAGA GGACTTGCAG GGACTTGGGG GGACTAGCG GGACTAGCAG GACCAGGC GGACTAGCAG GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC GACCAGGC CAAAGTGGGA CAAAGTGGGA CAAAGTGGGA CAAAGTGGGA CAAAGTGGGA CAAAGTGGGA CAAAGTGGGA CAAAGTGGGA CAAAGTGGGA CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGGAA GGCCCAGGC CAAAGTGCAA GGCCCAGGC CAAAGTGGAA GGCCAGAGC CAAAGTGGAA CAAAGC CAAAGTGGAA CAAAGC CAAAGC CAAAGC CAAAGC CAAAGC CAAAGC CAAAGC CAAAGC CAAAGC CAAACC CAAAGC CAAACC	GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTACCAGCT AGCATTGCTG GCCACAGTGT ATCTACCAGCT ACCATGCAG GAGGAGCTT ACCACAGGAG ACCAGGAGAGCT TGGCCAAGAGAGT TGGCCAAGAAAA AGGAGAAAAA AAGGAGAAAAA AAGGAGAAAAA AAGGAGAAAAA AAGGAGAAAAA AAGGAGAAAAAA	AGCCACAGA AGGACACAG AGGACTACAG AGGACTACAG AGGACTACAG AGGACTACAG AGGACTACAG AGGACTACAG AGGACTACAG AGGACTACAG AGGACTACAG AGGACTACACAG AGGACTACACAG AGACTACACAG AGACTACACAG ACAGACAG ACAGACACAC AGCACACACAC AGCACACAC	CONGUENCIA MANTESGACE COTTANDETT TOCHTOTOGE TOCHTOCHTOCHTOCHTOCHTOCHTOCHTOCHTOCHTOCH	CTTCSTTGCC CCCCTTTCTI COGCCLACTTG CAGGCTTGCA GTGCTGCAG TTCTCAGCC AACCGCAGTC TTTCAGCCA GGCCACCCA AGGGTTACC GGTTGCCAG GGTTGCCAG GTTGCAGC GTTTACACCT GTGGCCACT ACCAGGTTAC ACCAGGTACT ACCAGGTACT ACCAGGTACT CCCGGCTACT ACCAGGTAC ATCAACAGCA TGCAGCAGCA TGCAGCAGCAC TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA TACACTTGCA	600 660 720 780 840 900 900 1020 1260 1320 1380 1440 1560 1620 1680 1740 1800 1800

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	TCCATGACGT	GGCCCCTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAGGC	AACAGCTGCA	2160
	ACATCAMGCA	CACGGAGGCC	CCCCTACAAGA	TOTTGGACAA	CATTROOTEN	TOTOTOTO	2280
	COGCTGTGGC	CTACATCATT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
5	AAGCCAAGCG	GCTGCAGAAG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
	GAGGGCCTTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
		CGGCCCCGCG					2520
	TCCCACGGTC	TAGCCTGCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580 2640
10	COCTOGRAM	GGCTCAGGGC GAAGGATGAG	CACCACGAGG	GAGTGGCAGA	CACCCACTA	CITGIGAAGA	2700
10	GCETGCAGAC	CCACGCCAAC	GTGGTGGGG	TOTTGGGGGT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCTG	AGGATTTCCA	2820
	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTCGCCCTAT	2880
10	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
15	TGGCTGCGCG	TAACTGCCTG	GTCAGTGCCC	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCC	3000
	TCAGCAAGGA	TGTGTACAAC	AGTGAGTACT	ACCACTTCCG	CCAGGCCTGG	GTGCCGCTGC	3060 3120
	GCTGGATGTC	CCCCGAGGCC GCTGATGTGG	ATCCTGGAGG	CACATCCACA	CATCOCCAT	COTCCCCAC	3120
	CAGATGATGA	AGTACTGGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCCCGAGG	3240
20	GCTGCCCTTC	CARACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
		CCCGCTCAGG					3420
	CAGCATGATG	GGCAAGATCC	CTGTCCTCCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
0.5	TTGCTGAGGT	CTGAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCCTCA	TCCTTTGGGA	3540
25	GGCTGACTTG	GACCCAAACT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCCTGCCAC	3600
	CTCTTCCTCT	ATCAGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTTCT	GGCCTTCAAC	3660 3720
	TTCTCCCCTT	GACCGGGTCC TGAGCTGGGT	AACTUIGCCA	CTCATCIGCC	MACTITICATION	CTICCCCACAC	3780
	ACCUTACIONA	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
30	ACACAGCAAG	TGAGTCCTCC	CCACTCTGGG	CTTGTGCACA	CTGACCCAGA	CCCACGTCTT	3900
	CCCCACCCTT	CTCTCCTTTC	CTCATCCTAA	GTGCCTGGCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTCACAC	TATATABACC	COCCETTETS	TATISCACCAC	CCCCCCTTT	TATATITAAT	4020
	TGCAGCGTGG	GGTGGGTGGG CCCCACACTT	CATGGGAGGT	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
35	GCCATCCTTA	CCCCACACTT	TTATTGTTGT	CGTTTTTTGT	TIGITITGIT	TTTTTGTTTT	4140
33	TGTTTTTGTT	TTTACACTCG	CIGCICICAA	TAAATAAGCC	TTTTTTA		
	Seq ID NO:	667 Prote	in sequence				
	Protein Acc	ession #: 1	IP_002812				
40			_				
40	1	11	21	31	41	51	
	1	1	!	!	1	1	60
	MGAARGSPAR	PRRLPLLSVL PVQDTERRFA	COCCI COL	ALVYIKQPSS	QUALQUERRAL	DARCEVEAPOP	120
	TWITTERGRAN	LANDVOLVEL	COCCUCATION	BULLERDOOTE	OWNEDCTOR	DCOCNUTUSE	
45	IKWIEAGPVV	LKHPASEAEI	OPOTOVTLRC	HIDGHPRPTY	OWFRDGTPLS	DGOSNHTVSS	180
45	IKWIEAGPVV KERNLTLRPA EAMPHCOPSA	LKHPASEAEI GPEHSGLYSC OPPPSLOWLF	QPQTQVTLRC CAHSAPGQAC EDSTPITNRS	HIDGHPRPTY SSQNFTLSIA RPPHLRRATV	QWFRDGTPLS DESFARVVLA FANGSLLLTO	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR	180
45	IKWIEAGPVV KERNLTLRPA EAMPHCOPSA	LKHPASEAEI GPEHSGLYSC OPPPSLOWLF	QPQTQVTLRC CAHSAPGQAC EDSTPITNRS	HIDGHPRPTY SSQNFTLSIA RPPHLRRATV	QWFRDGTPLS DESFARVVLA FANGSLLLTO	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR	180 240 300 360
45	IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VRLPTHGRVY	LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA OKGHELVLAN	QPOTOVTLRC CAHSAPGQAC EDETPITNRS EIEDMPLPEP IAESDAGVYT	HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGOR	QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSNLKKPQD	180 240 300 360 420
	IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VRLPTHGRVY SOLFEGERGY	LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTOATPK	QPOTQVTLRC CAHSAFGQAC EDETPITNRS EIBDMPLFEP IAESDAGVYT PTVVWYRNOM	HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRPEV	QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR	180 240 300 360 420 480
45 50	IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VRLPTHGRVY SOLFEGERGY	LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTOATPK	QPOTQVTLRC CAHSAFGQAC EDETPITNRS EIBDMPLFEP IAESDAGVYT PTVVWYRNOM	HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRPEV	QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR	180 240 300 360 420 480 540
	IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPENVID	LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV	QPOTQVTLRC CAHSAFGQAC EDETPITNRS EIBDMPLPEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC	HIDGHPRPTY SSQNPTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRPEV QQCMEFDKEA IASNGPOGOI	QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT PKNGTLRINS TVPCSATGRE RAHVOLTVAV	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITPKVEPER	180 240 300 360 420 480 540
	IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VRLPTHGRVY SQLEBGKPGY CMSSTPAGSI GSSLPENVTD TTVYQGHTAL	LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK	QPOTQVTLRC CAHSAFGQAC EDETPITNRS EIBDMPLPEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR	HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRPEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR	QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT PKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITPRVEPER IHDVAPEDSG	180 240 300 360 420 480 540 600
50	IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCLAGNSC	LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY	QPOTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNOM KLKPTPPPQP TRDDAGNYTC PLIQWKGKDC VVDKPVPEES	HIDGHPRPTY SSQMPTLSIA RPPHLRRATV RVFTAGSEER CHAANIAGQR LISEDSRPEV QQCMEFDKEA IASMGPQGQI ILDPTKLGPR EGPGSPPPYK	QWFRDGTPLS DESFARVVLA FANGSLLLTA VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG	DGQSNHTVSS PQDVVVARYE VRPRNAGIYE PSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITPRVEPER IHDVAPEDSG AAVAYIIAVL	180 240 300 360 420 480 540
	IKWIEAGPVV KERNITLRPA EAMPHCOPSA CIGGOGRPP VRLPTHGRVY SQUEBSKPGYY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC KMENTSDKMH	LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCL/TQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE FPRSSLQPIT	QPQTQVTLRC CAHSAFGQAC EDETPITMRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLM TLGKSEFGEV	HIDGHPRPTY SSQNPTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFBV QQCMEFDKEA LASMGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE	QWFRDGTPLS DESFARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG ABIQEEVALT GVABILVLVK	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVMWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITPRVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQQ	180 240 300 360 420 480 540 600 660 720 780 840
50	IKWIEAGPVV KERNITLRPA EAMPHCOPSA CIGOGORGPP VRLPTHGRVY SQLEBUKPCY CMSSTPAGSI GSSLPEWVTD TTVYOGHTAL RYTCIAGNSC GLMPYCKKRC KRHSTSDKMH LDFFRELIMP	LKHPASEAEI GPEHSGLYSE GPEHSGLYSE IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAGGDPK NIKHTEAPLY KAKRLQKQPE PPRSSLQPIT GKINKAVVR	QPQTQVTLRC CAHSAFGAG EDSTPITMS EIEDMPLFEP IAESDAGVYT FTVVWYRNQM KLKPTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLM TLGKSEFGEV LIGLCRAEP	HIDGHPRPTY SSQNPTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRPEV QCMEFDKEA LASNGPQGQI ILLDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEVUL	OWFRDGTPLS DESFARVVLA PANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG ABIQEEVALT GVABTLVLVK GDLKOFLRIS	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSNLKKPQD VEVYDGTWYR KPTIKWERAD FITPKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQG KSKDEKLKSO	180 240 300 360 420 480 540 600 720 780 840 900
50	IKWIEAGPVV KERNITLRPA EAMPHCOPSA CIGOGORGPP VRLPTHGRVY SQLEBUKPCY CMSSTPAGSI GSSLPEWVTD TTVYOGHTAL RYTCIAGNSC GLMPYCKKRC KRHSTSDKMH LDFFRELIMP	LKHPASEAEI GPEHSGLYSE GPEHSGLYSE IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAGGDPK NIKHTEAPLY KAKRLQKQPE PPRSSLQPIT GKINKANVVR	QPQTQVTLRC CAHSAFGAG EDSTPITMS EIEDMPLFEP IAESDAGVYT FTVVWYRNQM KLKPTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLM TLGKSEFGEV LIGLCRAEP	HIDGHPRPTY SSQNPTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRPEV QCMEFDKEA LASNGPQGQI ILLDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEVUL	OWFRDGTPLS DESFARVVLA PANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG ABIQEEVALT GVABTLVLVK GDLKOFLRIS	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSNLKKPQD VEVYDGTWYR KPTIKWERAD FITPKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQG KSKDEKLKSO	180 240 300 360 420 480 540 600 720 780 840 900 960
50	IKWI BAGPVV KERNLTLEPA EAMPRCOPSA CIGQORGPP VRLPTHGRVY SQLEBGENOY CMSTPAGSI GSSLPEWTID TTVYQGHTAL RYTCIAGNSC GLMPYCKKRC GLMPYCKKRC KRESTSDKMH LDFRELEMP PLSTKQKVAL LDFRELEMP PLSTKQKVAL	LKHEASEARI GPEHSGLYSC QPPPSLOWLF IILEATLHLA QKGELVILAN LDCLTQATPK EAQARVQVILE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE FRESLQPIT GKLMHANVVR CTQVALGMEH RWMSPEAILE	OPOTOVTLAC CAHSAFQAC EDETPITMRS EIEBMPLFEP IAESDACY TOVWYRNOM KLKFTPPPOP TRDDAGNYTC PLIQWKGKOR VVDKPVPES GEEPEMECLM TLGKSEFGEV LLGLCREAEP LLSNNRFVHKD GDFSTKSDVM	HIDGHPRTY SSQNFTLSIA RPPHIRRATV RVFTAGSEER CHAANLAGGR LISEDSRFEV QCMEFDKEA LASNGPQGGI LIASNGPQGGI LIASNGPQGDE LIASNGPQGDE LIASNGPQGDE LIASNGPQGDE LIASNGPQGDE LIASNGLEE HYMVLEYUDL LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA	QWERDGTPLS DESPARVVLA DESPARVALA PRANGSLLITQ VTCLPPKGLP RQDVNITVAT FXNCTLRINS TVPCSATGRE RAHVQLTVAV MITOTIGLSVG AEIQEVALT GUARTLVLVK GDLKQFLRIS QRQVKVSALG QRQVKVSALG THGEMPRIGGQ	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSNLKKPQD VEVYDGTWYR KPTIKWERAD FITPKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQG KSKDEKLKSO	180 240 300 360 420 480 540 600 720 780 840 900
50 55	IKWI BAGPVV KERNLTLEPA EAMPRCOPSA CIGQORGPP VRLPTHGRVY SQLEBGENOY CMSTPAGSI GSSLPEWTID TTVYQGHTAL RYTCIAGNSC GLMPYCKKRC GLMPYCKKRC KRESTSDKMH LDFRELEMP PLSTKQKVAL LDFRELEMP PLSTKQKVAL	LKHPASEAEI GPEHSGLYSE GPEHSGLYSE IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAGGDPK NIKHTEAPLY KAKRLQKQPE PPRSSLQPIT GKINKANVVR	OPOTOVTLAC CAHSAFQAC EDETPITMRS EIEBMPLFEP IAESDACY TOVWYRNOM KLKFTPPPOP TRDDAGNYTC PLIQWKGKOR VVDKPVPES GEEPEMECLM TLGKSEFGEV LLGLCREAEP LLSNNRFVHKD GDFSTKSDVM	HIDGHPRTY SSQNFTLSIA RPPHIRRATV RVFTAGSEER CHAANLAGGR LISEDSRFEV QCMEFDKEA LASNGPQGGI LIASNGPQGGI LIASNGPQGDE LIASNGPQGDE LIASNGPQGDE LIASNGPQGDE LIASNGPQGDE LIASNGLEE HYMVLEYUDL LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA	QWERDGTPLS DESPARVVLA DESPARVALA PRANGSLLITQ VTCLPPKGLP RQDVNITVAT FXNCTLRINS TVPCSATGRE RAHVQLTVAV MITOTIGLSVG AEIQEVALT GUARTLVLVK GDLKQFLRIS QRQVKVSALG QRQVKVSALG THGEMPRIGGQ	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSNLKKPQD VEVYDGTWYR KPTIKWERAD FITPKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQG KSKDEKLKSO	180 240 300 360 420 480 540 600 720 780 840 900 960
50	IKWIEAGDWV KERNITILEPA EAMPHCQFSA CIGQGGREPY VELPTHERY SQLEBSHOFY CMSSTPAGSI GSSLEBWYTD TTVYQGHTAL TTVYQGHTAL TTVYCGHTAL KRESTSDKMH LDFRELBMF PLSTKQKVAL HERGAWVPL AGKARLPQPE	LKHPASEARI GPENSGLYAL OPPPSLOWLF IILEATHELA LGCLITOATPK RAGARAOVLE NAGTLHPARV LQCEAGODPK KARRLQKOPE FPRSSLQPIT GKLMHANVUR CTQVALGMEH RWMSPERILE GCPSKLYRLM	OPOTOVTLIC CAHSAFGAC EDETPITMES EIEDMPLEEP IAESDAGVIT PTVWWYRNOM KLKFTPPDT TRODAGNITC PLIQWIGKOR VYDNFVEES GERPEMECLM TLGKSEPGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW QRCMALSPKD	HIDGHPRTY SSQNFTLSIA RPPHIRRATV RVFTAGSEER CHAANLAGGR LISEDSRFEV QCMEFDKEA LASNGPQGGI LIASNGPQGGI LIASNGPQGDE LIASNGPQGDE LIASNGPQGDE LIASNGPQGDE LIASNGPQGDE LIASNGLEE HYMVLEYUDL LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA LAARNCLUSA	QWERDGTPLS DESPARVVLA DESPARVALA PRANGSLLITQ VTCLPPKGLP RQDVNITVAT FXNCTLRINS TVPCSATGRE RAHVQLTVAV MITOTIGLSVG AEIQEVALT GUARTLVLVK GDLKQFLRIS QRQVKVSALG QRQVKVSALG THGEMPRIGGQ	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSNLKKPQD VEVYDGTWYR KPTIKWERAD FITPKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQG KSKDEKLKSO	180 240 300 360 420 480 540 600 720 780 840 900 960
50 55	IKWIEAGDWV KERNITILEPA EAMPHCQFSA CIGGGGGFGFP VELPTHGRVY SQLEBGHDGY VMSSTFAGSI GSSLPEWVTD TTVYQGHTAL RYTCIACMSC GLMFYCKKRG KRESTSDKMM LDFRRELBMM LDFRRELBMA YHFRQAWVPL AGKARLPQPE SEQ ID MO: Nucleic Acid	LKHPASEARI GPENSGLYCO OPPPSLOWLF IILEATHHLA LDCLITOATPK RAQARVOVLE NAGTLHFARV LQCEAQGDPK NIRHTERPLY KARRLQKOPE FPRSSLOPIT GKLMRANVVR CTOVALGMER RWMSPEALLE GCPSKLYRLM 668 DNA sid d Accession	OPOTOVTLAC CAHSAFQAC EDETPITMES EIEDMPIFEP IAESDAGVT PTVWWYRNOM KLKFTPPOT TRODAGNYTC PLIOWKGNOR VVDRPVPEES GEEPEMECLAN TLGKSEFOEV LLGLCREAEP LSNNRPVHED GDFSTKSDVW QRCMALS PKD equence a &: Eos se	HIDGHPPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHANNIAGOR LISEDSRPEV QCMEFDKEA LASNGPGGT ILDPTKLGPR EGPGSPPLY GGPLQNGOPS FLAKAQGLEE LAARRCLUSA AFGVLMMEVF RPSFSEIASA	QWERDGTPLS DESPARVVLA DESPARVALA PRANGSLLITQ VTCLPPKGLP RQDVNITVAT FXNCTLRINS TVPCSATGRE RAHVQLTVAV MITOTIGLSVG AEIQEVALT GUARTLVLVK GDLKQFLRIS QRQVKVSALG QRQVKVSALG THGEMPRIGGQ	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSNLKKPQD VEVYDGTWYR KPTIKWERAD FITPKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQG KSKDEKLKSO	180 240 300 360 420 480 540 600 720 780 840 900 960
50 55	IKWIEAGDWV KERNITILEPA EAMPHCQFSA CIGGGGGFGFP VELPTHGRVY SQLEBGHDGY VMSSTFAGSI GSSLPEWVTD TTVYQGHTAL RYTCIACMSC GLMFYCKKRG KRESTSDKMM LDFRRELBMM LDFRRELBMA YHFRQAWVPL AGKARLPQPE SEQ ID MO: Nucleic Acid	LKHRASEARI GPEHSGLYSC OPPPSLOWLF IILBATLHIA LDCLIQATPK EAQARUQVLE EAQARUQVLE KIKHTEAPLY KARRLQKOPE PPRSSLQPIT GKLMKANVVR CTUVALGMEH GKCPSKLYRLM 668 DNA 84	OPOTOVTLAC CAHSAFQAC EDETPITMES EIEDMPIFEP IAESDAGVT PTVWWYRNOM KLKFTPPOT TRODAGNYTC PLIOWKGNOR VVDRPVPEES GEEPEMECLAN TLGKSEFOEV LLGLCREAEP LSNNRPVHED GDFSTKSDVW QRCMALS PKD equence a &: Eos se	HIDGHPPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHANNIAGOR LISEDSRPEV QCMEFDKEA LASNGPGGT ILDPTKLGPR EGPGSPPLY GGPLQNGOPS FLAKAQGLEE LAARRCLUSA AFGVLMMEVF RPSFSEIASA	QWERDGTPLS DESPARVVLA DESPARVALA PRANGSLLITQ VTCLPPKGLP RQDVNITVAT FXNCTLRINS TVPCSATGRE RAHVQLTVAV MITOTIGLSVG AEIQEVALT GUARTLVLVK GDLKQFLRIS QRQVKVSALG QRQVKVSALG THGEMPRIGGQ	DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSNLKKPQD VEVYDGTWYR KPTIKWERAD FITPKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQG KSKDEKLKSO	180 240 300 360 420 480 540 600 720 780 840 900 960
50 55 60	IKWIEAGDWV KERNITIEPA AMPRICOPSA CIGOGORGH VELPTHORWV SQLEBURHOV CMSTPAGGI GSSLEBURHOV CMSTPAGGI TTYVGGHTAL RYTCIAGNSC KHISTSDIMP PLSTKOKVAL HJERGAWVPL AGKARLPQPE Seq ID MO: Mucleic Act Coding sequ	LKHPASEAEI GPENSGLYSC OPPPSLOWLF ILBEATLEIA OKGHELVLAN LOCLINGATE RAGOLINE RAGOLIPE RAGOLIPE RAGOLIPE RAGOLIPE RAGOLIPE RAGOLIPE PERSILPE GCESKLYRLE 668 DNA sc dA Accession Lence: 11	OPOTOVTLEC CAMSAFGAC EDETPITMES LAESDAGVT TTVUWYRNOM KLKTTPPOPT FRDDAGNT TRDDAGNT TRDDAGNT TRDDAGNT TRDDAGNT TLOKSEFOEV LIGICARAEP LSNNRFVHKO QRCMALSPKD equence 1 % 8: 808 se 189	HIDGHPRPTY SSQMPTLSIA RPPHLRRATV RVFTAGSEER CHANNLAGOR LISEDSRPSV QCMEFDKEA LASNGPQGGI LIDDTKLGGP EGPGGPPPYK GGPLQNGOPS FLARAQGLEE HYMVLEYUDL LAARRCLUSA AFGVLMMEVF RPSFSEIASA	OWERDSTELS DESPARVVLA PANGSLLLTQ PANGSLLTQ RODVNITVAT FKNOTLRIVAT TVPCSATGRE RAHVOLTVAV HHIPONGSLV MICTIGLSVA AEIQBEVALT GVARTLVLVK GULKQFLGUS GULKQFLRIS QRQVKVSALG THGEMPRIGG LGDSTVDSKP	DGGSNHTVSS PQDVVVARYE VRPRNAGIYR PRPRNAGIYR VESYNGTWYR KPTIKMERAD FITFKWEPER HHDVAPEDSG ANVAYITAVL SLGSGPAATN SLGYTRDEQQG LSKOVYNSEY ADDEVLADLQ	180 240 300 360 420 480 540 600 720 780 840 900 960
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50 55 60 65 70 75 80	IKMIERAGPWY KERMITHERA PROPERTY OF THE PROPERT	LKHRASEARI GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GREENLAN LOCLTOATEK BADAROVILE GREENLAN LOCLTOATEK BADAROVILE GREENLAN LOCLTOATEK BADAROVILE GREENLAN LOCLTOATEK BADAROVILE GREENLAN CHARLES GREENLAN CHARLES GREENLAN LOCLTOATEK BADAROVILE LOCLTOATEK GREENLAN LOCLTOATEK GREENLAN LOCLTOATEK GREENLAN LOCLTOATEK LOCL	GEOTOTICAT LIASSAGAVIT LIASSAGAVIT LIASSAGAVIT PTVWYRENON KLEYTPP PGD GEOTOTICAT GE	HIDGEPPTY SEGMENTAL STATE SEMENTAL S	OWFEDSTPLS DESPARYULA PROPRIED PROPRIED PROPRIED ROMANIA ROM	DOGSMITUSE DOGSMITUSE DOGSMITUSE DOGSMITUSE DOGSMITUSE DEPHNIGHA VSNILKCOP V	180 240 300 420 480 540 660 660 780 900 1020
50 55 60 65 70 75	IKMIERAGHVE KERMITHERA IKM KERMITHER	LKHRASEARI GERISGLYSE GERISGLY GERISG	GEOTOTTATO TATAATAGET TATAATAGET	HIDGERPTY SEGNITUSIN SEGNITUSI SEGNITUSIN SEGNITUSIN SEGNITUSIN SEGNITUSIN SEGNITUSIN SEGNITUSI SEGNITUSIN SEGNITUSI SEGNITUSIN SEGNITUSIN SEGNITUSIN SEGNITUSIN SEGNITUSIN SEGNITUSI S	OWFEDOTPLS DESPARATURA DESPARATURA FOROTISTA FOROTISTA RATIONALIS ANALYTICAL ANALYT	DOGSMITUSE OCTOORSHIP STATEMENT	180 240 300 660 660 720 780 840 600 360 420 480 960 1020 840 960 1020 860 720 780 840 840 840 840 840 840 840 840 840 8
50 55 60 65 70 75 80	IKMIEROPHVE KERMITHERS EN EMERICA	LKHRASEARI GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GPERSOLYES GREENLAN LOCLTOATEK BADAROVILE GREENLAN LOCLTOATEK BADAROVILE GREENLAN LOCLTOATEK BADAROVILE GREENLAN LOCLTOATEK BADAROVILE GREENLAN CHARLES GREENLAN CHARLES GREENLAN LOCLTOATEK BADAROVILE LOCLTOATEK GREENLAN LOCLTOATEK GREENLAN LOCLTOATEK GREENLAN LOCLTOATEK LOCL	OPOTOVILICA CAMBA FORMA DE LA CAMBA FORMA DE LA SENDA LA CAMBA FORMA DE LA CAMBA FOR	HIDGEPPTY SEGNITISTS IN REPELIERATE REPELI	OWFEDOTFLS DESPARYUS DESPA	DOGSRITYSE POPPOVAPES PREVIOUS	180 240 300 420 480 540 660 660 780 900 1020

	CAAGACTGCA	/086443 cccatgggca agtctcatgt	GGAAATGTTC TCAGCAGACA	TACTGCTTTC ACACAACTTT	CTGACAATTT CTACTTTAAA	CTCTCTCACA TATTAGTATC	1320 1380
5	Seq ID MO: Protein Acc	669 Prote:	in sequence Sos sequence	1			
	1	11	21	31	41	51	
10	GFPLGILLLF IAMISYNIIA SLISTGLTTL YSSLEEPTVA	PPQRDLDDRE WVSYVTDFSL GDTLSKVFQR ILGIVNARAI KWSRLIHMSI	VLLIKGGALS IPGVDPENVF SLGPHIPKTE VISVFICIFF	GTDTYQSLVN IGRHPIIGLS DAWVPAKPNA ATCGYLTPTG	KTFGPPGYLL TVTPTLPLSL IQAVGVMSPA PTQGDLPENY	LSVLQFLYPF YRNIAKLGKV FICHHNSFLV CRNDDLVTFG	60 120 180 240 300
15	RFCYGVTVIL VLBLNGVLCA QDCTHGQEMF	TYPMECPVTR TPLIPIIPSA YCFPDNPSLT	EVIANVFFGG CYLKLSEEPR NTSESHVQQT				360 420
20		670 DNA se id Accession lence: 11	n #: Eos se 284				
	1	11	21	31	41	51	
25	AAGCAAGCTG TTTTCCCTTG TTGGTCAATA	AGAGGCAGGA GGTTTCCTTT TTTTATTGAT AAACTTTCGG TAGCAATGAT	GGGAATATTG AAAAGGAGGG CTTTCCAGGG	CITTTATTCT GCCCTCTCTG TATCTGCTCC	GGGTTTCATA GAACAGATAC TCTCTGTTCT GAGATACTTT	TGTTACAGAC CTACCAGTCT TCAGTTTTTG GAGCAAAGTT	60 120 180 240 300
30	GGACTTTCCA GGAAAGGTCT AGGGCAATTT	TCCCAGGAGT CAGTTACCTT CCCTCATCTC CACTGGGTCC TTCAGCGGT	TGATCCTGAA TACTCTGCCT TACAGGTTTA ACACATACCA CGGGGTTATG	AACGTGTTTA TTATCCTTGT ACAACTCTGA AAAACAGAAG TCTTTTGCAT	ACCGAAATAT TTCTTGGAAT ACGCTTGGGT TTATTTGCCA	CTTCATTATT AGCAAAGCTT TGTAATGGCA ATTTGCAAAG CCATAACTCC	360 420 480 540 600
35	TTTACTGGCT ACATTTGGAA GTGACAAGAG	TCACCCAAGG GATTTTGTTA AGGTAATTGC	GGACTTATTT TGGTGTCACT CAATGTGTTT	GAAAATTACT GTCATTTTGA TTTGGTGGGA	CATACCCTAT ATCTTTCATC	GGAATGCTTT	660 720 780 840 900
40	CTCGGGATAG CCATCAGCCT	CAGTGATGGT TTCTAGAACT GTTATCTGAA	CATCACTGTA CAATGGTGTG ACTGTCTGAA	GCCACGCTTG CTCTGTGCAA GAACCAAGGA	CTCCCCTCAT CACACTCCGA	GATTGATTGC TTTTATCATT TAAGATTATG CATGGCTATT TGACAATTTC TACTTTAAAT	960 1020 1080 1140 1200
45	TCTCTCACAA ATTAGTATCT Seq ID NO:	TTCAACTCGA	GTCTCATGTT GTAA in sequence	CAGCAGACAA	CACAACTTTC	TACTTTAAAT	1260
50	Protein Acc	cession #: 1		31	41	51	
	î	Ī.	1	i	1	1	
55	LVNKTFGFPG GLSTVTFTLP PNAIQAVGVM FTGFTQGDLF IVVTVMVITV	YLLLSVLQPL LSLYRNIAKL SPAFICHHNS ENYCRNDDLV ATLVSLLIDC	YPPIAMISYN GKVSLISTGL FLVYSSLEEP TFGRFCYGVT LGIVLELNGV	IIAGDTLSKV TTLILGIVMA TVAKWSRLIH VILTYPMECP LCATPLIPII	FQRIPGVDPE RAISLGPHIP MSIVISVFIC VTREVIANVP PSACYLKLSE	ALSGTDTYQS NVFIGRHPII KTEDAWVPAK IFPATCGYLT PGGNLSSVFH EPRTHSDKIM	120 180 240 300 360
60	ISIFQLE	VMVPGFVMAI	титорстноо	EMFYCFPONF	SLTNTSESHV	COTTQLSTLN	420
65	Seq ID NO: Nucleic Ac: Coding sequ	672 DNA so id Accession uence: 11	n#: Bos se	equence			
	1 ATGGGCTACC	11 J AGAGGCAGGA	21 GCCTGTCATC	31 CCGCCGCAGT TACCAGTCTT	41 TTTCCCTTGT TGGTCAATAA	51 TTTATTGATA AACTTTCGGC	60 120
70	AGTTACAATA GATCCTGAAA	TANTAGCTGG ACGTGTTTAT	AGATACTTTG TGGTCGCCAC	AGCAAAGTTT TTCATTATTG	TTCAAAGAAT GACTTTCCAC	AGCAATGATA CCCAGGAGTT AGTTACCTTT	180 240 300 360 420
75	GGGGTTATGT GAAGAACCCA TTTATCTGTA	CAGTAGCTAA TATTCTTTGC	GTGGTCCCGC TACATGTGGA	CATACCICCT CTTATCCATA TACTTGACAT	TCTTAGTTTA TGTCCATCGT TTACTGGCTT	ACTGGGTCCA TCAAGCGGTC CAGTTCTCTA GATTTCTGTA CACCCAAGGG	480 540 600 660 720
80	GGTGTCACTG	TCATTTTGAC	ATACCCTATG	GAATGCTTTG	TGACAAGAGA	ATTTTGTTAT GGTAATTGCC AGTGATGGTC TCTAGAACTC TTATCTGAAA GCTTCCCATT	780 840 900 960
85	CTGTCTGAAG GGTGCTGTGG CATGGGCAGG TCTCATGTTC	AACCAAGGAC TGATGGTTTT AAATGTTCTA AGCAGACAAC	ACACTCCGAT TGGATTCGTC CTGCTTTCCT ACAACTTTCT	AAGATTATGT ATGGCTATTA GACAATTTCT ACTTTAAATA	CTTGTGTCAT CAAATACTCA CTCTCACAAA TTAGTATCTT	AGACTGCACC TACCTCAGAG TCAACTCGAG	1020 1080 1140 1200

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5	Seq ID NO: Protein Acc	673 Protei ession #: F	n sequence los sequence						
10	MGYQRQEPVI SYNIIAGDTL TGLTTLILGI EEPTVAKWSR GVTVILTYPM NGVLCATPLI	SKVFQRIPGV VMARAISLGP LIHMSIVISV ECPVTREVIA FIIPSACYLK	21 KGGALSGTDT DPENVFIGRH HIPKTEDAW PICIFFATCG NVFFGGNLSS LSEEPRTHSD SHVQQTTQLS	FIIGLSTVTF FAKPNAIQAV YLTFTGFTQG VPHIVVTVMV KIMSCVMLPI	TLPLSLYRNI GVMSFAFICH DLFENYCRND ITVATLVSLL	AKLGKVSLIS HNSFLVYSSL DLVTFGRFCY IDCLGIVLEL	60 120 180 240 300 360		
13	Seq ID NO: Nucleic Aci Coding sequ		#: Eos se	quence					
20	1	11 -	21 GCCTGTCATC	31 CCGCCGCAGG	41 - TCAATAAAAC	51 TTTCGGCTTT	60		
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30	GAACCCACAG ATCTGTATAT TTATTTGAAA GTCACTGTCA	TAGCTAAGTG TCTTTGCTAC ATTACTGCAG TTTTGACATA	TTGCCACCAT GTCCCGCCTT ATGTGGATAC AAATGATGAC CCCTATGGAA	ATCCATATGT TTGACATTTA CTGGTAACAT TGCTTTGTGA	CCATCGTGAT CTGGCTTCAC TTGGAAGATT CAAGAGAGGT	CCAAGGGGAC TTGTTATGGT AATTGCCAAT	480 540 600 660 720		
35	ACTGTAGCCA GGTGTGCTCT TCTGAAGAAC GCTGTGGTGA	CGCTTGTGTC GTGCAACTCC CAAGGACACA TGGTTTTTGG	TTCATCGGTT ATTGCTGATT CCTCATTTTT CTCCGATAAG ATTCGTCATG	GATTGCCTCG ATCATTCCAT ATTATGTCTT GCTATTACAA	GGATAGTTCT CAGCCTGTTA GTGTCATGCT ATACTCAAGA	AGAACTCAAT TCTGAAACTG TCCCATTGGT CTGCACCCAT	780 840 900 960 1020	•	
40	CATGTTCAGC	AGACAACACA 675 Prote	CTTTCCTGAC ACTTTCTACT	TTAAATATTA	GTATCTTTCA	ACTOGAGTAA	1080		
			Sos sequence	•					
45	1	11	21 	31	41	51 1			
50	PENVFIGRHF IPKTEDAWVF ICIFFATCGY VPFGGNLSSV	IIGLSTVTFT AKPNAIQAVG LTFTGFTQGD FHIVVTVMVI IMSCVMLPIG	PGYLLLSVLQ LPLSLYRNIA VMSFAFICHH LFENYCRNDD TVATLVSLLI AVVMVFGFVM	NSFLVYSSLE LVTFGRFCYG DCLGIVLELN	EPTVAKWSRL VTVILTYPME GVLCATPLIF	MARAISLGPH IHMSIVISVF CFVTREVIAN IIPSACYLKL	60 120 180 240 300 360		
55	Nucleic Aci	676 DNA seld Accession lence: 26	2 #: NM_006	853.1					
60	ATCGGGCAGA CATGAGGATT	GGTCTCACAG	21 CGCAGATGCA CAGCCAAGGA TCCTGCTTGC AGTGCAAGCC	ACCTGGGGCC TCTGGCAACA	GGGCTTGTAG	CCCTCCAGGC GGGGAGAGAC	60 120 180 240		
65	CGAGAAGACG AGCCCACTGC GGAGGGCTGT CAGCCTCCCC	CGGCTACTCT CTCAAGCCCC GAGCAGACCC AACAAAGACC	GTGGGGCGAC GCTACATAGT GGACAGCCAC ACCGCAATGA	GCTCATCGCC TCACCTGGGG TGAGTCCTTC CATCATGCTG	CCCAGATGGC CAGCACACCCG CCCCACCCCG GTGAAGATGG	TCCTGACAGC TCCAGAAGGA GCTTCAACAA CATCGCCAGT	300 360 420 480 540		
70	CAGCTGCCTC CTTGCGATGC CAACATCACA CGGTGACTCC	ATTTCCGGCT GCCAACATCA GACACCATGG GGGGGCCCTC	TGTGTGCCAG TGGTCTGTAA	GTCCAGCCC GCACCAGAAG CGTGCAGGAA CCAGTCTCTT	CAGTTACGCC TGTGAGAACG GGGGGCAAGG CAAGGCATTA	TGCCTCACAC CCTACCCCGG ACTCCTGCCA TCTCCTGGGG	600 660 720 780		
75	GGACTGGATC ACCCTCCATT CAAGACCCTC	CAGGAGACGA TCCACTTGGT TACGAACATT GGGTTCGAAA	GTTTGGTTCC CTTTGGGCCT TCAGTGAGAC	TTAGACTGA TGTTCACTCT CCTGGACTAC CTGGATTCAA	GTTAATAAGA AGGAGATGCT ATTCTGCCTT	GCAAATATGT ACAGCCCATC AACCCTAAGC GTCACTTAAT GAAATATTGT CAAAGACAGC	840 900 960 1020 1080		
80	Seq ID NO:	677 Prote	TTCAATAAAT in sequence	ATTTGCTAAA	TGAGTG				
0.5			NP_006844.1						
85	1 .	11	21	31	41	51			

5	ANCLERRYIV HLOOMNLOKE ESCECTRIAT ESFPHPGFRN SLPNKDHRHD IMLVRMASFV SITMANFRIF LSSRCYTAGT SCLISGKGST SSPOLALPHIT LECANITILE HOKCEMNYFO HITTMYNCHS VQEOGKOSCO GDSGGPLVCN QSLQGIISMG QDPCAITREP GYYTKVCKIV DHIQETMONN	120 180 240
,	Seq ID NO. 678 DNA sequence Nucleic Acid Accession 8: Eos sequence Coding sequence: 1.933	
10	1 11 21 31 41 51 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	60 120 180
15	TTCCCCTGTG CCAGCGGCAT CLATTCACTCATTCACTCGCATCACCCGACTGTCCCCACCCGACTGTCCCCGATGGCAGCAA ACCCTCTGCT TTGCTCCACCCGCCCCTTCACTCG CGATGGACAGCAGCACCACCACCACCACCACCACCACCACCACC	240 300 360 420
20	ANTANCTOR: MAGNAMOR THANKINGHA MUTHINITHA MOCCOMOR CACCITATION GEOGRAPHY THYRACTIC MAGNAMOR CHIPTINITHA MAGNAMOR CACCITATION C	480 540 600 660 720
25	COLOCITICA ACTICOLOGIC CITACTURE CHIRALICA GEOGRAPICA CONCOCTATA CITATORICA GARACTERIA ALCONAGGO ACCITICACIONA CONCOCIONA CONTINU	780 840 900
30	Seq ID No: 679 Protein sequence Protein Accession #: Eos sequence	
35	1 11 21 11 1. 1 1 1. 1 1. 1 1. 1 1. 1 1	60 120 180 240 300
40	SEPSOTEEV Seg ID NO: 680 DNA sequence Nucleic Acid Accession 8: 978203.1 Coding sequence: 12190	
45.	1 11 21 31 41 51	
	ATGARTCCTT TCCAGAAAAA TGAGTCCAAG GAAACTCTTT TTTCACCTGT CTCCATTGAA GAGGTACCAC CTCGACCACC TAGCCCTCCA AAGAAGCCAT CTCCGACAAT CTGTGGTCC GAGGTACCAC CTCGACCACC TAGCCCTCCA AAGAAGCCAT CTCCGACGA CTTTTCCTAT	60 120 180
50	AACTATCCAC TRAGGATTEC CATCATION OF GRANCIAN TECTROCACT GAARGAAGA ACCTCCACAT CRATATACCA TECCTTCAGE ACCTCCACAT CTATATACCA TECCTTCAGAA ACCTCCACAT CTATATACCA TECCTTCAGAA ACCTCCACAT CTATATACCA TECCTTCAGAAA TECATACTAC CACCTTGGAAAA TECATACTAC CACCTTGGTG ACCTCACAT ACCTCACAT ACCTCACAT ACCTCACAT ACCTCACAT ACCTCACAT ACCTCACAT ACCTCACAT ACCTCACAT ACCTCACA	240 300 360 420 480
55	GTACACACAG TCCTATCATT GATCGGCCTG AGTCTAATAG CITIGGGGA AGAGGAACGG	540
33	ACTAGATACT TOTCAGTCTT CTACCTIC ATCAGTCGA AGACTGCTA TGCATTGGCT ATCACACCCA TGCTGAGAGG AGATGTGCAA TGTTTTGGAG AGACTGCTA TTTTGGAGTT GGAGAGCAAA TTTTGGAGTTC CAGGACCAAA TTTTGGAGTTC CAGGACCAAA TGCATGTGAGAGCAAA ATCATACTGG	600 660 720 780
60	MATACANTA ACCIOCCCCC (OGRACIONE ATTOCANCE) ROCACCACA TITOCANTATT COLORIGADA ATTOCANTAT COLORIGADA ATTOCANTA COLORIGADA ATTOCANTA COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA ATTOCANO COLORIGADA COLORIGADA ATTOCANO COLORIGADA COLORIGADA ATTOCANO COLO	840 900 960 1020 1080
65	TITIFICATIT ATGICTIGG CITCCTGGCA TITIGCAGTIG CGCCACCTGT AGAGATAANA ATGAATGANA TGGCCCCAGC CCAGTCAGGT CCCCAGGAGG TITICCTACA AGTCTTGAAT ATGAATGANA TGGCCCCAGC CCAGTCAGGT CCCCAGGAGG TITICCTACA AGTCTTGAAT ATGAATGANA TGGCCCCAGC	1200 1260 1320
70	GAGTCCATCA ARTCCTTTCA GRAMACKACK CACHTTGT CTCTCTACAC TGAGCATTCT AGCCAGGATT TTCACTTCCA CTGAAATAT CACAATTTGT CTCTCTACAC TGAGCATTCT GTGCAGGAGA AGAACTGGTA CAGTCTTGTC ATTCGTAAAG ATGGGAACAG TATTCTCCAGC GTGCAGGAGA AGAACTGGTA CAGTCTTGTC ATTCGTAAAG ATGGGAACTG GAGGTTTGTT	1440 1500 1560
75	AACACTITES ATAMAGATUT GUNCHITTAGAACT GTGCAMAGAG GAGAATACCC TGCAGTGCAG GAGACTATG GTGTTGTGC TTATAGAACT GTGCAMAGAG GAGATACCC TGCAGTCAGCA TGTAGAACAG AAGATAGAA CTTTTGTGT AATTTGGGTC TTCTAGACT TGTGCAGCA TATCGTTTG TTATTACTAA TAACACCAAT CAGGGTCTT AGGCCTGGAA GATTGAAGAT	1680 1740 1800
80	ATTOCKGCA ACAMANTIC CATTOCOTIO CHICARCAGE ANTINICOCOCCOCCOCAGO CONCORDANTICO CATTOCAGO CACAGORICATI GARITHICTI ATTOCTOCAGO EXCENTANO ACAMANCOLO TOTOCCAGO ACCITACATA TRACAMATO CATTOCAGO ACAMITICAGO TROCTOGRA CATOCAGO CATTOCAGO CACAMITICAGO TROCTOGRA CATOCAGO CATOCAGO CACAMITICAGO TROCTOGRA ACAMANCAGO TACOCAGO ACAMITICAGO CANCINICA ACAMANCAGO TACOCAGO CANCINICA ACAMANCAGO TACOCAGO CANCINICA ACAMANCAGO CANCINICA ACAMANCAGO CANCINICA CA	1980 2040
85	ACAMAGATA COAMAGAGC ANAACTCTA Seq ID No: 681 Protein Sequence Protein Accession S: AAB14386.1	

	W U U 2	/000443					
	MNPFQKNESK YGMKAVLILY	PLYPLHWNED	TSTSIYHAFS	SLCYPTPILG	AAIADSWLGK	FKTIIYLSLV	60 120
5	YVLGHVIKSL TRYFSVFYLS IYNKPPPEGN BVLFLYIDLP	GALPILGGQV INAGSLISTP IVAQVPKCIW MPWALLDOGG	VHTVLSLIGL ITPMLRGDVQ FAISNRFKNR SRWTLOAIRM	SLIALGTGGI CFGEDCYALA SGDIPKRQHW NRNLGFFVLO	KPCVAAPGGD FGVPGLLMVI LDWAAEKYPK PDOMOVLNPP	QFEEKHAEER ALVVFAMGSK QLIMDVKALT LVLIFIPLFD	180 240 300 360
10	LADDEVKVTV	VGNENNSLLI TREDGNSTSS	AVGMILACLA ESIKSFOKTP MMVKDTESKT CRTEDKNFSL GEVMFSVTGL	HYSKLHLKTK THEMTTVRFV	SQDFHFHLKY NTLHKDVNIS	HNLSLYTEHS LSTDTSLNVG	420 480 540 600 660
15	LVVAQFSGLV KLETKKTKL	QHAEFILFSC	LLLVICLIFS	IMGYYYVPVK	TEDMRGPADK	HIPHIQGNMI	720
	Seq ID NO: Nucleic Aci Coding sequ	682 DNA so id Accession sence: 128	ı#: NM_016	077.1			
20	1 I	11	21 CGGAACTTTG	31 -	41 ACCCCCGGAAG	51 AGGTAGCTCA	60
25	CGCGATAGAA ACTGTAGATG CTTGGCTGTT GATGCTCCCC	ACGTGTTCGC CCCTCCAAAT GGAGTTGCTT AAAAGCAAGA AGCGGGGAGT	TTGCCCAGAA CCTTGGTTAT GTGGCATGTG CGAGCAAGAC ACAAGATGAT	GAAGGGAAGG GGAATATTTG CCTGGGCTGG ACACACAGAT TCTTGTGGTT	CGCGAGTGAG GCTCATCCCA AGCCTTCGAG ACTGAAAGTG CGAAATGACT	GAAAGGAGGT GTACACTCGG TATGCTTTGG AAGCAAGCAT TAAAGATGGG	120 180 240 300 360
30	AAGAAGAAAT CAAAGCTCCT	CCTGAAATGC GATGAAGAAA TTAATTCAAG	AGTGCTCTCA TCAAACAATG CCCTGATTGC ATGCTGGACG CAGCAGACCT TGACAACAAC	GGAATACTGT ATTATTGGCC TACTCAGATT	GGCCAGCCCA CATGCAAAAA GCACCAGGCT	TGCTGGGACT CTCAAACTGT	420 480 540 600 660
35	GATTCTAACA	GACTTTGATA ACAAAAGCTG CCATGTTCTA	AATTTCTTCA	CCCTCCATCA	CAAGTGTTTG ATGTTCTTGA	GATGAAAATA	720 · 780
40	Seq ID NO: Protein Acc	cession #: 1	_				
	MPSKSLVMEY	LAHPSTLGLA	21 VGVACGMCLG KVAAQCSHAA	31 WSLRVCFGML VSAVKOTORR	41 PKSKTSKTHT NPRMLKOWEY	51 DTESEASILG CGOPKVVVKA	60 120
45	Sec ID NO:	684 DNA B	SLIQDAGRTQ equence	IAPGSQTVLG	IGPGPADLID	KVTGHLKLY	
	Nucleic Ac:	id Accession	n #: NM_004	1864.1			
50	1	11	21	31	41	51 1	
55	GGCCGAGGCG ATTCCGAGAG CTGGGAAGAT AGTCCGGCTG	TTGCGGAAAC TCGAACACCG	CAGCCATGCC TGGTGCTCTC GTTTCCCGGG GCTACGAGGA ACCTCGTCCC GCCACCTGCA	CCTGCTAACC GGCCCCTGCA CCTGCGTATC	AGGCTGCGGG GTCCGGATAC TCTCGGGCCG	CCAACCAGAG TCACGCCAGA CCCTTCCCGA	60 120 180 240 300 360
60	GGGGCTCCCC AAGGTCGTGG GCCCGCGCTG ATCTTCGTCC	GAGGCCTCCC GACGTGACAC CACCTGCGAC GCACGGCCCC	GCCTTCACCG GACCGCTGCG TGTCGCCGCC AGCTGGAGTT	GCCTCTGTTC GCCTCGCAG GCACTTGCGG CTGTCCGCTC	AGCCTTGCAA TCGGACCAAC CCGCAAGCCG GGGCCCGGGC	GACGCGAGC GACCCCAAGC TGCTGGCAGA CCAGGGGGCG GTTGCTGCCG	420 480 540 600 660
65	TCTGCACACG ACGGGAGGTG CATGCACGCG CTGCTGCGTG	CAAGTGACCA CAGATCAAGA CCCGCCAGCT ACCTATGATG	TGTGCATCGG CGAGCCTGCA ACAATCCCAT ACTTGTTAGC	CCTGGGCTGG CGCGTGCCG CCGCCTGAAG GGTGCTCATT CAAAGACTGC	AGCCACTTGGG AGCCAGTTCG CCCGACACGG CAAAAGACCG CACTGCATAT	GGGCGGCAAA AGCCAGCGCC ACACCGGGGT GAGCAGTCCT	720 780 840 900 960
70	GGGCTCAAGG	TTAATTTATT	GCGCGGGGGA ACCCGATTCC GGGGTGACCT TCTGGTGATA	TGCCCAAACA	TCGGGGGCTG	GTCTGATGGA	1020 1080 1140 1200
75	Seq ID NO: Protein Ac	685 Prote cession #:	in sequence NP_004855.1				
80						51 SRFRBLRKRY PEGLPEASRL AESSSARPQL SPREVQVINC GVSLQTYDDL	60 120 180 240 300
85	LAKDCHCI	686 DNA 8					

Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2

	Coding sequ	ence: 486	351				
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	GAGGCATGAG	TGAGCTACAG AACAAAAAAT	TGGGAACAGG	CTCAGGACTA	TCTCAAGAGA	TTTTATCTCT	180 240
10	ATGACTCAGA	ACCTATAACT	CCAACAGIT	ACTOCCOCCO	CATACAAATA	ATGCAGARGC	300
10	CCACATCTCC	ACCTATARCT	CTTCCACAA	ACTCACTATT	TOCALATACO	CCABABTGGB	360
		GGTCACCTAC					420
	TGGATCGATT	AGTGTCAAAG	GCTTTAAACA	TOTGGGGCAA	AGAGATCCCC	CTGCATTTCA	480
	GGAAAGTTGT	ATGGGGAACT	GCTGACATCA	TGATTGGCTT	TGCGCGAGGA	GCTCATGGGG	540
15	ACTCCTACCC	ATTTGATGGG	CCAGGAAACA	CGCTGGCTCA	TGCCTTTGCG	CCTGGGACAG	600
	GTCTCGGAGG	AGATGCTCAC	TTCGATGAGG	ATGAACGCTG	GACGGATGGT	AGCAGTCTAG	660
	GGATTAACTT	CCTGTATGCT	GCAACTCATG	AACTTGGCCA	TTCTTTGGGT	ATGGGACATT	720
	CCTCTGATCC	TAATGCAGTG	ATGTATCCAA	CCTATGGAAA	TGGAGATCCC	CAAAATTTTA	780
20	AACTTTCCCA	GGATGATATT GAAACTTCAG	AAAGGCATTC	AGAAACTATA	TGGAAAGAGA	AGTAATTCAA	840 900
20	GAAAGAAATA	TCAGAATTGA	GCAGAACATC	CATTCATTCA	CATTEGORA	TGTATATCAT	960
	CTTTTTTTTTT	CAGARTIGA	TTTGBBTGTC	TTTCACTCCT	TTTATTGGTT	AAACTCCTTT	1020
	ATGGTGTGAC	TOTOTOTAT	TCCATCTATG	AGCTTTGTCA	GTGCGCGTAG	ATGTCAATAA	1080
	ATGTTACATA	CACAAATAAA	TAAAATGTTT	ATTCCATGGT	AAATTTA		
25							
		687 Protei cession #: N					
	1	11	21	31	41	51	
30	Ī	ì	1	1	1	1	
		LLPGSLALPL					60
	EMOKFFGLPI	TGMLNSRVIE	IMQKPRCGVP	DVAEYSLPPN	SPKWTSKVVT	YRIVSYTRDL	120
	PHITVDRLVS	Kalninwikei	PLHFRKVVWG	TADIMIGFAR	GAHGDSYPFD	GPGNTLAHAP	180 240
35				AATHELGHSL	GMGHSSDPNA	VMYPTYGNGD	240
33	PONFKTSOND	IKGIQKLYGK	KSNSKKK				
40	Nucleic Ac	688 DNA se ld Accession Lence: 18	n#: NM_005	3221.3			
	1	11	21	31	41	51	
	ī	i	Ī	1	1	1	
	ATGACAGGAG	TGTTTGACAG	AAGGGTCCCC	ACCATCCGAT	CCGGCGACTT	CCAAGCTCCG	60
	TTCCAGACGT	CCGCAGCTAT	GCACCATCCG	TCTCAGGAAT	CGCCAACTTT	GCCCGAGTCT	120
45	TCAGCTACCG	ATTCTGACTA	CTACAGCCCT	ACGGGGGGAG	CCCCGCACGG	CTACTGCTCT	180
	CCTACCTCGG	CTTCCTATGG	CANAGCTCTC	AACCCCTACC	AGTATCAGTA	TCACGGCGTG	240 300
	AACGGCTCCG	CCGGGAGCTA ACGGCGGCGC	CCCAGCCAAA	GCTTATGCCG	ACTATAGCTA	COCHAGCICC	360
	CAACCACCAGT	ACCCCGAGGT	CACANGGE	AATGGCAAAC	CARAGABAGT	TOGTABACCC	420
50	POCACLA LEL	ATTOCAGOT	TCAGCTGGCC	GCATTACAGA	GAAGGTTTCA	GAAGACTCAG	480
-	TACCTOGCCT	TGCCGGAACG	CGCCGAGCTG	GCCGCCTCGC	TGGGATTGAC	ACAAACACAG	540
	GTGAAAATCT	GGTTTCAGAA	CARAGATCC	AAGATCAAGA	AGATCATGAA	AAACGGGGAG	600
	ATGCCCCCGG	AGCACAGTCC	CAGCTCCAGC	GACCCAATGG	CGTGTAACTC	GCCGCAGTCT	660
	CCAGCGGTGT	GGGAGCCCCA	GGGCTCGTCC	CGCTCGCTCA	GCCACCACCC	TCATGCCCAC	720
55		CCAACCAGTC					780
				CTGCCGCCGC	CGGGCTCCTT	ACAGCACCCG	840.
	CTGGCGCTGG	CCTCCGGGAC	ACTCTATTAG				
	a en 110	600 D					
60		689 Protei cession #: 1					
	1	11	21	31	41	51	
	1	1	1	1	1	1	
10	MTGVFDRRVP	SIRSGDFOAP	FOTSAAMKHP	SQESPTLPES	SATDSDYYSP	TGGAPHGYCS	60
65	PTSASYGKAL	NPYQYQYHGV	NGSAGSYPAK	AYADYSYASS	YHQYGGAYNR	VPSATNOPEK	120
	EVTEPEVRMV	NGKPKKVRKP	RTIYSSFQLA	ALQREFORTO	THATPERAEL	MASIGITUTUTU	180 240
	VALWFONKRS	SYLENSASWY	TCALCCINCU	LDDDGGLOHD	LALASCILY	RSLSHHPHAH	240

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein neorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- The method of claim 1, wherein the polynucleotide selectively

 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue 2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
 2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- The method of claim 4, further comprising the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.
- The method of claim 1, wherein the polynucleotide comprises a sequence as shown in Tables 1A-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on 2 a solid surface.
- The method of claim 1, wherein the patient is undergoing a therapeutic
 regimen to treat lung cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having lung 2 cancer.
- 1 13. A method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of:

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3	(i) providing a biological sample from a patient undergoing the therapeutic
4	treatment; and
5	(ii) determining the level of a lung cancer-associated transcript in the
6	biological sample by contacting the biological sample with a polynucleotide that selectively
7	hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8	thereby monitoring the efficacy of the therapy.
1	14. The method of claim 13, further comprising the step of: (iii) comparing
2	the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3	transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4	treatment.
1	15. The method of claim 13, wherein the patient is a human.
1	16. A method of monitoring the efficacy of a therapeutic treatment of lung
2	cancer, the method comprising the steps of:
3	(i) providing a biological sample from a patient undergoing the therapeutic
4	treatment; and
5	(ii) determining the level of a lung cancer-associated antibody in the biological
6	sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7	that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8	Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9	antibody, thereby monitoring the efficacy of the therapy.
1	17. The method of claim 16, further comprising the step of: (iii) comparing
2	the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3	antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4	treatment.
1	18. The method of claim 16, wherein the patient is a human.

A method of monitoring the efficacy of a therapeutic treatment of lung

(i) providing a biological sample from a patient undergoing the therapeutic

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treatment; and

cancer, the method comprising the steps of:

5	(ii) de	termining the level of a lung cancer-associated polypeptide in the			
6	biological sample by contacting the biological sample with an antibody, wherein the antibody				
7	specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to				
8	a sequence at least 80	0% identical to a sequence as shown in Tables 1A-16, thereby			
9	monitoring the effica	cy of the therapy.			
1	20.	The method of claim 19, further comprising the step of: (iii) comparing			
2	the level of the lung	cancer-associated polypeptide to a level of the lung cancer-associated			
3	polypeptide in a biol	ogical sample from the patient prior to, or earlier in, the therapeutic			
4	treatment.				
1	21.	The method of claim 19, wherein the patient is a human.			
1	22.	An isolated nucleic acid molecule consisting of a polynucleotide			
2	sequence as shown i	n Tables 1A-16.			
1	23.	The nucleic acid molecule of claim 22, which is labeled.			
1	24.	The nucleic acid of claim 23, wherein the label is a fluorescent label			
1	25.	An expression vector comprising the nucleic acid of claim 22.			
1	26.	A host cell comprising the expression vector of claim 25.			
1	27.	An isolated polypeptide which is encoded by a nucleic acid molecule			
2	having polynucleotic	de sequence as shown in Tables 1A-16.			
1	28.	An antibody that specifically binds a polypeptide of claim 27.			
1	29.	The antibody of claim 28, further conjugated to an effector component.			
1	30.	The antibody of claim 29, wherein the effector component is a			
2	fluorescent label.				
1	31.	The antibody of claim 29, wherein the effector component is a			
2	radioisotope or a cyl	totoxic chemical.			
1	32.	The antibody of claim 29, which is an antibody fragment.			

WO 02/086443 PCT/US02/12476 33. The antibody of claim 29, which is a humanized antibody 1 34. A method of detecting a lung cancer cell in a biological sample from a 1 patient, the method comprising contacting the biological sample with an antibody of claim 2 3 28. 35. The method of claim 34, wherein the antibody is further conjugated to 1 2 an effector component. 36. The method of claim 35, wherein the effector component is a 1 fluorescent label. 2 A method of detecting antibodies specific to lung cancer in a patient, 37. 1 the method comprising contacting a biological sample from the patient with a polypeptide 2 3 encoded by a nucleic acid comprises a sequence from Tables 1A-16. 1 38. A method for identifying a compound that modulates a lung cancerassociated polypeptide, the method comprising the steps of: 2 (i) contacting the compound with a lung cancer-associated polypeptide, the 3 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 4 80% identical to a sequence as shown in Tables 1A-16; and 5 (ii) determining the functional effect of the compound upon the polypeptide. 6 The method of claim 38, wherein the functional effect is a physical 1 39. 2 effect. The method of claim 38, wherein the functional effect is a chemical 40. 1 2 effect. 1 41. The method of claim 38, wherein the polypeptide is expressed in a 2 eukarvotic host cell or cell membrane.

 The method of claim 38, wherein the functional effect is determined by measuring ligand binding to the polypeptide.

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43. The method of claim 38, wherein the polypeptide is recombinant.

A method of inhibiting proliferation of a lung cancer-associated cell to 1 44 treat lung cancer in a patient, the method comprising the step of administering to the subject a 2 therapeutically effective amount of a compound identified using the method of claim 38. 3 The method of claim 44, wherein the compound is an antibody. 45. 1 The method of claim 45, wherein the patient is a human. 1 46. 47. A drug screening assay comprising the steps of 1 (i) administering a test compound to a mammal having lung cancer or a cell 2 3 isolated therefrom: (ii) comparing the level of gene expression of a polynucleotide that selectively 4 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a 5 treated cell or mammal with the level of gene expression of the polynucleotide in a control 6 cell or mammal, wherein a test compound that modulates the level of expression of the 7 polynucleotide is a candidate for the treatment of lung cancer. 8

- 1 48. The assay of claim 47, wherein the control is a mammal with lung 2 cancer or a cell therefrom that has not been treated with the test compound.
- 1 49. The assay of claim 47, wherein the control is a normal cell or mammal.
- 1 50. A method for treating a mammal having lung cancer comprising administering a compound identified by the assay of claim 47.
- 1 51. A pharmaceutiPcal composition for treating a mammal having lung
 2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
 3 physiologically acceptable excipient.

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Declaration under Rule 4.17:

of inventorship (Rule 4.17(iv)) for US only

Published:

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PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13ter.1(c) and 39)

Applicant's or agent's the reference	IMPORTANT DECL	ARATION	15 AUG 2003				
18501-15-3PC International application No.	International filing date (day/m	anth (vear)	(Earliest) Priority date (day/month/year)				
PCT/US02/12476		,					
PCT/US02/12476 18 April 2002 (18.04.2002) 10 May 2001 (10.05.2001) International Patent Classification (IPC) or both national classification and IPC							
1							
IPC(7): C07H 21/02, 21/04; C12Q 1/68 Applicant	and US Ct.: 435/6, 536/23.1, 23	3.3					
EOS BIOTECHNOLOGY, INC			•				
will be established on the international	This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.						
	ernational application relates to:						
a scientific theories.							
b mathematical theor	les						
c. plant varieties.							
d. animal varieties.							
e. ssential biological and the products of		lants and animals,	, other than microbiological processes				
f. schemes, rules or n	ethods of doing business.						
	g. schemes, rules or methods of performing purely mental acts.						
h. schemes, rules or methods of playing games.							
	1 methods for treatment of the human body by surgery or therapy.						
j methods for treatment of the animal body by surgery or therapy.							
k, diagnostic methods practised on the human or animal body.							
mere presentations of information. computer programs for which this international Searching Authority is not equipped to search prior art.							
iii. [_] computer programs	for which this international Sear	ching Authority is	not equipped to search prior art.				
2. The failure of the following parts of the international application to comply with prescribed requirements prevents a							
meaningful search from being							
the description	the claims	ш	the drawings				
3. The failure of the nucleotide	and/or amino acid sequence listin	g to comply with	the standard provided for in Annex C				
of the Administrative Instructions prevents a meaningful search from being carried out:							
the written form has not been furnished or does not comply with the standard.							
the computer readable form has not been furnished or does not comply with the standard.							
4. Further comments:							
Name and mailing address of the ISA/US	Name and mailing address of the ISA/US Authorized officer						
Mail Stop PCT, Atm: ISA/US							
P.O. Box 1450			PRIMARY EXAMINER				
Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230 Telephone No. 703-308-0196							
Form PCT/ISA/203 (July 1998)							

PATENT COOPERATION TREATY

From the INTERNATIONAL SEARCHING AUTHORITY

To: TOWNSEND AND TOWNSEND AND CREW LLP TWO EMBARCADERO CENTER	PCT NOTIFICATION OF TRANSMITTAL OF THE INTERNATIONAL SEARCH REPORT OR THE DECLARATION			
EIGHTH FLOOR SAN FRANCISCO, CA 94111-3834				
	(PC)	Rule 44.1)		
	Date of Mailing (day/month/year)	15 AUG 2003		
Applicant's or agent's file reference 18501-15-3PC	FOR FURTHER ACTION	See paragraphs 1 and 4 below		
International application No. PCT/US02/12476	International filing date (day/month/year) 18 April 2002 (18,04,2002)			
Applicant EOS BIOTECHNOLOGY, INC	•			
The applicant is hereby notified that the international sea	orb report has been established and i	e transmitted because		
Filing of amendments and statement under Article 19 The applicant is entitled, if he so wishes, to amend the c				
When? The time limit for filing such amendments international search report.	s normally two months from the dat	e of transmittal of the		
Where? Directly to the International Bureau of WIPO, 34, chemin des Colombettes 1231 Geneva 20, Switzerland, Facetmile No.: (41-22) 740.14.35				
For more detailed instructions, see the notes on the accompanying sheet.				
The applicant is hereby notified that no international search report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.				
3. With regard to the protest against payment of (an) addi	tional fee(s) under Rule 40.2, the ap	plicant is notified that:		
the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.				
no decision has been made yet on the protest; the a	plicant will be notified as soon as a	decision is made.		
 Reminders Shortly after 18 months from the priority date, the internstiapplicant wisher to avoid or postpous publication, a notice of w reach the International Bureau as provided in Rules 50 bits preparations for international publications. 	ithdrawal of the international applica	tion, or of the priority claim, must		
Wittin 19 attends from the priority date, but only in suspect of some designated Offices, a demand for international preliminary examination must be filed if the applicant whiches to postpose the entry into the autional place until 30 annuals from the priority date (in some Offices own later); otherwise the applicant must, within 20 months from the priority date, perform the prescribed acts for entry into the national places before these designated Offices;				
In respect of other designated Offices, the time limit of 30 months (or later) will apply even if no demand is filed within 19 months.				
See the Annex to Form PCT/IB/301 and, for details about the a Volume II, National Chapters and the WIPO Internet site.	pplicable time limits, Office by Offi	ice, see the PCT Applicant's Guida,		
Name and mailing address of the ISA/US Mall Sup PCT, Atm: ISA/US Commissioner for Patents	Authorized officer Carle Myers	Bell-Harrisfo		
P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230	Telephone No. 703-30	V I		

(See notes on accompanying sheet)